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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 03:53:49 ; Search time 228 Seconds
(without alignments)
5462.084 Million cell updates/sec

Title: US-09-593-793A-113

Perfect score: 553

Sequence: 1 MVQRLLWSRLRRKRAQLL.....AIYFATQVVFQKSLAKYSA 553

Scoring table:

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Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Word size: 3

Total number of hits satisfying chosen parameters: 3387848

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
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-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-WARN_TIMEOUT=30 -THREADS=60 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DSELP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	553	100.0	1662	24	ABN81324	Human mast cell re
2	553	100.0	2582	24	ABK92217	Prostate cancer-as
3	553	100.0	3320	24	AAS14962	DNA encoding human
4	553	100.0	3410	19	AAV61201	Full length cDNA s
5	553	100.0	3410	19	AAV58586	Prostate tumour sp
6	553	100.0	3410	21	AAW79473	cDNA sequence of h
7	553	100.0	3410	21	AAW63349	Human immunogenic
8	553	100.0	3410	22	AAW63557	Human prostate cDN
9	553	100.0	3410	22	AAW63557	Human prostate tum
10	553	100.0	3410	22	AAH93465	Human prostate-spe
11	553	100.0	3410	22	AAH84779	Human prostate-spe
12	553	100.0	3410	22	AAH02530	Prostate tumour an
13	553	100.0	3410	24	ABL94929	Human L1-12 cDNA s
14	553	100.0	3410	24	ABK29017	Human breast tumou
15	501	90.6	2133	24	ABA91283	Thioredoxin-ubiqui
16	320	57.9	1593	24	ABA91284	Thioredoxin-ubiqui
17	320	57.9	4034	22	AAS64040	Human prostate cDNA
18	320	57.9	4034	22	AAS93868	P53S cDNA splice
19	320	57.9	4034	24	ABL95411	Human P53S splice
20	263	47.6	1203	22	AAS64153	Human /M. tubercul
21	263	47.6	1203	22	AAH93917	Ral2-P501S-E2 cons
22	263	47.6	1203	24	ABL95524	Ral2-P501S-E2 cons
23	263	47.6	3878	22	AAD05230	Human secreted pro
24	263	47.6	4894	22	AAS64038	Human prostate cDNA
25	263	47.6	4894	22	AAH93866	P53S cDNA splice
26	263	47.6	4894	24	ABL95409	Human P53S splice
27	263	47.6	6976	22	AAS64041	Human prostate cDNA
28	263	47.6	6976	22	AAH93869	P53S cDNA splice
29	263	47.6	6976	24	ABL95412	Human P53S splice
30	255	46.1	2133	21	AAC64928	Human prostate-rel
31	255	46.1	2133	22	AAW71555	Prostate gene PS10
32	255	46.1	2152	20	AAV71181	Consensus sequence
33	252	45.6	2124	21	AAC64927	Human prostate-rel
34	252	45.6	2124	20	AAW7601	Prostate gene PS10
35	252	45.6	2143	20	AAV71180	Clone 1711346IH, t
36	235	42.5	2904	22	AAS64039	Human prostate cDNA
37	235	42.5	2904	22	AAH93867	P53S cDNA splice
38	235	42.5	2904	24	ABL95410	Human P53S splice
39	209	37.8	2462	21	AAZ45677	cDNA sequence of a
40	187	33.8	3663	24	ABN81320	Human mast cell re
41	122	22.1	789	19	AAV61144	3' cDNA sequence o
42	122	22.1	789	19	AAV58487	3' fragment of pro
43	122	22.1	789	21	AAW58487	Human immunogenic
44	122	22.1	789	22	AAS63458	Human prostate cDN
45	122	22.1	789	22	AAS10009	Human prostate tum
46	122	22.1	789	22	AAH93366	Human prostate-spe
47	122	22.1	789	22	AAH84680	Human prostate-spe
48	122	22.1	789	22	AAH02431	Prostate tumour an
49	122	22.1	789	24	ABL94830	Human L1-12 3' cDN
50	85	15.4	258	20	AAV71166	PS108 gene-specifi
51	85	15.4	258	21	AAC63191	Human prostate-rel
52	85	15.4	258	22	AAW71167	Prostate gene PS10
53	82	14.8	247	20	AAV71169	PS108 gene-specifi
54	82	14.8	247	21	AAC63194	Human prostate-rel
55	82	14.8	247	22	AAW71168	Prostate gene PS10
56	76	13.7	742	21	AAZ45675	cDNA sequence of a
57	71	12.8	217	20	AAV71167	PS108 gene-specifi
58	71	12.8	217	21	AAC63192	Human prostate-rel
59	71	12.8	217	22	AAW71168	Prostate gene PS10
60	71	12.8	255	20	AAV71168	PS108 gene-specifi
61	71	12.8	255	21	AAC63193	Human prostate-rel
62	71	12.8	255	22	AAW71169	Prostate gene PS10
63	35	6.3	432	22	AAW71170	Human secreted pro
64	34	6.1	231	20	AAW71170	PS108 gene-specifi
65	34	6.1	231	21	AAC63195	Human prostate-rel
66	34	6.1	231	22	AAW71171	Prostate gene PS10
67	34	6.1	510	21	AAZ45681	cDNA sequence of a

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68 32 5..8 828 24 ABK93112 Human prostate spe
69 26 4..7 271 24 ABK93110 Human prostate spe
70 24 4..3 612 24 ABK93111 Human prostate spe
71 20 3..6 60 22 AAS64154 Human prostate cDN
72 20 3..6 60 22 AAS64154 Human prostate cDN
73 20 3..6 60 22 AAS64154 Human prostate cDN
74 18 3..3 435 20 ABL95525 Human P501S epitop
75 12 2..2 57 22 ABL95525 Human secreted pro
76 12 2..2 57 22 ABL95525 Human prostate cDN
77 12 2..2 57 22 ABL95525 Human prostate cDN
78 10 1..8 30 22 ABL95525 Human prostate cDN
79 10 1..8 30 22 ABL95525 Human prostate cDN
80 10 1..8 30 22 ABL95525 Human prostate cDN
81 10 1..8 40 24 ABA91300 Prostate antigen P
82 10 1..8 75 24 ABA91299 Thiorodoxin-ubiqui
83 10 1..8 75 24 ABA91299 Prostate antigen P
84 10 1..8 208 22 ABL20168 Human breast cance
85 10 1..8 308 22 ABL20168 Human breast cance
86 10 1..8 1808 21 AAZ29231 Human cell signall
87 10 1..8 2352 23 ABV22257 Human prostate exp
88 10 1..8 2352 23 ABV22257 Human prostate exp
89 9 1..6 27 22 AAS64156 Human prostate cDN
90 9 1..6 27 22 ABL95527 Human P501S epitop
91 9 1..6 27 22 ABL95527 Human P501S epitop
92 9 1..6 27 24 AAS14966 Human PROST 03 PCR
93 9 1..6 33 22 AAS63908 Human prostate cDN
94 9 1..6 33 22 AAS63908 Human prostate cDN
95 9 1..6 33 22 AAS63908 Human prostate-spe
96 9 1..6 33 22 AAS63908 Human prostate-spe
97 9 1..6 40 22 ABL95279 Human PCR primer A
98 9 1..6 40 22 ABL95279 Human prostate cDN
99 9 1..6 40 22 ABL95279 Human prostate-spe
100 9 1..6 54 24 ABA91298 Human coding sequ
Thiorodoxin-ubiqui
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ALIGNMENTS

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RESULT 1
ABN81324
ID ABN81324 standard; cDNA; 1662 BP.
XX AC ABN81324;
XX DT 30-AUG-2002 (first entry)
XX DE Human mast cell related splice variant gene MC14 SEQ ID NO 12.
XX DE Human; mast cell; MC; antiallergic; antiinflammatory; antiasthmatic;
XX DE vasotrophic; dermatological; allergy; hypersensitivity; rhinitis; asthma;
XX KW gene; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT 1..1662
XX FT /*tag= a
XX FT /product= "MC14 alternatively spliced variant"
XX PN WO200246389-A2.
XX PD 13-JUN-2002.
XX PF 07-DEC-2001; 2001WO-US46180.
XX PR 08-DEC-2000; 2000US-251835P.
XX PR 14-MAR-2001; 2001US-275479P.
XX PR 28-MAR-2001; 2001US-279115P.
XX PR 02-APR-2001; 2001US-280143P.
XX PA (UNIO ) UCB SA.
XX PI Nocka K, Pirozzi G, Einstein R;
XX
```

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DR WPI; 2002-508560/54.
XX P-PSDB; ABB77575.
XX Novel isolated nucleic acids that are differentially expressed in mast
PT cells in patients with allergic hypersensitivity, encoding proteins
PT associated with mast cell regranulation and allergic hypersensitivity
PT
XX Claim 1; Page 115-117; 119pp; English.
XX The invention relates to isolated nucleic acid (ABN81319-ABN81324),
CC corresponding to genes differentially expressed in mast cells following
CC activation or in patients with allergic hypersensitivity disease, (I)
CC that encodes proteins (ABB77569-ABB77575) (II) or a protein fragment of
CC (II) if at least 6 amino acids. (II) is useful for identifying binding
CC partners. (I) or (II) is useful for diagnosing or treating a disease
CC state (e.g. allergic hypersensitivity, seasonal rhinitis, asthma,
CC urticaria or atopic dermatitis or mastocytosis) in a subject which
CC involves determining the level of expression of (I) or (II). A computer
CC system, comprising a database containing information identifying the
CC expression level in a tissue or at least one mast cell of (I), is useful
CC for presenting information to identify the relative expression level of
CC (I). (II) is used as a marker to detect, diagnose or identify an allergic
CC response in a patient. The protein can also serve as a target that
CC modulate gene expression or activity and as an antigen to raise
CC polyclonal or monoclonal antibodies. (II) is useful for identifying
CC agents that modulate expression of the protein or agents, such as
CC agonists or antagonists. The agonists or antagonists are useful for
CC modulating biological activity and function of (II) and thus are useful
CC for alleviating disease conditions such as allergic hypersensitivity,
CC seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis.
XX SQ Sequence 1662 BP; 229 A; 551 C; 511 G; 371 T; 0 other;
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Alignment Scores:

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
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QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGlyIleThrTyValPro 40
DB 61 GTCAACCTGCTAACCTTTGGCGCTGGAGGTGTGTTGGCGCGCAGGCATCACCTATGTGCCG 120
QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
DB 121 CCTCTGCTGTGGAGTGGGGGTAGAGAGAGTTCATGACCATGTGTCTGGGCATTTGGT 180
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
DB 181 CCAGTGTCTGGGCTGTCTGTCTGCTGCTGCTAGGCTCAGCCAGTACCCAGCTGGCTGGA 240
QY 81 ArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
DB 241 CGCTATGGCGCGCGCGCGCTTCATCTGGGCACCTGCTCTGGGCATCTCTGTGAGCCTC 300
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
DB 301 TTTCTCATCCCAAGGCGCGGCTGGCTAGCAGGCTCTGCTGGCGCATCCAGGCCCTC 360
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyValGlyLeuAspPheCysGlyGlnValCysPhe 140
DB 361 GAGCTGGCACTGCTCATCTCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
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Db 421 ACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCGGACCACTGTGCCAGGCC 480
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 481 TACTCTGTCTATGCTTCATGATGATGCTGTGGGGCTGCTGGGCTACCTCTGCTGCTGCC 540
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
Db 541 ATTGACTGGACACCACTAGTCCCTGGCCCCCTACCTGGGACCCAGGAGGAGTGCCTCTT 600
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 601 GGCTCTCTCACCTCATCTCTCTACCTGCTAGCAGCCACACCTGCTGCTGCTGAGGAG 660
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 661 GCAGCCTGGGCCCCACCGGAGCAGAGGGCTGCGGCCCCCTCTCTGCTGCGCCCCAC 720
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 721 TGTGTTCATGCGGGCCGCTTGGCTTCCGGAACCTGGGCGCCCTGCTTCCCGGCTG 780
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 781 CACCAGCTGTGCTGCGCATGCGCCGACCCCTGCGCGGCTCTCTGCTGCTGAGCTGTC 840
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPheValGlyGluGlyLeu 300
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Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 901 TACCAGGGCTGCCAGAGCTGAGCGGCGCAGGAGCCCGGAGACACTATGATGAGGC 960
Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 961 GTTCGATGGCAGCGCTGGGGCTGTCTCTGCACTGCGGCACTCCCTGCTCTCTCTG 1020
Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1021 GTCATGGACCGGCTGGTGAGGATTCGGCACTCGAGCACTATTTGGCCAGTGTGCA 1080
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1081 GCTTTCCTGTGCTGCGGTCGCCACATGCTCTGCCACAGTGTGCCGCTGGTGCAGCT 1140
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1141 TCAGCGCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1200
Qy 401 SerLeuTyrHisArgGluGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1201 TCCCTCTACCCACCGGAGAGCAGGTGTCTCTGCCCAATACCGAGGGGACACTGGAGGT 1260
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1261 GCTACAGTGGAGCAGCCTGTATGACCACTTCTTCCAGGCCCCAAGCCTGGAGCTCCC 1320
Qy 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
Db 1321 TTCCCTTAATGGACAGCTGGGTCTGGAGCAGTGGCTCTCCACCTCCACCCCGGCTC 1380
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1381 TCGGGGGCTCTGCTGCTGATGCTCTCGGTACGTGTGGTGGTGGTGGTGGTGGTGGTGG 1440
Qy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1441 AGGGTGGTTCGGGGCGGGGATGTCGCTGGACCTTCGGCATCCTGGATGCTTCCTG 1500
Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520

Db 1501 CTGTCCAGGTGGCCCCCATCCCTGTTTATGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1560
Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1561 ACTGCTATATGCTGTCTGCCGAGCCCTGGGTCTGGTCCCATTTACTTTCTCTACACAG 1620
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1621 GTAGTATTGTGACAGAGCGACTTGGCCAAATACTCAGCG 1659
RESULT 2
ABK92217
ID ABK92217 standard; DNA; 2582 BP.
XX AC ABK92217;
XX DT 15-AUG-2002 (first entry)
XX Prostate cancer-associated DNA sequence #103.
DE Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW gene therapy; gene; ds.
XX Mammalia.
XX PN WO200230268-A2.
XX PD 18-APR-2002.
XX PF 12-OCT-2001; 2001WO-US32045.
XX PR 13-OCT-2000; 2000US-0687576.
PR 08-DEC-2000; 2000US-0733288.
PR 08-DEC-2000; 2000US-0733742.
PR 24-JAN-2001; 2001US-263957P.
PR 16-MAR-2001; 2001US-276791P.
PR 16-MAR-2001; 2001US-276888P.
PR 06-APR-2001; 2001US-281922P.
PR 24-APR-2001; 2001US-286214P.
PR 30-APR-2001; 2001US-0847046.
PR 04-MAY-2001; 2001US-288589P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX WPI; 2002-471335/50.
XX P-PSDB; ABC61900.
PT Detecting a prostate cancer-associated transcript in a cell in a
PT patient, useful for diagnosing prostate cancer (PC) or screening
PT modulators of PC, by determining if prostate cancer-associated genes
PT are expressed in a prostate tissue
XX
PS Claim 22; Page 386; 436pp; English.
XX
CC The present invention relates to methods of detecting a prostate
CC cancer-associated transcript in a cell from a patient. The method
CC comprises contacting a biological sample from the patient with
CC prostate cancer-associated polynucleotides (designated PC genes) that
CC selectively hybridize to a sequence that is at least 80% identical
CC to them. The prostate cancer-associated polynucleotide sequences
CC are differentially expressed in prostate tumour tissue or in
CC prostate cancer and are derived from the tissues of various
CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
CC The methods of the invention are useful for diagnosing and treating
CC prostate cancer in mammals. The prostate cancer-associated genes are
CC useful for diagnosing or treating prostate cancer, as well as for
CC identifying modulators of prostate cancer or agents that inhibit
CC prostate cancer. The nucleic acid sequences are particularly useful
CC in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences.

XX 01-NOV-2001.
PD
XX
XX 26-APR-2001; 2001WO-US13323.
PF
XX
XX 27-APR-2000; 2000US-200065P.
PR
XX 20-APR-2001; 2001US-0200065.
PR
XX (SCHD) SCHERING AG.
PA
XX
XX Lau T, Lin RJ, Parkes D, Parry G, Schneider DW, Steinbrecher R;
PI Van Heut PT, Wu J;
PI
XX WPI; 2002-041404/05.
DR
XX P-PSDB; AAU10324.
DR
XX Novel PROST 03 polypeptides and polynucleotides useful in research,
PT diagnosis and therapeutic applications, particularly for use in cancer
PT therapeutics -
PT
XX
PS Claim 6; Fig 1; 77pp; English.
XX
XX The invention relates to an isolated PROST 03 polypeptide (I) and to
CC the polynucleotide (II) encoding PROST 03. Fragments of (I) were used
CC to generate antibodies (III) to PROST 03. (III) is useful for selectively
CC destroying a cell expressing (I), and for treating a disease-state
CC associated with expression of PROST 03 in a human patient. (III) is
CC useful for diagnosing metastasis associated with (I), in a subject.
CC (I) is also useful for diagnosing and treating diseases of cell
CC proliferation such as prostate cancers. (I) is also useful for generating
CC antibodies to PROST 03. (III) is useful in detecting the levels of PROST
CC 03 polypeptides in cells and tissues, and in targeting drugs to primary
CC and metastatic tumours. (I) is also useful for stimulating immune
CC response to PROST 03 containing cells. (II) is useful in diagnostic
CC assays for detecting the levels of polynucleotides encoding PROST 03 in
CC cells and tissues. (II) is useful as DNA probes, as targets for antisense
CC and ribozyme therapy, and as templates for the production of antisense
CC polynucleotides. (I) and (II) are useful in research, biological,
CC clinical and therapeutic purposes. The present sequence represents
XX the coding sequence of human PROST 03.
SQ Sequence 3320 BP; 585 A; 1013 C; 944 G; 778 T; 0 other;

Alignment Scores:
Pred. No.: 0 Length: 3320
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-593-793A-113 (1-553) x AAS14962 (1-3320)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db
QY 282 ATGGTCCAGAGGCTGGGTGAGCGCCCTGCTGCGCACCAGAAAGCCAGCTCTTGCTG 341
Db
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db
QY 342 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCCGCAGGCATCACCTATGTGCGG 401
QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db
QY 402 CCTCTGCTGGAAGTGGGGTAGAGGAGAGTTCATGACCATGGCTGGGCATTTGGT 461
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
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QY 462 CCAGTGTGGGCTGTGCTGTCTCCCGCTCTAGGCTCAGCCAGTACCACTGGCGTGA 521
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
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QY 522 CGCTATGGCCGCCGCCGCCCTTTCATCTGGGCACCTGTCTTGGGCATCTCTGCTGAGCCTC 581

QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db
QY 582 TTTCTCATCCCAAGGGCGGCTGGCTAGCAGGGCTGCTGTGCCGGATCCAGGCCCTG 641
Db
QY 121 GluLeuAlaLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db
QY 642 GAGCTGGCACTGCTCATCTGGCGCTGGGGCTGCTGGACTTCTGTGGCAGGTGCTTC 701
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db
QY 702 ACTCCACTGGAGGCCCTGCTCTACCTCTTCCGGGACCCGGACCACTGTGCCAGGCC 761
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db
QY 762 TACTCTGTATGCCTTCATGATCAGTCTGGGGCTGCTGGGCTACCTCTGCTGCC 821
QY 181 IleAspTrpAspTrpSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlnCysLeuPhe 200
Db
QY 822 ATTGACTGGGACACCACTGCTGGCCCTTACCTGGGCACCCAGAGGAGTGCCTCTTT 881
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db
QY 882 GGCCTGCTCACCCTCATCTTCTCCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAG 941
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db
QY 942 GCAGCGCTGGGCCCCACCGAGCCAGCAGAGGGCTGTGGGCCCTCTCTGTGCGCCAC 1001
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db
QY 1002 TGCTGTCCATGCGGGCGCGCTGGCTTTCGGAAACCTGGGGCGCTGCTTCCCGGGTG 1061
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaLeuLeuCys 280
Db
QY 1062 CACCAGCTGTGTCGGCATGCCCGCACCTTGGCCCGGCTCTTGGTGGCTGAGTGTGC 1121
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlyLeu 300
Db
QY 1122 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACAGGATTCGTGGCGAGGGGTG 1181
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGly 320
Db
QY 1182 TACCAGGGCGTGCCAGAGCTGAGCGGGCACCCGAGGGCCCGAGACACTATGATGAAGC 1241
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db
QY 1242 GTTCGGATGGCGAGCCTGGGGCTGTTCTGTCAGTGGCCATCTCCCTGCTCTCTCTG 1301
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db
QY 1302 GTCATGGACCGGCTGGTCGCGGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGCA 1361
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
Db
QY 1362 GCTTTCCCTGTGGCTGGCTGCCACATGCTGTCCACAGTGTGCCGTGGTGCAGACT 1421
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db
QY 1422 TCAGCGCCCTCACCGGTTTACCTTCTCAGCCCTGCGAGATCCTGCCCTACACACTGCC 1481
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db
QY 1482 TCCCTCTACCAACCGGAGACAGGTGTCTTCCCAANTACCGAGGGGACACTGGAGGT 1541
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db
QY 1542 GCTAGCAGTGGAGCAGCCTGATGACCACTTCTTCCCGAGGCCCTTAAGCCTGGAGCTCC 1601
QY 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
Db
QY 1602 TTCCCTAATGACAGCTGGGTGCTGGAGGAGTGGCTTCCCACTCCACCCCGCGCTC 1661
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480

```

1662 TCGGGGCGCTCTCCCTGTGATGTCCTCCGTACGTGTGGTGGGTGAGCCACCGAGGCC 1721
481 AtgValValproGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
1722 AGGGTGGTTCGGCGCGGGCGGCACTCCCTGGACCTCGCCATCTGGATAGTGGCTTCCGTG 1781
501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
1782 CTGTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTGTCCAGTCAGCCAGTCTGTC 1841
521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
1842 ACTGCCTATATGGTGTCTGCGCAGGCGCTGGGTCTGGTGGCCATTACTTTGCTACACAG 1901
541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
1902 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1940

RESULT 4
AAV61201
ID AAV61201 standard; cDNA; 3410 BP.
AC AAV61201;
XX
DT 06-JAN-1999 (first entry)
XX
DE Full length cDNA sequence of prostate tumour clone L1-12.
XX
KW Prostate; cancer; tumour; vaccine; immunogen; clone; ss.
XX
OS Homo sapiens.
XX
PN W09837093-A2.
XX
PD 27-AUG-1998.
XX
PF 25-FEB-1998; 98WO-US03492.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Xu J;
XX
PR WPI; 1998-609886/51.
DR P-PSDB; AAW71869.
XX
PT Polypeptides comprising immunogenic portions of prostate proteins -
PT used in a vaccine for the treatment of prostate cancer
XX
PS Claim 3; Page 79-80; 130pp; English.
XX
CC The present sequence is a new DNA which encodes an immunogenic portion
CC of a prostate tumour protein. The encoded immunogen, or the DNA itself,
CC can be used as a vaccine for the treatment of prostate cancer. The DNA
CC was identified by analysis of a subtracted cDNA library obtained by
CC subtracting a prostate tumour cDNA expression library with a normal
CC tissue cDNA library.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-09-593-793A-113 (1-553) x AAV61201 (1-3410)
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```

1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
284 ATGGTCCACGAGGCTGTGGGTGAGCCGCTGCTGGCGCACCGGAAAGCCAGCTCTTGGCTG 343
21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
344 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTTGGCGCAGGCATCACCTATGTGCCG 403
41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
404 CCTCTGCTCTGGAAAGTGGGGGTAGAGAGAAAGTTTCATGACCATGGTGTGGGCATTTGGT 463
61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTyrArgGly 80
464 CCAGTGTGGGCTGTGTCTGTCCGCTCCTAGGCTAGCCAGTACCACCTGGCGTGGGA 523
81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
524 CGCTATGGCGCGCGCGGCTTTCATCTGGGCACTGCTTGGGCATCTCTGTGAGCCCTC 583
101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
584 TTCTCATCCCAAGGCGCGGCTGGCTAGCAGGCTCTGTGCCCGGATCCAGGCCCTCG 643
121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
644 GAGTGGCACTGCTCATCTGGCGTGGGCTGCTGAGACTTCTGTGCCAGGTGCTCTTC 703
141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
704 ACTCCACTGGAGGCGCTGCTCTGACCTCTTCCGGAGCCCGGACCACCTGTGCCAGGCC 763
161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
764 TACTCTGTCTATGCCCTCATGATCAGTCTTGGGGGCTGCTGGGCTACCTCTGCTGCC 823
181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
824 ATTGACTGGGACACCCAGTCCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTT 883
201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
884 GGCTCTGCTCACCTCATCTTCTACCTGCTAGCAGCCACACTGCTGGTGGGTGAGGAG 943
221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
944 GCAGGCGCTGGGCCCCACCAGGACGAGGAGGCTGTCGGCCCCCTCTCTGTGCCCCAC 1003
241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
1004 TGCTGTCCATGCGGGCGCGCTTGGCTTTCGGGAACCTGGCGGCGCTGCTTCCCGGCTG 1063
261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
1064 CACCACTGTGCTGGCGCATGCCCGCACCTGGCGGCTCTTCGTGGCTGAGCTGTGC 1123
281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGCGGAGGGCTG 1183
301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
1184 TACCAGGCGCTGCCAGAGCTAGCGGGGACCGAGGCCCGGAGACACTATATGATGAGGC 1243
321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
1244 GTTCGGATGGCAGCGCTGGGCTGTTCCTGCAGTGGCCATCTCCCTGGTCTCTCTCTG 1303
341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
1304 GTCATGAGCCGCTGTGCAGCGATTTCGCACTCGAGCACTCTATTTGGCCAGTGGCA 1363
```

Qy	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla	380
Db	1364	GGTTTCCTGCTGGCTGCCGTCACATGCTGTCCACAGTGTGGCTGTGTGACAGCT	1423
Qy	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400
Db	1424	TCAGCGCCCTCACCGGTTTCACCTTCTCAGCCCTGCAGATCTCTCCATACACATGGCC	1483
Qy	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	420
Db	1484	TCCCTCTACACCGGAGACAGGTGTCTCTGCCCAATACCGAGGACACTGGAGGT	1543
Qy	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440
Db	1544	GCTAGCAGTGGAGCAGCCTGATGACCACTTCTCTGCCAGGCCCTTAAGCCTGGAGCTCC	1603
Qy	441	PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu	460
Db	1604	TTCCTTAATGACACGTGGGTGCTGGAGGACGTGGCTCTCCACCTCCACCGCGCTC	1663
Qy	461	CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla	480
Db	1664	TGGGGGCTCTGCTGTGATGTCTCCGTAGCTGTGTGGTGGTGAGCCACCAGGCTC	1723
Qy	481	ArgValValProGlyArgGlyLeuCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500
Db	1724	AGGTGTGTCCGGCGGGGCATCTGCCTGGACCTCGCATCTGGATAGTGCCTTCCTG	1783
Qy	501	LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
Db	1784	CTGTCCCAAGTGGCCCATCTGTTATGGGCTCCATTTGTCCAGCTCAGCCAGTCTGTC	1843
Qy	521	ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	540
Db	1844	ACTGCTATATGGTGTCTGCCGCGAGGCTGGGTCTGGTCGCCATTTACTTTGCTACACAG	1903
Qy	541	ValValPheAspLysSerAspLeuAlaLysTyrSerAla	553
Db	1904	GTAGTATTTGACAGAGGACTTGGCCAAATACTCAGCG	1942
RESULT 5			
AAV58586	standard; cDNA; 3410 BP.		
XX	AC	AAV58586;	
XX	DT	08-DEC-1998 (first entry)	
XX	DE	Prostate tumour specific gene clone Ll-12.	
XX	KW	Prostate tumour specific gene; human; prostate cancer; detection;	
XX	KW	therapy; ss.	
XX	OS	Homo sapiens.	
XX	FH	Location/Qualifiers	
FT	CD5	284..1945	
FT		/*tag= a	
XX	WO9837418-A2.		
XX	27-AUG-1998.		
XX	25-FEB-1998;	98WO-US03690.	
XX	09-FEB-1998;	98US-0904809.	
XX	25-FEB-1997;	97US-0806596.	
XX	01-AUG-1997;	97US-0904809.	
XX	(CORI-) CORIXA CORP.		
XX	Dillon DC, Xu J;		
XX			

DR	WPI; 1998-480805/41.		
XX	P-PSDB; AAW69385.		
XX	Novel human prostate specific tumour protein and fragments - useful		
PT	for detecting and treating prostate cancers		
XX	Claim 1; Page 84-85; 141pp; English.		
XX	This sequence represents a human prostate tumour specific gene, and can		
CC	be used in the method of the invention. The method is for detecting		
CC	prostate cancer comprises contacting a biological sample with an agent		
CC	able to bind an immunogenic portion of a prostate protein (such as		
CC	encoded by this sequence). An antibody which binds to an immunogenic		
CC	portion of the prostate protein, and the method can be used to detect,		
CC	monitor progression of, or treat prostate cancers. The antibody may		
CC	also be conjugated to a therapeutic agent for use in therapy of prostate		
CC	cancers.		
XX			
SQ	Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;		
Alignment Scores:			
Pred. No.:	0	Length:	3410
Score:	553.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	19	Gaps:	0
US-09-593-793A-113 (1-553) x AAV58586 (1-3410)			
Qy	1	MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu	20
Db	284	ATGCTCCAGAGCGCTGGGTGAGCGCTGCTGGCGACCGAAGCCAGCTCTTGCTG	343
Qy	21	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro	40
Db	344	GTCACCTGCTTAACCTTTGGCTGGAGGTGTGTTGGCGCGAGGCATCACCTATGCGG	403
Qy	41	ProLeuLeuGluValGlyValGluLysPheMetThrMetValLeuGlyIleGly	60
Db	404	CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAGTTCATGACCATGGTCTGGGCATTGGT	463
Qy	61	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly	80
Db	464	CCAGTGTGGCGCTGGTGTGTCCTCCCTAGCTCAGCCAGTGCACCTGGCGTGA	523
Qy	81	ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu	100
Db	524	CGCTATGGCGCGCGCGCCCTTCATCTGGGCACTGTCTTGGGCATCCTCTGAGCCTC	583
Qy	101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu	120
Db	584	TTTCTCATCCCAAGGCGCGCTGCTAGCAGGCTGTGTCGCCGATCCCGAGGCCCTG	643
Qy	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe	140
Db	644	GAGCTGGCAGTGTCTCATCTGGCGTGGGCTGTGGACTTCTGTGGCAGAGTGTGCTTC	703
Qy	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160
Db	704	ACTCCACTGGAGGCGCTGCTCTCTGACCTCTCCGGGACCGGACCACTGTGCGCAGGCC	763
Qy	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180
Db	764	TACTCTGTCTATGCTTTCATGATCAGTCTGGGGGCTGCTGGGCTACCTCTGCTGCC	823
Qy	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe	200
Db	824	ATTGACTGGGACACAGTGCCTGCCCTACCTACCTGGGCAACCCAGGAGGAGTGTCTTT	883
Qy	201	GlyLeuLeuThrIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
Db	884	GGCTGTCTCACCTCTCTCTCACCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAG	943

QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
|||||
Db 944 GCAGCGCTGGCGCCACCAGGAGCCAGAGAGGCTGTGGCGCCCTCTCTGTGTGGCGCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
|||||
Db 1004 TGCTGTCCATGCCGGCGCCGCTGTGGCTTTCGGAACCTTGGCGCCCTGCTTCCCGGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
|||||
Db 1064 CACCAGCTGTGTGGCGATGCCCGCACCTTCCCGGGCTTCTGTGGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrThrAspPheValGlyGluGlyLeu 300
|||||
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTCACAGGATTTCTGTGGCGAGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisThrAspGluGly 320
|||||
Db 1184 TACCAGGGGCTGCCAGAGCTGAGCGGGCACCCGAGGGCCGAGACACTATGATGAAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
|||||
Db 1244 GTTCGATGGCAGCGCTGGGGCTGTCTTCAGTGCAGTGCCTATCTCCTGTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValValThrLeuAlaSerValAla 360
|||||
Db 1304 GTCTGGACCGCTGGTCAGCGATTCGCACTCGAGCAGTCTATTGGCCAGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
|||||
Db 1364 GCTTTCCCTGTGGCTGCCAGTGCCTGTCCACAGTGTGGCGTGTGGTGCAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProThrThrLeuAla 400
|||||
Db 1424 TCAGCGCCCTCACCAGGTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
|||||
Db 1484 TCCTCTACCAACCGGAGAGCAGGTGTTCTTCGCCAAATACCGAGGGGACACTGGAGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
|||||
Db 1544 GCTAGCAGTGAGGACAGCTGTATGCCAGCTTCTCTGCCAGGCCCTAAGCCTGGAGCTCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
|||||
Db 1604 TTCCCTAATGGACAGTGGGTGCTGGAGCAGTGGCTCTCCACCTCCACCCCGGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
|||||
Db 1664 TCCGGGGCTCTGCCTGTGTATGCTCCGTACGTGTGGTGGTGAGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
|||||
Db 1724 AGGGTGGTTCCGGCGGGGCACTCTCCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
|||||
Db 1784 CTGTCCCAAGTGGCCCAATCCCTGTTTATGGGCTCATTTGTCAGCTCAGCCAGCTGTGC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
|||||
Db 1844 ACTGCCATATGCTGTGCCCGAGCGCTGGGTCTGGTGCCTATTACTTTGCTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||
Db 1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
RESULT 6
AAC79473
ID AAC79473 standard; cDNA: 3410 BP.
XX

AC AAC79473;
XX 07-FEB-2001 (first entry)
XX
XX cDNA sequence of human breast tumour clone P501S.
XX
KW Human; breast tumour antigen; cytostatic; immunotherapy;
KW breast cancer; vaccine; ss.
XX
OS Homo sapiens.
PN WO200061756-A2.
XX
XX 19-OCT-2000.
XX
XX 10-APR-2000; 2000WO-US09688.
XX
XX 09-APR-1999; 99US-0288950.
XX 02-JUL-1999; 99US-0346327.
XX
XX (CORI-) CORIXA CORP.
PA
PI Reed SG, Xu J, Dillon DC;
XX
DR WPI; 2000-638568/61.
DR P-PSDB; AAB28527.
XX
PT A novel isolated polypeptide comprising an immunogenic portion of a
PT breast cancer protein useful in the detection and treatment of breast
PT cancer -
XX
PS Claim 26; Page 91-92; 95pp; English.
XX
CC The present sequence was isolated from a breast tumour cDNA library. It
CC is provided in a specification relating to compounds for immunotherapy
CC and diagnosis of breast cancer. Breast tumour antigens and the
CC polynucleotides that encode them may be used in the production of a
CC pharmaceutical composition to be used in the treatment of breast cancer.
CC Proliferated T cells and incubated antigen presenting cells are also
CC required. The polypeptides and polynucleotides may also be used to
CC produce a vaccine.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
US-09-593-793a-113 (1-553) x AAC79473 (1-3410)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
|||||
Db 284 ATGGTCCAGAGGCTGTGGGTGAGCCCTGCTGCGCACCGGAAAGCCAGCTCTGTCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTrpValPro 40
|||||
Db 344 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCGCGAGGCATCACCTATGTGCG 403
QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
|||||
Db 404 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAGTTCATGACCATGGTGTGGCATTTGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
|||||
Db 464 CCAGTGTGGGCTGTGTGTCTGCTCCCTAGGCTCCTAGGCTCAGCCAGTGCACCTGGGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
|||||
Db 524 CGCTATAGCCGCCGCCCTTCATCTGCGGCACGTGTCCTTGGGCACGTCTGCTGAGCCTC 583

Qy	101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu	120
Db	584	TTTTCTCATCCAAAGGGCCGCTGGCTAGCAGGGCTGCTTGCCCGGATCCAGGCCCTG	643
Qy	121	GlutLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyValCysPhe	140
Db	644	GAGCTGGCATGCTCATCCCTGGGCGTGGGGCTGCTGGAGCTTCTGTGGCCAGGTGTGCTTC	703
Qy	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160
Db	704	ACTCCACTGGAGGCCCTGCTCTGACCTTCTCCGGGACCGGACCACTGTGCGCAGGCC	763
Qy	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180
Db	764	TACTTCTCTATGCTTTCATGATCACTTGTGGGGCTGCTGGGTACTCTCGCTGCCGCC	823
Qy	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe	200
Db	824	ATTGACTGGGACACCACTAGTGGCCCTGGCCCTACTCTGGGCACCCAGAGGAGTGGCTCTTT	883
Qy	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
Db	884	GGCTGTCTACCCCTCATCTTCCTCACTCGGTAGCAGCCACACTGCTGGTGGCTTGAGGAG	943
Qy	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
Db	944	GCAGCGCTGGGCCCCACCGAGCCAGCAGAAAGGGCTGTGGGCCCTCTCTGCGCCCCAC	1003
Qy	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260
Db	1004	TGCTGTCTCAATGCCGGGCGCGCTTGGCTTTCCGGAACTGGGGCGCCCTGCTTCCCGGGCTG	1063
Qy	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280
Db	1064	CACCAGCTGTGCTGCCGCATGCCGCCACCCCTGGCGCGGGCTCTTGGTGGCTTGAGCTGGCC	1123
Qy	281	SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu	300
Db	1124	AGCTGGATGGCACTCATGACCTTCACGCTGTTTTACAGGATTTCTGGTGGCGAGGGGCTG	1183
Qy	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly	320
Db	1184	TACACGGGCTGCCACAGCTGAGCGGCGGACCGAGGCCCGAGGACACTATGATGAAGGC	1243
Qy	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340
Db	1244	GTTCCGATGGGCAAGCTGGGGCTGTTCCTTCAGTGGGCCATCTCCCTGGCTTCTCTCTGT	1303
Qy	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla	360
Db	1304	GTCATGGACCGGCTGTGTGACGGATTTCGGCACTCTGAGCAGTCTATTGCGCCAGTGTGSCA	1363
Qy	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValIleThrAla	380
Db	1364	GCYTTCCCTGTGCTCCGGTGCCATGCCCTGTCCACAGTGTGGCGTGGTGACAGCT	1423
Qy	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400
Db	1424	TCAGCGCCCTCACCGGGTTCACTTCTCAGCCCTGCAGATCTTCCCTTACACACTGGCC	1483
Qy	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	420
Db	1484	TCCCTCTACCAACCGGAGAAGCGGTGTTCCTGCCCAAAATCCGAGGGGACACTGGAGGT	1543
Qy	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440
Db	1544	GCTAGCAGTGGAGACACGCTGATGACACGCTTCCTGCCAGGCCCTTAAGCCCTGGAGCTCC	1603
Qy	441	PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeu	460
Db	1604	TTCCCTTAATGGACACGTGGGTGCTGGAGCGAGTGGCCCTGCCACCTTCCACCTCCACCGCGCTC	1663

Qy	461	CysGlyAlaSerIlaCysAspValSerValArgValValValGlyVglUpProThrGluaLa	480
Db	1664	TGCGGGGCCCTCGCTCGTGTATGTCCTCCGTACCTGGTGTTGGTGGTGAGCCCCACCGAGGCC	1723
Qy	481	ArgValValProGlyArgGlyrleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500
Db	1724	AGGGTGGTTCGGGGCCGGGCACTGCCCTGGACCCTCGCCCATCTCGATAGTGCCCTTCCTG	1783
Qy	501	LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
Db	1784	CTGTCCCAGGTGGCCCCCATCCCTGTTATTATGGGCTCCATGTCCAGCTCAGCCAGTCTGTC	1843
Qy	521	ThrAlaTyrrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrrPheAlaThrGln	540
Db	1844	ACTGCCATATAGTGTCTGCCGAGGCCCTGGGTCCTGGTCGCATTTACTTTGCTACACAG	1903
Qy	541	ValValPheAspLysSerAspLeuAlaLysTyrrSerAla	553
Db	1904	GTAGATTTCACAGAGCGACTTGGCCAATACTCAGCG	1942
RESULT 7			
AAA06349			
ID	ID AAA06349 standard; cDNA; 3410 BP.		
XX AC	AAA06349;		
XX DT	13-JUN-2000 (first entry)		
XX DE	Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:110.		
KW	Human; prostate cancer; diagnosis; tumour; gene therapy; detection;		
KW	immunogenic; cytostatic; vaccine; ss.		
OS	Homo sapiens.		
PN	WC200004149-A2.		
PD	27-JAN-2000.		
PF	14-JUL-1999; 99WO-US15838.		
PR	14-JUL-1998; 98US-0115453.		
PR	14-JUL-1998; 98US-0116134.		
PR	23-SEP-1998; 98US-0159812.		
PR	23-SEP-1998; 98US-0159822.		
PR	15-JAN-1999; 99US-0232149.		
PR	15-JAN-1999; 99US-0232880.		
PR	09-APR-1999; 99US-0288946.		
PA	(CORI-) CORIXA CORP.		
PI	Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;		
XX	WPI; 2000-171268/15.		
DR	New polypeptide useful for treating and diagnosing prostate cancer		
PT	comprises an immunogenic portion of prostate tumor protein -		
XX PS	Claim 1; Page 135-136; 263pp; English.		
CC CC	The present invention describes isolated polypeptides, comprising an		
CC CC	immunogenic portion of a prostate tumour protein (ptp). The polypeptide		
CC CC	and polynucleotides encoding them have cytotstatic activity and can be		
CC CC	used in vaccines and in gene therapy. The polypeptides and		
CC CC	polynucleotides encoding them, antigen presenting cells which express		
CC CC	the polypeptides, antibodies against the polypeptides and vaccines		
CC CC	comprising them can be used for inhibiting the development of prostate		
CC CC	cancer in a patient. The polypeptides can be used to generate antibody		
CC CC	or anti-idiotypic antibodies for passive immuno therapy. A portion of		
CC CC	the polynucleotides encoding the polypeptides can be used as a probe o		
CC CC	to modulate the expression of the polypeptides. AAA06241 to AAA06691 and		
CC CC	AA82000 to AA82020 represent sequences used in the exemplification o		
CC CC	the present invention.		


```
XX
SQ Sequence 3410 BP: 667 A; 1015 C; 945 G; 782 T; 1 other;
Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
US-09-593-793a-113 (1-553) x AAA06349 (1-3410)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
DB 284 ATGGTCCAGAGCGTGTGGGTGAGCGCGCTGCTGCGGCACCGAAGGCCAGCTTGTGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
DB 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGACGATCACCTTATGTGCCG 403
QY 41 ProLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGly 60
DB 404 CTTCTGCTGCTGGAAGTGGGGGTAGAGGAGAGTTCATACCCATGCTGGGCGATTGCT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
DB 464 CCAGTGTGGGCTGTGTGTGTCGCGCTCCTAGGCTCAGCCAGTGCACCTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
DB 524 CCCTATGGCCGCGCGCGCTTCACTTGGGCACCTGTCTTGGGCATCTGCTGAGCCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
DB 584 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGCGTGTGTGCCGATCCCCAGGCCCTTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
DB 644 GAGCTGGCACCTCTCATCTGGCGCTGGGGCTGTGGACTTCTGTGGCCAGGTGTCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
DB 704 ACTCCACTGGAGCGCTGTCTCTGACCTCTTCCGGGACCCGACCACTGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
DB 764 TACTCTGTCTATGCCCTTCATGATCAAGTCTTGGGGCTGTGGCTGGCTACCTCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
DB 824 ATTGACTGGGACACCACTGCCCTGCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
DB 884 GGGCTGCTCAACCTCATCTTCTCCTACCTGCGTAGGACCCACACTGTGTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
DB 944 GCAGCGCTGGGCCCCACCGAGCCAGCAGAGGGCTGTGGCCCCCTCTCTTGTGGCCCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
DB 1004 TGTCTGTCCATGCGGCGCGCTTGGCTTTCGCGAACCTGGGCGCCTGTCTTCCCGGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
DB 1064 CACCAAGCTGTGTGCGCATGCCCCCGACCCCTGCGCGCGCTCTTCTGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlyLeu 300
DB 1124 ACCTGGATGGCACTCATGACCTTCACGCTGTGTTTACAGGATTTCTGTGGCGAGGGCTG 1183
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```
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
DB 1184 TACCAGGGCGTCCAGAGCTGAGCGGGCACCGAGGCCGAGACACTATGATGAAGCC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
DB 1244 GTTCGGATGGGAGCGCTGGGGCTGTTCCTGCAGTGGCGCATCTCCCTGGTCTTCTCTCG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
DB 1304 GTCATGGACCGGCTGGTGCAGCGATTCCGCACTCGAGCAGTCTATTTGGCCAGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
DB 1364 GCTTTCCCTGTGGCTGCCGGTGCACATGCCTGTCCACAGTGTGGCCGTGGTGACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
DB 1424 TCAGCGCGCCTCAGCGGTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
DB 1484 TCCTCTACCACCGGAGAGCAGGTTCCTGCCCAATACCGAGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
DB 1544 GCTAGCAGTGAAGACAGCCTGATGACCACTTCTCTGCCAGGCCCTAAGCCTGGAGTCCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProProAlaLeu 460
DB 1604 TTCCCTTAATGGACAGTGGGTGCTGGAGCAGTGGCGCTGCTCCACCTCCACCCGCGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
DB 1664 TCGCGGGCTCTGCTGCTGTGATGTCTCCGTACCTGTGGTGGTGGTGGAGCCAGCGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
DB 1724 AGGCTGGTTCCGGCGCGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTCTCG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
DB 1784 CTGTCCCAAGTGGCCCCATCCCTGTTTATGGGCTCCATTTGTCCAGCTCAGCCAGTCTGC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
DB 1844 ACTGCTATATGGTGTCTGCCGAGCGCTGGGTGGTGGCGCCATTTACTTTGCTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 1904 GTAGTATTTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
RESULT 8
AAS63557
ID AAS63557 standard; cDNA; 3410 BP.
XX
AC AAS63557;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA sequence #109.
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN WO2001/73032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
```

PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX (CORI-) CORIXA CORP.
XX
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Ratter MW, Stolk JA, Day CR, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX WPI: 2001-639232/73.
DR P-PSDB; AAU69763.
XX
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
XX Claim 1; Page 267-268; 579pp; English.
XX
XX The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes,
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-593-793A-113 (1-553) x AAS63557 (1-3410)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db ATGGTCCAGAGGCTGTGGGTGAGCGCCCTGCTGGCGCACCGAAGCCAGCTTTGCTG 343

QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyLeuTrpValPro 40
Db GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTGGCGCGCAGGATCACCTATGTGCG 403

QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyLeGly 60
Db CCTCTGCTGCTGGAGTGGGGGTAGAGGAGAAGTTTCATGACCATGGTGGTGGCATTTGT 463

QY 61 ProValLeuLeuValCysValProLeuLeuGlySerAlaSerAlaSerAspHisTrpArgGly 80
Db CCAGTGTGGGCTGTGTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 463

QY 81 ArgTyrGlyArgArgProPheLeuTrpAlaLeuSerLeuGlyLeuLeuLeuSerLeu 100
Db CGCTATGGCGCGCGCGCGCTTCATCTGGGACATGTCTTGGGGATCTGCTGCTGAGCCCTC 583

QY 101 PheLeuLeuProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db TTTTCTCATCCCAAGGGCGGCTGGTGTAGCAGGGCTGCTGTGCTGCTGCTGCTGCTGCTG 643

QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db GAGCTGGCACTGCTCATCTGGCGGTGGGGCTGCTGAGACTTCTGTGGCCAGGTGTCTTC 703

QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db ACTCCACTGGAGGCCCTGCTCTGTGACCTCTTCCGGAGCCGACACCTGTGCCAGGCC 763

QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db TACTCTGTCTATGCTTCATGATCAGCTGTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 823

QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db ATTGACTGGACACAGTCCCTGCGCCCTACCTGGGGACCCAGGAGGTGCTCTTT 883

QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db GGCCTGCTCACCTCATCTTCTCCTACCTGCTAGCAGCCACACTGCTGCTGCTGCTGCTG 943

QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db GCAGCGCTGGGGCCCGCCAGCGAGCGAGGGCTGTGCGGCCCTCTCTTGTGCGCCAC 1003

QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db TCGTGTCCATGCGGGCCCGCTTGGCTTCCGGAACCTGGCGCCCTGCTTCCCGGCTG 1063

QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db CACCACTGTGCTGCGCATGCGCCACCCCTGCGCGGCTCTTCTGCTGCTGCTGCTGCTG 1123

QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTGCTGGCGAGGGCTG 1183

QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db TACCAGGGCTGCCAGAGCTGAGCGGGCCGAGGCGCCGAGACACTATCATGAAGCC 1243

QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db GTTCGGATGGCAGCTGGGGCTGTCTGTCAGTGGCGCATCTCCCTGCTCTCTCTCTG 1303

QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db GTTCATGGACCGCTGGTGGCAGCATTCGCGCACTTCGAGCAGTCTATTTGGCCAGTGTG 1363

QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db GCTTTTCCCTGCTGGCTGGCGTCCCATGCTGCTCCACAGTGTGGCGGTGGTACAGCT 1423

QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db TCAGCGCCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCCTGCGCTACACACTGGCC 1483

QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db TCCCTCTACACCGGGAGAGAGGTGTCTTCTGCGCAATACCGAGGGGACACTGGAGGT 1543

QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProGlyAlaPro 440
Db GCTAGCAGTGGAGCAGCTGATGACCTTCTTCCGAGGGCCCTAAGGCTGGAGCTCC 1603

QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
Db TTCCCTTAATGGACAGTGGGTCTGGAGGCTGGCTGCTCCACCTCCACCCGGCTC 1663

QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db TGCGGGGCTCTGCTGCTGATGCTCTCCGTACGTGTGGTGGTGGTGGTGGTGGTGGTGG 1723

```
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
DB 1724 AGGGTGGTCCCGGGCGGCATCTGCCCTGGACCTCGCCATCTCGATAGTGCTTCCCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
DB 1784 CTGTCCAGGTGGCCCATCTCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
DB 1844 ACTGCCATATAGTGTCTGCCGAGCGCTGGGCTGGTCTGGTCCCATTTACTTGTGTACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTACGCG 1942

RESULT 9
AAS10108
ID AAS10108 standard; cDNA; 3410 BP.
XX
AC AAS10108;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human prostate tumour cDNA L1-12.
XX
KW Human; prostate tumour protein; prostate cancer; ss.
XX
OS Homo sapiens.
XX
PN US6262245-B1.
XX
PD 17-JUL-2001.
XX
PF 25-FEB-1998; 98US-0030607.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC;
XX
DR WPI; 2001-440862/47.
DR P-PSDB; AAU04961.
XX
PT Novel polynucleotide encoding polypeptide comprising a portion of
PT prostate tumour protein useful for inhibiting development of prostate
PT cancer or for treating prostate cancer in a patient
XX
PS Claim 3; Column 118-121; 105pp; English.
XX
CC The sequence is a human prostate tumour cDNA which encodes a
CC partial tumour protein. The DNA is useful for inhibiting the development
CC of prostate cancer or for treating prostate cancer in a patient.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-593-793A-113 (1-553) x AAS10108 (1-3410)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
DB 284 ATGGTCCAGAGGCTGTGGGTAGCCCGCTGTGCGGCACCGGAAAGCCAGCTCTTGGCTG 343
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... QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
DB 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGCTTTTGGCGCGAGGCATCACCTATGTGCCG 403
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
DB 404 CCTCTGCTGCTGGAAGTGGGGGTAGAGAGAGAGTTTACCATGGTGTGGCGCATGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTyrPheGly 80
DB 464 CAGTCTGGCCCTGCTGTGTCTCCGCTCTAGAGGTCTAGCCAGTACCACTGCGCGTGG 523
QY 81 ArgTyrGlyArgArgProPheIleTyrAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
DB 524 CGCTATGGCGCGCGCGCCCTTTCATCTGGGCACCTGCTTGGGCATCTCTGCTGAGCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
DB 584 TTTCATCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCAGCGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
DB 644 GAGCTGGCACTGCTCATCTCTGGCGTGGGCTGCTGGACTTCTGTGCCAGGTGTGCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
DB 704 ACTCCACTGGAGGCCCTGCTCTGACCTTCTCCGGGACCCGAGACCACCTGTCGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
DB 764 TACTCTGTCTATGCCCTTCATGATCAGTCTTGGGGGTGCTTGGGCTACCTCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
DB 824 ATTGACTGGGACACCAAGTGGCCCTGGCCCTCTCTGCGGCACCCAGGAGGAGTCTCTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
DB 884 GGCTGCTCACCCCTCATCTTCTCACCTGCTAGCAGCCACACCTGCTGGTGGTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
DB 944 GCAGCGCTGGGCCCCACCGAGCGAGCAGAGGGGCTGTGGCGCCCTCTTGTGCGCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
DB 1004 TGCTGTCCATGCCGGCGCGCTGGCTTTCGGGAACCTGGCGCCCTGCTTCCCGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
DB 1064 CACCAGCTGTGCTGCCGCATGCCCGCACCTGCGCGGCTCTTCGTGGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlyLeu 300
DB 1124 AGCTGGATGGCATCTCATACCTTTCACGGATTTCTGTGGCGAGGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
DB 1184 TACCAGGGGTGCCAGAGCTGAGCGCGGACGAGCGCGGAGACACTATGATGAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
DB 1244 GTTCGGATGGCAGCGCTGGGCTGTTCCTGCAGTGGCCATCTCCCTGGTCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
DB 1304 GTCATGGACCGGCTGCTGCGAGCATTCGGCACTCGAGCAGTCTATTGGCCAGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
DB 1364 GCTTTCCCTGTGGCTGCCGTGCCACATGCTCTGCCACAGTGTGGCGGTGGTACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnLeuProTyrThrLeuAla 400
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Db 1424 TCAGCGCCCTCACCGGGTTACCTCTCAGCCCTCAGATCCTGCCCTACACACTGGCC 1483
Qy 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCTCTACACCGGGAGAGCAGGTGTTCTTCCGCCCAATACAGGGGACACTGGAGGT 1543
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGAGCACAGCCTGATGACACAGCTTCTTCCAGGCCCTAAGCCTGGAGCTGCC 1603
Qy 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCTTAATGGACACGTGGGTGCTGGAGCAGTGGCTCTCTCCACCTCCACCCGGCTC 1663
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TCGGGGCCCTTCCTCTGATGTCCTCCGTACGTGGTGGTGAGCCACCGAGGCC 1723
Qy 481 ArgValValProGlyArgGlyLeuCysLeuAspLeuAlaLeuAspSerAlaPheLeu 500
Db 1724 AGGTGTTCCTCCGGCGGGGATCTGCTGGACCTGCGCCATCTGGATAGTGCCTTCCTG 1783
Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1843
Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGTTGTCCTCCGAGCCCTGGGTCTGGTGGCCATTACTTTGCTACACAG 1903
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTGACAAGCGGCACTTGGCCAAATACTACGCG 1942
RESULT 10
AAH93465
ID AAH93465 standard; cDNA; 3410 BP.
XX AAH93465;
AC
XX
DT 04-OCT-2001 (first entry)
DE Human prostate-specific full length cDNA sequence L1-12.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX
DR WPI; 2001-425873/45.
XX
XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient
PT for use in vaccines -
XX
PS Claim 1; Page 265-266; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode

CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used to treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;
Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-09-593-793A-113 (1-553) x AAH93465 (1-3410)
Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 284 ATGGTCCAGAGCTGTGGGTGAGCCGCTGCTGGCGCAGCCGGAAGCCAGCTTGTCTG 343
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCGCGCAGGCATCACCTATGTGCG 403
Qy 41 ProLeuLeuGluValGlyValGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAGTTCATGACCATGGTGTGGGCAATTGGT 463
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGGCTGGTCTGTGTCCTGCTTAGGCTCAGCCAGTGACCATGGCGTGA 523
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGCGCGCGCGCCCTTCATCTGGGCACATGCTCTGGGCATCTCTGTGAGCCTC 583
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGGCGGGCTGGCTAGCAGGGCTGCTGTGCCGGATCCCAAGGCCCTG 643
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGACACTGCTCATCTGGGCGTGGGCTGCTGGACATCTCTGTGGCAGGTGCTTC 703
Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGACCATGTGCGCAGGCC 763
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrIleLeuProAla 180
Db 764 TACTCTGTATATGCTTTCATGATCAGTCTTGGGGCTGCTGGGCTACCTCTCTGCTGCC 823
Qy 181 IleAspTTPAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 824 ATTGACTGGGACACCGAGTGGCTTGGCCCCCTTACCTGGGACCCAGGAGAGTGCCTCTTT 883
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GSCCTGCTCACCTTCATCTCTACCTACCTGCGGTAGCAGCCACACTGCTGTGTGGTGGAG 943
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGGCTGGGCCCCACCGAGCCAGCAGAGAGGCTGTGCGGCCCTCTCTTGTGCGCCAC 1003

```
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
DB 1004 TGTGTCCATGCGCGCGCGTGGCTTTCGGAACCTGGCGCCCTGCTGCCCGCGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgPheValAlaGluLeuCys 280
DB 1064 CACCAGCTGTGTGCGCGATGCCCGCACCCCTGCGCGCGCTCTTGTGGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPheValGlyGluGlyLeu 300
DB 1124 AGCTGGATGGCACTCATGACCTTCAGCGTGTGTTTACACGGATTTCGTGGCGAGGGCGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
DB 1184 TACCAGGCGCTGCCAGAGCTGAGCGCGGCACCGAGCGCGGAGACACTATGATGAAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
DB 1244 GTTCGGATGGGAGCGCTGGGGCTGTTCCTGCAGTGGCCATCTCCCTGCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
DB 1304 GTCATGACCGCGCTGTGTCAGCGATTCGGCACTCGAGCAGTCTATTGGCCAGTGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
DB 1364 GCTTTCCTGTGCTGCCGTGCCATGCTGCTCCACAGTGTGCCGTGGTGACAGCT 1423
QY 381 SerAlaAlaLeuThrClyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
DB 1424 TCAGCGCGCTCACC GGTTCCACTTCTCAGCGCTGCAGATCTGCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
DB 1484 TCCTCTACACCGGAGAGAGAGGTGTTCTCGCCCAATACGAGGAGGACACTGGAGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
DB 1544 GCTAGCAGTGAGACAGCTGATGACCACTTCTGCCAGGCGCTAAGCCTGGAGCTCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
DB 1604 TTTCCCTTAATGGACACGTGGGTGCTGGAGCAGTGGCGCTGCTCCACCTCCCGCGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
DB 1664 TCGGGGGCTCTGCTGTGATGTCCTCGGTGCTGGTGGTGGTGGAGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
DB 1724 AGGGTGTTCGGCGCGGGGCATCTGCCCTGGACCTCGCCATCTGGATAGTGCCTCCCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
DB 1784 CTGTCCAGGTGGCCCAATCCCTGTTTATGGCTCCATTTGTCAGCTCAGCCAGCTGTGC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
DB 1844 ACTGCTATATGTTGTCGCCGAGCGGCTGGGTCTGGTCCCATTTACTTCTTCACAGAC 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
RESULT 11
AAH84779
ID AAH84779 standard; cDNA; 3410 BP.
AC AAH84779;
XX
XX
DT 25-SEP-2001 (first entry)
XX
```

Human prostate-specific cDNA sequence L1-12/P501S.

Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
chromosome 22q11.2; prostate-specific protein; chromosome 1;
prostate specific antigen; PSA; ss.

Homo sapiens.

WO200134802-A2.

17-MAY-2001.

09-NOV-2000; 2000WO-US30904.

12-NOV-1999; 99US-0439313.

18-NOV-1999; 99US-0443686.

(CORI-) CORIXA CORP.

Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;

WPI; 2001-308785/32.

Isolated polypeptide comprising at least an immunogenic portion of a
prostate-specific protein, useful in the diagnosis and therapy of
prostate cancer -

Claim 5; Page 164-165; 325pp; English.

The present invention describes an isolated polypeptide (P1) comprising
at least an immunogenic portion of a prostate-specific protein, or its
variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
(N1) have cytostatic activity and can be used in vaccine production.
The polypeptides, nucleic acids and antibodies from the present
invention are useful in the diagnosis and therapy of prostate cancer.
Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
region. Prostate specific antigen (PSA) P501S was located on
chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
polynucleotide and polypeptide sequences used in the exemplification
of the present invention.

Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:

Pred. No.:	0	Length:	3410
Score:	553.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-593-793A-113 (1-553) x AAH84779 (1-3410)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20

DB 284 ATGGTCCAGAGCGCTGGGTGAGCGCCTGCTGCGGCACCGGAAAGCCAGCTCTTGGCTG 343

QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40

DB 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCCGAGGCATCATGTGCGCG 403

QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60

DB 404 CCTGCTGCTGGAAGTGGGGGTAGAGAGAAAGTTCTATGACCATGCTGCTGGCATTTGT 463

QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80

DB 464 CCAGTGTGGGCTGTGCTGTCTGCCGCTCCCTAGGCTCAGCCAGTCACCCAGTGGCGTGA 523

QY 81 ArgTyrGlyArgArgProPheIleThrAlaLeuSerLeuGlyIleLeuLeuSerLeu 100

DB 1000

Qy	461	CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla	480
Db	1664	TGCGGGGCCCTCTGCCCTGTATGCTCCGTACGTGTGGTGGGTGGAGCCACCCAGAGGCC	1723
Qy	481	ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500
Db	1724	AGGTTGGTTCCGGCGGGGGGCATCTGCCCTGGACCTCGGCATCCCTGGATAGTGCCTTCCCTG	1783
Qy	501	LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
Db	1784	CTGTCCCAGGTGGCGCCATCCCTGTTTATGGGCTCCATTTGTCCAGCTCAGCCAGCTCTGTC	1843
Qy	521	ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	540
Db	1844	ACTGCCATATATGGTGTCTCCCGCAGGCCCTGGGTCTGGTCGCCATTTTACTTTTGCTACACAG	1903
Qy	541	ValValPheAspLysSerAspLeuAlaLysTyrSerAla	553
Db	1904	GTACTATTTCACAAAGCGACCTTGGCCAAATACTCAGCG	1942

RESULT 12

AAH02530.
ID AAH02530 standard; cDNA; 3410 BP.
XX
AC AAH02530;
XX
DT 14-JUN-2001 (first entry)
XX
DE Prostate tumour antigen determined full length cDNA sequence for LI-12
XX
XX Human; prostate tumour antigen; prostatic tumour; therapy; diagnosis;
KW prostate cancer; immunogenic; cytostatic; vaccine; ss.
KW

Prostate tumour antigen determined full length cDNA sequence for L1-12

05 Homo sapiens.

PN W0200125272-A2.

12-APR-2001.

XX
PF 04-OCT-2000: 2000W0-IIS27464XX
04-007-1999. 991157155XX
D
CORT -
CORTVA
CORPXX
PI Xu J, Skeiky YAW, Reed SG, Cheever MA;XX
DR
WPT: 2001-245062/25XX
DR P-PSDB; AAB/4800.

prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer -

PS Claim 4: page 155-156: 276pp: English:

The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or its variant. (I) have cytostatic activity and can be used in vaccine production. (I), prostate tumour antigen polynucleotides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the development of cancer in a patient. Antibodies specific for prostate specific proteins and oligonucleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression the progression of a cancer, especially prostate cancer. AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences used in the exemplification of the present invention.

XX
SQ
Sequence 3410 BP: 667 A: 1014 C: 945 G: 783 T: 1 other:

Alignment Scores:

Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-593-793a-113 (1-553) x AAH02530 (1-3410)

```
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
|||||
DB 284 ATGGTCCAGAGGCTGTGGGTGAGCCCTGCTGCGGCACCGGAAAGCCAGCTCTGTGCG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||||
DB 344 GTCAACCTCTTAACCTTTGGCTGGAGGTGTGTTGGCGCGCAGGCATCACCTATGTGCGG 403
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
|||||
DB 404 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGGTGTGCGGCATTTGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
|||||
DB 464 CCAGTGTGGGCTGTGTGTGCTCCGCTCCTTAGGCTCAGCCAGTGCACCTGGCGGTGGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
|||||
DB 524 CGCTATGGCGCGCGCGCCCTTCATCTGGGCACATGTCTCTGGGCATCCTGTGTGAGCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
|||||
DB 584 TTTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCACAGGCCCTTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
|||||
DB 644 GAGCTGGCACTGCTCATCTGGCGGTGGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
|||||
DB 704 ACTCCACTGGAGGCCCTGCTCTGACCTCTTCGCGGACCCGAGCACCTGTGCGCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
|||||
DB 764 TACTCTGTCTATGCTTTCATGATCATGCTTGTGGGGCTGCTGGGCTAGCTCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
|||||
DB 824 ATTGACTGGGACACCACTGCTTGGCCCCCTACCTGGGACCCAGGAGGAGTGCCTCTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGly 220
|||||
DB 884 GGCCTGCTCACCTCTTCTCCTACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
|||||
DB 944 GCAGGCGTGGGCCCCACCGAGCCAGCAGAGGGCTGTGCGGCCCTCTCTTGTGCGCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
|||||
DB 1004 TGCTGTCCATGCGGGCGCGCTTGGCTTTCGGGAACCTGGGCGCCCTGCTTCCCGCGGTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
|||||
DB 1064 CACCAAGTGTGTGCGCGATGCCCGCACCTGCGCGCGCTCTTCTGGCTGAGCTGTGCG 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
|||||
DB 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTTTACACGAGATTTCTGTGGCGAGGGGTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTrpAspGluGly 320
|||||
DB 1184 TACCAGGGCGTCCCCAGAGCTAGCGCGGCACCCGAGGGCCCCGAGACACTATGATGAAGGC 1243
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QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
|||||
DB 1244 GTTCGATGGCAGCGCTGGGGCTGTTCCTGCAGTGCAGCCATCTCCCTGGTCTTCTCTCG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
|||||
DB 1304 GTCATGGACCGGCTGTGTCAGCATTCGGCAGTTCGAGCAGTCTATTGGCCAGTGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
|||||
DB 1364 GCTTTCCTGCTGGCTGCGCGTGCACATGCCCTGTCCACAGTGTGGCGTGGTGCAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
|||||
DB 1424 TCAGCGCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
|||||
DB 1484 TCCTCTTACCACCGGAGAGCAGGTGTTCCTGCCCAATACCGAGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
|||||
DB 1544 GCTACAGTACAGACAGCCTGATGACAGCTTCTGCCAGGCCCTAAGCCTGGAGCTGCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProProAlaLeu 460
|||||
DB 1604 TTCCCTAATGGACACGTGGTGTCTGGAGCAGTGGCTGTCTCCACCTCCACCCGCGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
|||||
DB 1664 TCGCGGGCTCTGCTGCTGTGATGCTCCGTACGTGTGGTGGTGGTGGAGCCACCGAGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
|||||
DB 1724 AGGGTGGTTCGGGGCGGGGCATCTGCCTGGACCTGCGCATCTCGATAGTGCCTCTCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
|||||
DB 1784 CTGTCCAGGTGGCCCATCCCTGTTTATGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
|||||
DB 1844 ACTGCTATATGGTGTCTGCCAGCGCTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||
DB 1904 GTAGTATTGTACAGAGGCACTTGGCCAAATACTCAGCG 1942
RESULT 13
ABL94929
ID ABL94929 standard; cDNA; 3410 BP.
XX
AC ABL94929;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human L1-12 cDNA sequence SEQ ID NO 110.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US200202248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
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PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0289946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
(XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
XU J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
WPI; 2002-255649/30.
XX
New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer -
XX
Claim 1; SEQ ID NO 110; 87pp; English.
XX
The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-593-793A-113 (1-553) x ABL94929 (1-3410)
QY 1 MetValGlnArgLeuTyrValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
DB 284 ATGGTCCAGAGCGTGTGGGTGAGCCCTGCTGGCGGACCGGAAAGCCAGCTCTTGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
DB 344 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTCTTTGGCGCGCAGGCATCACCTATGTGCCG 403

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QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
DB 404 CCTCTGCTGCTGGAAGTGGGGGTAGAGAAAGTTCAATACCATTGCTGGCGATGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
DB 464 CCAGTGTGGGCTGTGCTGTCTCCCGCTCTAGCTAGCTAGCCAGTCACCACTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
DB 524 CGCTATGGCGCGCGCGGCTTCTATCTGGGCATCTGCTGGGCATCTGCTGAGCCTC 583
QY 101 PheLeuIleProArgAlaGlyTyrLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
DB 584 TTTCTCATCCCAAGGCGGCTGGCTAGCAGGGCTGTGTGCCCGGATCCAGGCCCTCG 543
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
DB 644 GAGCTGGCAGCTGCTCATCTGGGCGTGGGGCTGCTGGAGACTTCTGTGGCCAGGTGCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
DB 704 ACTCCACTGGAGGCGCTGCTCTGACCTCTTCCGGGACCCGGACACTGTGCGCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
DB 764 TACTCTGTCTATGCTTCTATGATCAGTCTTGGGGCTGCTGGGCTACCTCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
DB 824 ATTGACTGGGACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 883
QY 201 GlyLeuLeuThrIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
DB 884 GGCCTGCTCACCTCTCATCTTCTCCTGCTAGCAGCCACACTGCTGCTGCTGCTGCTG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
DB 944 GCAGCGCTGGGCGCCACCGAGCCACGAGAGGGCTGTGCGGCCCTCTCTTGTGCGCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
DB 1004 TGCTGTCCATGCGGCGCGCTTGGCTTTCGGAACCTGGGCGCTGCTTCCCGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
DB 1064 CACCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
DB 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACAGGATTCGTGGCGGAGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
DB 1184 TACCAGGGCGTGCCAGAGCTGAGCGGCGCACCGAGGCCGAGGACACTATGATGAAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
DB 1244 GTTCGGATGGGCGAGCTGGGGCTGTTCCTGTCAGTGGCGCATCTCCCTGCTTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
DB 1304 GTCATGGACCGGCTGTGTCAGCGCATTCGGCACTCAGGAGCTATTTTGGCCAGCTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
DB 1364 GCTTTCCCTGTGGCTGCCGTCACATGCTGTCACAGGTGCGCGTGTGTGACAGCT 1423
QY 381 SerAlaLeuLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
DB 1424 TCAGCGCGCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1483

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QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCTCTTACACCGGAGAGAGGTGTTCTCCCAATACCGAGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGCAGACAGCTGATGACACGCTTCTGCCAGGCCCTAAGCCTGGAGCTCCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCTGCTCCACACTCCACCGCGCTC 1663
QY 461 CysGlyAlaSerAlaCysaspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TGGGGGGCTCTCCCTGCTGATGCTCCGTACGTGTGTGGTGGTGGAGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGTGGTTCGGGGCGGGGCATCTGCTGGACCTCGCCATCTGGATAGTGCCTTCCCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCCTATATGTGCTGCCGAGGCTGGGTCTGGTGCCTATTTACTTTGCTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTTGACAAGACCGACTTGGCCAAATACTACGCG 1942
RESULT 14
ID ABK29017
XX ABK29017 standard; cDNA; 3410 BP.
AC ABK29017;
XX
DT 23-APR-2002 (first entry)
XX
DE Human breast tumour polypeptide full length cDNA clone #3.
XX
XX Human; breast tumour polypeptide; gene; ss; breast cancer; cytostatic;
KW immunostimulant.
XX
OS Homo sapiens.
XX
PN W0200198339-A2.
XX
PD 27-DEC-2001.
XX
XX 12-JUN-2001; 2001WO-US19032.
PF
XX
PR 22-JUN-2000; 2000US-0602877.
PR 12-OCT-2000; 2000US-0687507.
PR 06-FEB-2001; 2001US-0778381.
XX
XX (CORI-) CORIXA CORP.
XX
XX Reed SG, Xu J, Dillon DC, Retter MW, Harlocker SL;
PI WPI; 2002-147792/19.
XX
DR Polynucleotides encoding breast tumour polypeptides, useful for treating
XX breast cancer or stimulating an immune response -
PT
XX
XX Claim 1; Page 143-144; 150pp; English.
PS
XX
XX The invention relates to polynucleotides encoding breast tumour
CC polypeptides. The sequences are useful for treating cancer; preferably
CC breast cancer, in a patient or for stimulating an immune response. The
CC polynucleotides and polypeptides are also useful in the diagnosis and
CC monitoring of breast cancer. A method for detecting the presence of a

CC cancer in a patient, comprises obtaining a biological sample from the
CC patient, contacting the biological sample with a binding agent that binds
CC to a breast tumour polypeptide, detecting in the sample an amount of
CC polypeptide that binds to the binding agent, and comparing the amount of
CC polypeptide to a predetermined cut-off value, and therefore determining the
CC presence of a cancer in the patient. Sequences ABK28920-ABK29025
CC represent cDNA clones encoding human breast tumour polypeptides of the
CC invention.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;
Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
US-09-593-793A-113 (1-553) x ABK29017 (1-3410)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 284 ATGGTCCAGAGGCTGGGTGAGCCGCTGCTGGGCACCGGAAACCCAGCTCTTGGCTG 343
... QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCCGAGGCATCATGTATGTGCCG 403
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGGTAGAGAGAAATTTCATGACCATGTTGTGGGCATTTGTT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTyrPheArgGly 80
Db 464 CCAGTGTGGGCTGTGTGTGTCGCGCTCTAGGCTCAGCCAGTACCCACTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCGGCTTCATCTGGGCATCTGCTTGGGCATCTGCTGAGCCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGCGCGGCTGGCTAGCAGGGCTCTGTGCCCGCATCCAGGCCCTTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTGGCGTGGGCTGTGGACTTCTGTGCCAGGTGTGCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCCCTGCTCTGACCTTCTCCGGGACCCGGAGCCACTGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTCTATGCCCTTCATGATCAGTCTTGGGGGTGCTGGGCTACCTCTGCCCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 824 ATTGACTGGACACCACTGCTGCTGCGCCCTACCTGGGCACCCAGGAGGAGTGCCTCTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGCCTGCTCACCTCATCTTCTCACCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGCGCTGGGGCCCCACCGAGCGAGAGGGGCTGTCGGCCCCCTCTCTGTGTCGCCCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATGCGGGCGCGCTTGGCTTTCCGGAACCTGGCGGCCCTGTCTCCCGGCTG 1063

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Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGTCGCCGATGCCGCCACCCCTGCCGCGCTCTTCGTGCTGAGCTGTGC 1123
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrArgPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTTCGTGGCGAGGGGTG 1183
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCGTCCAGAGCTGAGCGGCGCCAGGCGCCGAGACACTATGATGAAGGC 1243
Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGGCAGCTGGGGCTGTCTCTGAGTGCAGTCCTCCTGCTCTCTCTCTG 1303
Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCAATGGACCGGCTGGTCAGCGATTCGGCACTCGAGCAGTCTATTGGCCAGTGTGCA 1363
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCCTGTGGCTGCCGGTGCACATGCCGTGCCACAGTGTGGCGTGGTGACACT 1423
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCCTCACCGGTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1483
Qy 401 SerLeuTyrHisArgGluGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCCTCTACCCAGCGGGAAGCAGGTGTCTGTGCCAAATACCGAGGGGACACTGGAGGT 1543
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTAGGACAGCCTGATGACAGCTTCTGCCAGCCCTTAAGCCTGGAGCTCCC 1603
Qy 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCCTAATGGACAGCTGGGTGCTGGAGGCAGTGGCTTCCCACTCCACCCCGCTC 1663
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TGCGGGGCTTGGCTGTGATGTCCTCCAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1723
Qy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGTGTGTCCGGCGCGGGGCGCATCTGCCTGGACCTCGCCATCTCGGATAGTTCCTG 1783
Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCCAAGGTGGCCCATCCCTGTTTATGGCTCCATTGTCAGCTCAGCCAGTCTGTC 1843
Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGTGTCTGCCGCGAGCGCTGGGTCTGTGGTCCCATTTACTTTGCTACAG 1903
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTGACAGAGCGACTTGGCCAAATACTCAGCG 1942

RESULT 15
ID ABA91283
XX ABA91283 standard; DNA; 2133 BP.
XX AC ABA91283;
XX DT 08-APR-2002 (first entry)
XX DE Thioredoxin-ubiquitin-P501S(aa55-553)His triple gene fusion.
XX KW Thioredoxin; trxA; ubiquitin; P501S; tumour; prostate; antigen;
XX KW cancer; vaccine; therapy; human; gene; ds.
XX
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OS Chimeric - Homo sapiens.
OS Chimeric - Escherichia coli.
XX
PN WO200200892-Al.
XX
PD 03-JAN-2002.
XX
PF 19-JUN-2001; 2001WO-EP06952.
XX
PR 26-JUN-2000; 2000GB-0015619.
PR 30-OCT-2000; 2000GB-0026484.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
PI Cabezon Silva TEV, Delisse AEF;
XX
XX WPI; 2002-147888/19.
DR P-PSDB; AAM50661.
XX
XX Novel DNA sequence encoding triple fusion protein comprising ubiquitin
fused between thioredoxin and polypeptide of interest, useful for
producing recombinant polypeptide of interest suitable for medicinal
use
XX
XX Example 5; Fig 9a; 87pp; English.
XX
XX The present sequence is that of a triple gene fusion comprising,
from the 5' end, the trxA thioredoxin gene from Escherichia coli,
the human ubiquitin coding sequence, the prostate antigen P501S,
(amino acids 55-553) coding sequence, and DNA encoding a histidine
tail. The triple fusion was constructed in plasmid pRIT5063,
which included the Saccharomyces cerevisiae CUP1 promoter and
yeast alpha prepro signal sequence. The triple fusion protein
(see AAM50661) was produced in E. coli G1724 transformants. This
is an example of the production of triple fusion proteins of the
invention comprising ubiquitin fused between thioredoxin and a
protein of interest, in this case P501S(aa55-553). A claimed method
of producing a recombinant protein of interest involves: culturing
a host cell (preferably E. coli) under conditions which allow
for co-expression of the triple fusion and a ubiquitin-specific
endoprotease (especially UBPI from Saccharomyces cerevisiae);
and recovering the recombinant protein directly from the bacterial
cells after it has been subjected to the action of the
ubiquitin-specific endoprotease in vivo. In the present case,
a p501-like protein of 509 amino acids is generated. The
recombinant protein can used as a vaccine for cancer therapy.
XX
SQ Sequence 2133 BP; 384 A; 656 C; 614 G; 479 T; 0 other;

Alignment Scores:
Pred No.: 0 Length: 2133
Score: 501.00 Matches: 501
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 90.60% Indels: 0
DB: 24 Gaps: 0

US-09-593-793A-113 (1-553) x ABA91283 (1-2133)
Qy 53 MetThrMetValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGly 72
Db 604 ATGACCATGGTGTGGGCATTTGGTCCAGTGTGGGCCCTGTGTGTCCCGCTCCTAGCG 663
Qy 73 SerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAlaLeu 92
Db 664 TCAGCCAGTGACCATGGCGTGGACGCTATGGCCGCCCGCCCTTCATCTGGGCACTG 723
Qy 93 SerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeu 112
Db 724 TCCTTGGGCATCTGCTGAGCCTCTTTCTCATCCAAAGCGCGGCTGGCTAGCAGGGCTG 783
Qy 113 LeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeu 132
```

Db 784 CTGTGCCCCGGATCCACAGGCCCTGGAGCTGGCACTGCTCATCTGGCGCTGGGGCTGCTG 843
Qy 133 AspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArg 152
Db 844 GACTTCTGTGGCCAGGTGCTTCACTCCACTGGAGGCCCTGCTCTGTGACCTCTTCCGG 903
Qy 153 AspProAspHisCysArgGlnAlaThrSerValTyrAlaPheMetIleSerLeuGlyGly 172
Db 904 GACCCGGACCACTGTGCGCAGGCCCTACTCTGTCTATGCGCTTATGATCAGTCTTGGGGC 963
Qy 173 CysLeuGlyTyrIleuLeuProAlaIleAspThrProAlaLeuAlaProTyrLeu 192
Db 964 TGCTGGGCTACTCTGCTGCCATGACTGGGACACAGTGCCTGGCCGCCCTACCTG 1023
Qy 193 GlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAla 212
Db 1024 GGCACCCAGAGAGTGCCTCTTGGCGTGTCCACCTCATCTTCTCACCTGGGTAGCA 1083
Qy 213 AlaThrLeuLeuValAlaGluGluAlaLeuLeuGlyProThrGluProAlaGluGlyLeu 232
Db 1084 GCCACACTGCTGCTGGCTGAGGAGCGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTG 1143
Qy 233 SerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsn 252
Db 1144 TCGGCCCCCTCTCTGTGGCCCCACTGCTGTCCATGCGGGGCGCGCTTGGCTTTCCGGAA 1203
Qy 253 LeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArg 272
Db 1204 CTGGGGGCCCTGCTCCCGGGCTGCACCAAGCTGTGCTGCCGATGCCCGCACCTGCGC 1263
Qy 273 ArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyr 292
Db 1264 CGGCTCTTCTGCTGCTGAGCTGTCAGCTGTCAGTGGCACTCATGACCTTCACGCTGTTTAC 1323
Qy 293 ThrAspPheValGlyGluCysLeuThrGlnGlyValProArgAlaGluProGlyThrGlu 312
Db 1324 ACGGATTTCTGGGGAGGGGCTGTACAGGGCGGTGCCAGAGCTGAGCGGGCACCGAG 1383
Qy 313 AlaArgArgHisTyrAspGluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCys 332
Db 1384 GCCCGAGACACTATGATGAAGCGGTTCGGATGGCAGCGCTGGGGCTGTCTCTGCAAGTGC 1443
Qy 333 AlaIleSerLeuValIlePheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArg 352
Db 1444 GCCATCTCCCTGCTCTCTCTGCTGTCATGGACCGCGTGGTCAGCGATTCCGCACCTCGA 1503
Qy 353 AlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSer 372
Db 1504 GCAGTCTATTTGGCCAGTGTGGCAGCTTTCCTGTGGCTGCCGGTGCACATGCTGCTGCC 1563
Qy 373 HisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeu 392
Db 1564 CACAGTGTGGCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTTCACTTCTCAGCCCTG 1623
Qy 393 GlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluGlyGlnValPheLeuPro 412
Db 1624 CAGATCTCCCTACACACTGGCTCCCTCTACCAACCGGGAGCAGCGTGTCTCTGCGCC 1683
Qy 413 LysTyrArgGlyAspThrClyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeu 432
Db 1684 AAATACCGAGGGGACACTGGAGGTGCTAGCAGTAGGACAGCCTGATGACCAAGCTTCTCTG 1743
Qy 433 ProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGly 452
Db 1744 CCAGGCCCTAAGCTTGGAGCTCCCTTCCCTAATGGACAGCTGGGTGCTGGAGCAGTGGC 1803
Qy 453 LeuLeuProProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgVal 472
Db 1804 CTGCTCCCACTCCACCGCGCTCTGCGGGGCTCTGCTGTGTGATGCTCTCCCTACGCTGTG 1863
Qy 473 ValValGlyGluProThrClyAlaArgValValProGlyArgGlyIleCysLeuAspLeu 492
Db 1864 GTGGTGGGTGAGCCACCGAGGCCAGGGTGGTTCGGGGCGGGGCATGCTGCTGGACCTC 1923

Qy 493 AlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySer 512
Db 1924 GCCATCTGGATAGTGCCTTCTGCTGCCAGTGGCCCCCATCCCTGTTATGGGCTCC 1983
Qy 513 IleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeu 532
Db 1984 ATTGTCCAGCTCAGCAGTCTGTCTACTGCTATATGGTGTCTGCCGAGCCCTGGGCTCG 2043
Qy 533 ValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSer 552
Db 2044 GTCGCATTTACTTTGCTACAGGTAGTATTGTGACAGCGACTTGGCCAAATACTCA 2103
Qy 553 Ala 553
Db 2104 GCG 2106
RESULT 16
ABA91284
ID ABA91284 standard; DNA; 1593 BP.
XX
AC ABA91284;
XX 08-APR-2002 (first entry)
DT 08-APR-2002 (first entry)
XX
DE Thioredoxin-ubiquitin-P501S(aal-320)His triple gene fusion.
XX
KW Thioredoxin; trxA; ubiquitin; P501S; tumour; prostate; antigen;
KW cancer; vaccine; therapy; human; gene; ds.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Escherichia coli.
FH Key Location/Qualifiers
FT CDS 1..1593
FT /*tag= a
FT /trans_except= (pos:607..609,aa:Xaa)
FT /note= "Xaa not given in amino acid sequence of
FT Figure 12b (AAM50662), which has a Val
FT residue at amino acid position 208 not
FT not encoded by the present sequence"
XX
PN WO200200892-A1.
XX
PD 03-JAN-2002.
XX
PF 19-JUN-2001; 2001WO-EP06952.
XX
PR 26-JUN-2000; 2000GB-0015619.
PR 30-OCT-2000; 2000GB-0026484.
XX
PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Cabezon Silva TEV, Delisse ABF;
XX
DR WPI; 2002-147888/19.
DR P-PSDB; AAM50662.
XX
PT Novel DNA sequence encoding triple fusion protein comprising ubiquitin
PT fused between thioredoxin and polypeptide of interest, useful for
PT producing recombinant polypeptide of interest suitable for medicinal
PT use
XX
PS Example 8; Fig 12b; 87pp; English.
XX
CC The present sequence is that of a triple gene fusion comprising,
CC from the 5' end, the trxA thioredoxin gene from Escherichia coli,
CC the human ubiquitin coding sequence, the prostate antigen P501S
CC (amino acids 1-320) coding sequence, and DNA encoding a histidine
CC tail. The triple fusion was constructed in plasmid pRIT15115,
CC under the control of the lambda pL promoter. Triple fusion
CC protein (see AAM50662) was produced in E. coli G1724 transformants.
CC This is an example of the production of triple fusion proteins of

CC the invention comprising ubiquitin fused between thioredoxin and a
CC protein of interest, in this case P501S(aal-320). A claimed method
CC of producing a recombinant protein of interest involves: culturing
CC a host cell (preferably E. coli) under conditions which allow
CC for co-expression of the triple fusion and a ubiquitin-specific
CC endoprotease (especially UBP1 from *Saccharomyces cerevisiae*);
CC and recovering the recombinant protein directly from the bacterial
CC cells after it has been subjected to the action of the
CC ubiquitin-specific endoprotease in vivo. In the present case,
CC expression was controlled by addition of tetracycline. The
CC recombinant protein can be used as a vaccine for cancer therapy.

XX Sequence 1593 BP; 308 A; 472 C; 461 G; 352 T; 0 other;

Alignment Scores:

Pred. No.: 3 93e-288 Length: 1593
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 24 Gaps: 0

US-09-593-793A-113 (1-553) x ABA91284 (1-1593)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuHisArgLysAlaGlnLeuLeuLeu 20
DB 604 ATGGTCCAGAGGCTGTGGGTGAGCGCGCTGCTGGCGACCCGAAAGCCAGCTCTGTG 563
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyLeuTrpValPro 40
DB 664 GTCAACCTGCTAACCTTTGGCGTGGAGGTGCTTTGGCGCGAGGCATCACCTATGTGCG 723
QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyLeuGly 60
DB 724 CCTCTGCTGCTGGAGTGGGGGTAGAGGAGAGTTCATGACCATGCTGGCGCATTTGGT 783
QY 61 ProValLeuGlyValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
DB 784 CCAGTGTGGGCTGTGCTGTCCCGCTCTAGCTAGCTAGCCAGTACCAGCTGGCGTGA 843
QY 81 ArgTyrGlyArgArgProPheLeuTrpAlaLeuSerLeuGlyLeuLeuSerLeu 100
DB 844 CGCTATGGCGCGCGCGCGCTTCTCTGGGCACTGTCTTGGGCACTCTGCTGAGCCTC 903
QY 101 PheLeuLeuProArgAlaGlyTrpLeuAlaGlyLeuLysProAspProArgProLeu 120
DB 904 TTTCATCCCCAAGGCGCGGCTGGCTAGCAGGGGCTGCTGTGCCCGGATCCCGAGCCCTG 963
QY 121 GluLeuAlaLeuLeuLeuValGlyLeuLeuLeuAspPheCysGlyGlnValCysPhe 140
DB 964 GAGCTGGCACTGCTCATCTCTGGCGCTGGGGCTGCTGGACTCTGTGGCAGGTGTGCTTC 1023
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
DB 1024 ACTCCACTGGAGGCGCTGCTCTGCTACCTCTTCCGGGACCCGACCTGTGCCAGGCGC 1083
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
DB 1084 TACTGTGTATGCTTATGATATGATGCTTGGGGCTGCTGGGCTACCTCTGCTGCTGCC 1143
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
DB 1144 ATTGACTGGACACAGTGGCTGCTGGCGCTTACCTTGGGACCCAGAGAGTGCCTCTTT 1203
QY 201 GlyLeuLeuThrLeuLeuPheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
DB 1204 GGCCTGCTCACCTCATCTTCTACCTACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAG 1263
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
DB 1264 GCAGGCTGGGCGCCACCGAGCAGAGAGGGCTGTGGCGCCCTCTCTGTGCGCCAC 1323
QY 241 CysCysProCysArgAlaAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260

DB 1324 TGCTGTCCATGCGGGCGCGCTTGGCTTCCGGAACCTGGCGCCCTGCTTCCCGGCTG 1383
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAlaGluLeuCys 280
DB 1384 CACCAGCTGTGTCGCGCATGCCCGCACCCCTGCGCGCGGCTCTTGGTGGCTGAGCTGTC 1443
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
DB 1444 ACCTGGATGGCACTCATGACCTTCACGCTGTGTTTACACGGATTTCTGCGCGGAGGCTG 1503
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
DB 1504 TACCAGGGCGTCCCGAGAGCTGAGCGCGGACCGGAGCCCGAGACACTATGATGAAGGC 1563
RESULT 17
AAS64040
ID AAS64040 standard; cDNA; 4034 BP.
XX
AC AAS64040;
XX
XX 29-JAN-2002 (first entry)
XX
DE Human prosate cDNA P553S splice variant #3.
XX
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US099919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick JS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
WPI; 2001-639232/73.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Claim 1; Page 483-484; 579pp; English.
XX
CC The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
XX polynucleotide of the invention.

SQ Sequence 4034 BP; 721 A; 1226 C; 1141 G; 946 T; 0 other;

Alignment Scores:
Pred. No.: 9.75e-288 Length: 4034
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 22 Gaps: 0

US-09-593-793A-113 (1-553) x AAS64040 (1-4034)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
|
DB 281 ATGCTCAGAGGCTGTGGTGTAGCGCGCTGCTGGCGCACCGAAGCCAGCTTTGGCTG 340
|
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGlyIleThrTyrValPro 40
|
DB 341 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTGGCCGACGACATCACTATGTGCCG 400
|
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
|
DB 401 CCTCTGCTGTGAGAGTGGGGTAGAGGAGAGTTATGACCATGTGTGCTGGGCATTGGT 460
|
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
|
DB 461 CCAGTGTGGCGCTGGTGTGTGTCGCCGCTCTAGGCTCAGCCAGTGCACCTGGCGTGA 520
|
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
|
DB 521 CGTATATGGCGCGCGCGGCTTCATCTGGGCACCTGCTTGGGCATCTCTGTGAGGCCTC 580
|
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
|
DB 581 TTTCTCATCCAGAGCGCGCTGGCTAGCAGGCTGCTGTGCCCGCATCCAGCCGCCCTG 640
|
QY 121 GluLeuAlaLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
|
DB 641 GAGCTGGCACTGTCTATCTCTGGCGTGGGCTGCTGTGACCTCTGTGGCCAGGTGTGCTTC 700
|
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
|
DB 701 ACTCCACTGGAGCGCCGCTCTCTGACCTCTTCCGGACCGGACCACTGTGCCAGGCC 760
|
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAla 180
|
DB 761 TACTCTGTCTATGCCTTCATGATCAGTCTTGGGGCTGCTGGGCTACCTCTCTGCTGCC 820
|
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
|
DB 821 ATTGACTGGGACACCACTGCTGCTGGCGCCCTTACCTGGGCACCCAGGAGGAGTGCCTTT 880
|
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
|
DB 881 GGCTGTCTACCTCATCTTCCTCACCTGCTAGCAGCCACACTGTGTGGTGGCTGAGGAG 940
|
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
|
DB 941 GCAGGCTGGGCCCCACCGAGCCAGCAGAGGCTGTGGCCCCCTCTCTGTGTGGCCCCAC 1000
|
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
|
DB 1001 TGCTGTCCATGCGCGCGCTGGCTTTCCGGAACCTTGGCGCCCTGTCTTCCCGCGCTG 1060
|
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
|
DB 1061 CACACAGCTGTGTGCGCGCATGCCCCGACCCCTGCGCGGCTCTTCGTGGCTGAGCTGTGC 1120
|
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
|
DB 1121 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCTGTGGCGAGGGCTG 1180
|
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
|

DB 1181 TACCAGGGCTGCCAGAGCTGAGCCGGCAGCGGCGGACACTATGATGAGGT 1240
|
RESULT 18
AAH93868
ID AAH93868 standard; cDNA; 4034 BP.
XX
AC AAH93868;
XX
DT 04-OCT-2001 (first entry)
XX
DE P553S cDNA splice variant P553S-10.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stoik JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX
DR WPI; 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
PS Claim 1; Page 460-461; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used to treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 4034 BP; 721 A; 1226 C; 1141 G; 946 T; 0 other;
|
Alignment Scores:
Pred. No.: 9.75e-288 Length: 4034
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 22 Gaps: 0
|
US-09-593-793A-113 (1-553) x AAH93868 (1-4034)
|
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
|
DB 281 ATGCTCAGAGGCTGTGGTGTAGCGCGCTGCTGGCGCACCGAAGCCAGCTTTGGCTG 340
|
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGlyIleThrTyrValPro 40
|

Db 341 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCGCAGGCATCACCTATGTGGCG 400
Qy 41 ProLeuLeuGluValGlyValGlyValGluGluLysPheMetThrMetValLeuGlyLeuGly 60
Db 401 CCTCTGCTGCTGAAGTGGGGGTAGAGAGAGTTTCAATGACCATGGTCTGGGCATTGGT 460
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 461 CCAGTGGCTGGGCTGTGCTGTGCTCCCGCTCTAGCTCAGCCAGTGACCACTGGCGTGA 520
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 521 CGCTATGGCGCGCGCGGCTTCACTCTGGGCACGTGCTTGGGCATCTGCTGAGCCCTC 580
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTCTCATCCCAAGGCGCGGCTGGCTAGCAGGGCTGTGTGCGCGGATCCCAAGGCCCTG 640
Qy 121 GluLeuAlaLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyClnValCysPhe 140
Db 641 GAGCTGGCACGTCTATCTGGGCGTGGGCTGTGACTTCTGTGGCCAGGTGTGCTTC 700
Qy 141 ThrProLeuGluAlaLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGGCGCTGCTCTGACCTCTTCCGGGACCCGACCACTGTGCGCAGGCC 760
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 761 TACTCTGTATGCTTCATGATCAGTCTTGGGGGCTGCTGGGCTACCTCTGCTGCTGCC 820
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
Db 821 ATTGACTGGACACAGTGCCTGCGCCCTACCTGGGCGCCACCCAGGAGGTGCTCTTT 880
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 881 GGCCTGCTCAGCCTCATCTTCTCACCTCGCTAGCAGCCACACTGCTGCTGCTGAGGAG 940
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 941 CGAGCGCTGGGCGCCACCGACGACAGAGGCTGTGCGCCCTCTCTGTGCGCCCGAC 1000
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1001 TGCTGTCCATCGCGGCGCGCTTGCTTCCGGACCTGGGCGGCTCTTCCCGGCTG 1060
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1061 CACCAGCTGTGTCGCGCATGCGCGCACCCCTGCGCGGCTCTTCTGCTGAGCTGTGC 1120
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluClyLeu 300
Db 1121 ACCTGGATGGCACTCATGACCTTCAGCTGTGTTTACACGGATTTGCTGGCGAGGGGCTG 1180
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1181 TACCAGGCGTGCCAGAGCTGAGCGGCGCACCGGAGCCCGGAGACACATGATGAAGGT 1240

RESULT 19
ABL95411
ID ABL95411 standard; cDNA; 4034 BP.
XX AC ABL95411;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human P53S splice variant SEQ ID NO 704.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX

PN US2002022248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
(XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2002-255649/30.
XX
PT New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer
XX
PS Claim 1; SEQ ID NO 704; 87pp; English.
XX
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
SQ Sequence 4034 BP; 721 A; 1226 C; 1141 G; 946 T; 0 other;
Alignment Scores:
Pred. No.: 9,75e-288 Length: 4034
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 24 Gaps: 0

US-09-593-793A-113 (1-553) x ABL95411 (1-4034)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
DB 281 ATGGTCACAGGCTGTGGGTGAGCGCCGTCTGGCGCACCGAAGACCCAGCTCTTGCTG 340
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
DB 341 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTTGGCCGACAGGCATCACCATTATGTGCGG 400
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
DB 401 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAAGTTTCATGACCATTGGTGTGGGCATTGGT 460
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
DB 461 CCAGTCTGGGCTGTGCTGTGTCGCGCTCCCTAGGCTCAGCGAGTACACCTGGCGTGA 520
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
DB 521 CGTATGGCGCGCGCGGCTTCATCTGGGCACGTCTCTTGGGCATCCTGCTGAGCCCTC 580
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
DB 581 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCAGGCCCTG 640
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
DB 641 GAGTGGCACTGCTCATCTCGGGGTGGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTC 700
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
DB 701 ACTCCACTGGAGCCCTGCTCTGACCTCTTCGGGACCCGACCACTGTGCCAGGCC 760
QY 161 TyrSerValTyrAlaPheMetIleSerLeuLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
DB 761 TACTCTGTATGCCTTCATGATCATGCTTGGGGGTGCTGGGTACCTCTGCTGCTGCC 820
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
DB 821 ATTGACTGGGACCACTGCTGCTGCGCCCTACCTGGGCGACCCAGGAGGTGCTCTTT 880
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
DB 881 GGCTGCTCACCTCATCTCTCCTACCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAG 940
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
DB 941 GCAGCGCTGGGCGCCACCGAGCCAGCAGAGGGCTGTGCGGCCCTCTCTTGTGCGCCAC 1000
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuLeuGlyAlaLeuLeuProArgLeu 260
DB 1001 TGCTGTTCATGCGGGCGCGCTGGCTTTCCGGAACCTGGGCGCGCTGCTTCCCGGGCTG 1060
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
DB 1061 CACCACTGTGCTGGCGATGCCCGCACCTGCGCGGCTCTTGTGGCTGAGTGTGC 1120
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlyLeu 300
DB 1121 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTCTGTTGGCGCAGGGGCTG 1180
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
DB 1181 TACCAGGGCGTCCCAAGCTGAGCGGGGACCCGAGGCGCGGAGACACTATGATGAAGGT 1240

RESULT 20

AA564153

ID AA564153 standard; cDNA: 1203 BP.

XX AA564153;

AC AA564153;

XX

DT 29-JAN-2002 (first entry)
XX Human /M. tuberculosis fusion protein RA12-P501S-E2 cDNA.
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX Chimeric - Homo sapiens.
OS Chimeric - Microbacterium tuberculosis.
XX WO200173032-A2.
XX 04-OCT-2001.
PD 27-MAR-2001; 2001WO-US09919.
PF 27-MAR-2001; 2000US-0536857.
XX 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX (CORI-) CORIXA CORP.
PA Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI: 2001-639232/73.
DR P-PSDB; AAU69907.
XX New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
PS Example 17; Page 542-543; 579pp; English.
XX The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX Sequence 1203 BP; 175 A; 415 C; 368 G; 245 T; 0 other;
Alignment Scores:
Pred. No.: 3, 85e-235 Length: 1203
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 22 Gaps: 0
US-09-593-793A-113 (1-553) x AA564153 (1-1203)
QY 36 IleThrTyrValProLeuLeuLeuGluValGlyValGluLysPheMetThrMet 55
DB 412 ATCACTATGTGCCGCTCTGCTGTGGAAGTGGGGTAGAGGAAGTTCATGACCATG 471
QY 56 ValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSer 75
DB 472 GTGCTGGCATTGGTCCAGTGTGGCGCTGGTGTGTGTCGCCGCTCTAGGCTCAGCCAGT 531

Db 892 GAGGAGTGGCTCTTTGGCTGTGCACCTCATCTTCCCTCACCTGCGTAGCAGCCACACTG 951
Qy 216 LeuValAlaGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaPro 235
Db 952 CTGGTGGCTGAGGAGGAGCGCTGGGGCCACCGAGCCAGAGGGCTGTGGGCCCGC 1011
Qy 236 SerLeuSerProHisCysCysProCysArgAlaAraGluAlaPheArgAsnLeuGlyAla 255
Db 1012 TCCTTGTGCGCCACACTGCTTCATCGCGGCGCGCTTGGCTTCCGGAACCTGGGCGCC 1071
Qy 256 LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe 275
Db 1072 CTGCTTCCCGGCTGACACAGCTGTGCTGCGCATGCCCGCACCTGGCGCGCTCTTC 1131
Qy 276 ValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPhe 295
Db 1132 GTGGCTGAGCTGTCAGCTGGATGGCAGCTCATGACCTTCACGCTGTTTACACGGATTTC 1191
Qy 296 ValGlyGlu 298
Db 1192 GTGGCGGAG 1200

RESULT 22
ABL95524
ID ABL95524 standard; cDNA; 1203 BP.
AC ABL95524;
XX
DT 19-JUL-2002 (first entry)
DE Ra12-P501S-E2 construct cDNA sequence SEQ ID NO 851.
XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX Chimeric - Mycobacterium tuberculosis.
OS Chimeric - Homo sapiens.
XX
PN US2002022248-A1.
XX
PD 21-FEB-2002.

XX 12-JAN-2001; 2001US-0759143.
XX 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.

XX (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.

PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEL/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer
XX
XX Example 17; SEQ ID NO 851; 87pp; English.
XX
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
XX Sequence 1203 BP; 175 A; 415 C; 368 G; 245 T; 0 other;

Alignment Scores:
Pred. No.: 3,85e-235 Length: 1203
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 24 Gaps: 0
US-09-593-793A-113 (1-553) x ABL95524 (1-1203)
Qy 36 IleThrTyrValProProLeuLeuLeuGluValGlyValGluLysPheMetThrMet 55
Db 412 ATCACCTATGTCCGCTCTGCTGTGAAGTGGGGTAGAGAGAAGTTCATGACCATG 471
Qy 56 ValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuGlySerAlaSer 75
Db 472 GTGCTGGGCATTGGTCCAGTGTGGGCTGTGTCTCCCTCCTAGGCTCAGCCAGT 531
Qy 76 AspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGly 95
Db 532 GACCACTGGCTGGAGCGCTATGGCGCGCGCGCTTCATCTGGGCACTGTCTTGGGC 591
Qy 96 IleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysPro 115
Db 592 ATCTCTGCTGAGCTCTTCTCTCATCCAGGCGCGGTGGCTGTGTGCTGTGCTGCCG 651
Qy 116 AspProArgProLeuGluLeuAlaLeuLeuLeuGlyValGlyLeuLeuAspPheCys 135
Db 652 GATCCAGGCGCTGAGCTGCTGCTATCCCTGGGCTGGGCTGTGACTTCTGT 711
Qy 136 GlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAsp 155
Db 712 GGCCAGGTGTGTTACTCCACTGGAGGCGCTGCTCTGACCTCTCCGGGACCGGAC 771
Qy 156 HisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyCysLeuGly 175
Db 772 CACTGTGCGCAGCGCTTACTCTGTCTATGCTTCTATGCTCAGTCTTGGGGCTGCCCTGGC 831
Qy 176 TyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln 195
Db 832 TACCTCTGCTGCCATTGACTGGGACACAGTGGCGCTGGCGCTTACCTGGGACCGCCAG 891

QY 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277
|||||
Db 1911 CCGCGCTGCACAGCTGTGCTGCCGATGCGCCGACCTGCGCGGCTCTTCGTGGCT 1970
|||||
QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheThrThrAspPheValGly 297
|||||
Db 1971 GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTGTTTACACGGATTTCGTGGGC 2030
|||||
QY 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
|||||
Db 2031 GAGGGCTGTACACGGGCTGCCAGAGCTGAGCGGGCAGCCAGCGGAGACACTAT 2090
|||||
QY 318 AspGluGly 320
|||||
Db 2091 GATGAAGT 2099
|||||
RESULT 25
ID AAH93866 standard; cDNA; 4894 BP.
AC
XX AAH93866;
XX
DT 04-OCT-2001 (first entry)
XX
DE P553S cDNA splice variant P553S-14.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01574.
PR
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SC;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX
DR WPT; 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
PS Claim 1; Page 457-459; 543pp; English.
XX
SS
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AA01115 to
CC AA01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 4894 BP; 928 A; 1448 C; 1354 G; 1163 T; 1 other;
Alignment Scores:
Pred. No.: 1.52e-234 Length: 4894

Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 22 Gaps: 0
US-09-593-793A-113 (1-553) x AAH93866 (1-4894)
QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
|||||
Db 1311 GGCATTGGTCAGCTGCTGGGCTGTGTCTGTCTCCGCTCTAGGCTCAGCAGTGCACAC 1370
|||||
QY 78 TrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
|||||
Db 1371 TGGCGTGGACGCTATGCGCGCGCGGCTTCATCTGGGCACGTCTCTGGGCATCTG 1430
|||||
QY 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
|||||
Db 1431 CTGAGCCTCTTTCTCATCCCAAGGCGGCTGGCTAGCAGGCTGCTGTGCCGATCCC 1490
|||||
QY 118 ArgProLeuGluLeuAlaLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
|||||
Db 1491 AGCCCCCTGGAGCTGGCACCTGCTCATCTGGCGTGGGCTGTGTGGCCAG 1550
|||||
QY 138 ValCysPheThrProLeuGluAlaLeuSerAspLeuPheArgAspProAspHisCys 157
|||||
Db 1551 GTGTCTTCACTCCACTGGAGGCTGCTCTCTGACCTCTTCCGGGACCCGACCACTGT 1610
|||||
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
|||||
Db 1611 CGCCAGGCTACTCTGTCTATGCTCTCATGATCATGCTGTGGGCTGTGGGTACCTC 1670
|||||
QY 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGlu 197
|||||
Db 1671 CTGCTGCCATTGACTGGGACACAGTGCTGCTGGCCCTACCTGGGCACCCAGAGAG 1730
|||||
QY 198 CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
|||||
Db 1731 TGCCTCTTTGGCTGCTCACCTCTCATCTCCTACCTGCTAGCAGCCACACTGCTGGTG 1790
|||||
QY 218 AlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
|||||
Db 1791 GCTGAGGAGGCGGCTGGGCCCCACCGAGCCAGAGGCTGTGCGCCCTCCTCTG 1850
|||||
QY 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
|||||
Db 1851 TCGCCCACTGCTGTCCATGCCGGGCGCTGTGGCTTTCCGGAACCTGGGCGCTGCTT 1910
|||||
QY 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277
|||||
Db 1911 CCGCGCTGCACAGCTGTGCTGCCGATGCGCCGACCTGCGCGGCTCTTCGTGGCT 1970
|||||
QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheThrThrAspPheValGly 297
|||||
Db 1971 GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTGTTTACACGGATTTCGTGGGC 2030
|||||
QY 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
|||||
Db 2031 GAGGGCTGTACACGGGCTGCCAGAGCTGAGCGGGCAGCCAGCGGAGACACTAT 2090
|||||
QY 318 AspGluGly 320
|||||
Db 2091 GATGAAGT 2099
|||||
RESULT 26
ABL95409
ID ABL95409 standard; cDNA; 4894 BP.
XX
AC ABL95409;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human P553S splice variant SEQ ID NO 702.

XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX Homo sapiens.
XX US2002022248-A1.
XX 21-FEB-2002.
XX 12-JAN-2001; 2001US-0759143.
XX 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0569100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI; 2002-255649/30.
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer -
XX
XX Claim 1; SEQ ID NO 702; 87pp; English.
PS
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
SQ Sequence 4894 BP; 928 A; 1448 C; 1354 G; 1163 T; 1 other;
Alignment Scores:

Pred. No.: 1.52e-234 Length: 4894
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 24 Gaps: 0
US-09-593-793a-113 (1-553) x ABL95409 (1-4894)
QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
Db 1311 GGCATTGGTCCAGTGTGGCCCTGTGTCTGCCGCTCCTAGGCTCAGCCAGTACCAC 1370
QY 78 TrpA:qGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
Db 1371 TGGCGTGGAGCGTATGGCCGCCGCCCTTCATCTGGGCACTGTCTTGGGCATCTCG 1430
QY 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
Db 1431 CTGAGCCTCTTTCTCATCCAAAGGCGCGCTGGCTAGCAGGGCTGTCTGTCCCGGATCCC 1490
QY 118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
Db 1491 AGGCCCTGGAGCTGGCACTGTCTCATCTGGCGTGGGCTCTGTGACTTCTGTGCCAG 1550
QY 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
Db 1551 GTGTGCTTCACTCCACTGGAGCCCTGTCTCTGACCTTCTCCGGGACCCGACCACTGT 1610
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
Db 1611 CGCCAGGCTACTGTCTATGCCCTTCATGATCAGTCTTGGGGGCTGTCTGGGCTACCTC 1670
QY 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGlu 197
Db 1671 CTGCTGCCATTGACTGGGACACCACTGCCCTGGCCCTTACTGGGACCCGAGGAGGAG 1730
QY 198 CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
Db 1731 TGCTCTTTGGCTGCTCACCTCATCTTCCTCACCTGCTAGCAGCACCACTGTCTGTG 1790
QY 218 AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
Db 1791 GCTAGGAGGCGAGCGCTGGGCCCCACCAGCCAGCAGAGGGCTGTGCGGCCCTCTCTTG 1850
QY 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
Db 1851 TCGCCCCACTGTCTCCATGCGGGCGCGCTTGGCTTTCCGGAACTGGGCCCTCTGT 1910
QY 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277
Db 1911 CCCCAGCTGCACCACTGTGTGTCGCCCATGCCGCCACCTTGGCGGCTCTTCTGTGGCT 1970
QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
Db 1971 GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGGC 2030
QY 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyr 317
Db 2031 GAGGGGCTGTACCAGGGCTGCCAGAGCTAGCGGGGACCGAGGGCCCGGAGACACTAT 2090
QY 318 AspGluGly 320
Db 2091 GATGAGGT 2099
RESULT 27
AAS64041
ID AAS64041 standard; cDNA: 6976 BP.
XX
AC AAS64041;
XX
DT 29-JAN-2002 (first entry)
XX

DE Human prostate cDNA P553s splice variant #4.
XX
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
OS Homo sapiens.
XX
PN WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
FA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2001-639232/73.
DR P-PSDB; AAU69873.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Claim 1; Page 484-486; 579pp; English.
XX
CC The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
SQ Sequence 6976 BP; 1312 A; 1996 C; 1961 G; 1706 T; 1 other;

Alignment Scores:
Pred. No.: 2.15e-234 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 22 Gaps: 0

US-09-593-793A-113 (1-553) x AAS64041 (1-6976)

Qy 58 GlylleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
Db 1202 GGCATTGGTCCAGAGCTGGGCTGGTCTGTCTCCCGCTCTAGGCTCAGCCAGTGACCAC 1261
Qy 78 TrpArgGlyArgTyrglyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
Db 1262 TGGCGTGGACCGCTATGGCCCGCCCGCCCTTCATCTGGGACACTGTCTTGGGCACTCTG 1321
Qy 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
XX

Db 1322 CTGAGCCCTCTTTCTCATCCCAAGGGCCGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCC 1381
Qy 118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
XX
Db 1382 AGGCCCTGGAGCTGGCACTGCTCATCTGGGCGTGGGCTGCTGGACTTCTGTGGCCAG 1441
Qy 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
XX
Db 1442 GTGTGCTTCACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGAGCCGACCACTGT 1501
Qy 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
XX
Db 1502 CGCCAGGCCCTACTGCTCTATGCTTTCATGATCAGTCTTGGGGCTGCTGGGTACCTC 1561
Qy 178 LeuProAlaIleAspTTPAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
XX
Db 1562 CTGCTGCCATTTGACTGGGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1621
Qy 198 CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
XX
Db 1622 TGCCTCTTTGGCCTGCTCACCTCATCTTCTCCTACCTGCTAGCAGCCACACTGCTGCT 1681
Qy 218 AlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
XX
Db 1682 GCTGAGGAGGAGCGCTGGGCCCCCAGCAGCAGCAGGAGGCTGCTGGGCCCTCCTTG 1741
Qy 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
XX
Db 1742 TCGCCCCCACTGCTGCCATGCCGGGCCGCTGGCTTTCGGGAACCTGGGGCCCTGCTT 1801
Qy 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277
XX
Db 1802 CCCGGGCTGCACAGCTGCTGCTGCGCATGCCCGCCGCTGCGCCGGCTCTTCTGCTGCT 1861
Qy 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
XX
Db 1862 GAGCTGTGACGTGGATGGCACTCATGACCTTACGCTGTTTACACGGATTTCGTGGGC 1921
Qy 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyr 317
XX
Db 1922 GAGGGGCTGTACCAAGGGCGTGGCCAGAGCTGAGCGGGCACCCGAGGCCCCGAGACACTAT 1981
Qy 318 AspGluGly 320
XX
Db 1982 GATCAAGCT 1990
RESULT 28
AAH93869
ID AAH93869 standard; cDNA; 6976 BP.
XX
AC AAH93869;
XX
DX 04-OCT-2001 (first entry)
XX
DE P553s cDNA splice variant P553S-6.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;

PI Wang A, Meagher MJ;

DR WPI; 2001-425873/45.

XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -

XX Claim 1; Page 461-463; 543pp; English.

XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used to treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.

XX Sequence 6976 BP; 1312 A; 1996 C; 1961 G; 1706 T; 1 other;

Alignment Scores:

Pred. No.: 2,15e-234 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 22 Gaps: 0

US-09-593-793a-113 (1-553) x AAH93869 (1-6976)

QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
DB 1202 GGCATTGGTCCAGTGTGGCGCTGCTGTGTCGCCGCTCCTAGGCTAGCCAGTACCCAC 1261
QY 78 TrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
DB 1262 TGCGCTGGACGCTATGGCGCGCGCGCCCTTCATCTGGGCACTGCTCCTGGGCATCCTG 1321
QY 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
DB 1322 CTGAGCCCTCTTCTCATCCAGGCGCGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCC 1381
QY 118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
DB 1382 AGGCCCTTGGAGCTGGCACTGCTCATCTGGCGTGGGGCTGCTGGACTTCTGTGGCCAG 1441
QY 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
DB 1442 GTGTGCTTCACTCCACTGGAGCGCTGCTCTGTGACCTCTTCGCGGACCCCGGACCTGT 1501
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
DB 1502 CGCCAGGCTTACTCTGTCTATGCCCTCATGATCATGCTTGGGGGCTGCTGGGTACCTC 1561
QY 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
DB 1562 CTGCGCTGCCATTGCTGGACACCACTGCCCTGGCCCCCTACCTGGGCACTCCAGGAGGAG 1621
QY 198 CysteupheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
DB 1622 TGCCCTCTTTGGCGCTGCTCACCGCTCATCTCTCCTACCTGCTAGCAGCCACACTGCTGTG 1681
QY 218 AlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
DB 1682 GCTGAGGAGGAGCCGCTGGGCCCCCACCAGCCAGCAGGAAGGCGTGTGGGCCCCCTCTTG 1741

QY 238 SerProHisCysCysProCysArgAlaArgIleuAlaPheArgAsnLeuGlyAlaLeuLeu 257
DB 1742 TCGCCCCACTGCTGTCCATGCGGGCGCTGTGCTTTCCGGAACCTGGGCGCTGCTT 1801
QY 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAla 277
DB 1802 CCGCGGCTGACACAGCTGTGCTGCGCATGCCCGCCACCCCTGCGCGGCTCTTCTGTGGCT 1861
QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
DB 1862 GAGCTGTGCAGCTGGATGGATGCATCATGACCTTCAGGCTGTTTACACGATTTCTGTGGC 1921
QY 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
DB 1922 GAGGCGCTGTACACAGGCGCTGCCAGAGCTGAGCGGGCACCGAGGCCCGGAGACACTAT 1981
QY 318 AspGluGly 320
DB 1982 GATGAAGT 1990
RESULT 29
ABL95412
ID ABL95412 standard; cDNA; 6976 BP.
XX
AC ABL95412;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human P53S splice variant SEQ ID NO 1705.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002022248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636213.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (XUJ)/ XU J.
PA (DILL)/ DILLON D C.
PA (MITC)/ MITCHAM J L.
PA (HARL)/ HARLOCKER S L.
PA (JIAN)/ JIANG Y.
PA (KALO)/ KALOS M D.
PA (FANG)/ FANGER G R.
PA (RETT)/ RETTER M W.
PA (STOL)/ STOLK J A.

PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX WPI; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer -
XX
XX
PS Claim 1; SEQ ID NO 705; 87pp; English.
XX
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
XX
SQ Sequence 6976 BP; 1312 A; 1996 C; 1961 G; 1706 T; 1 other;
Alignment Scores:
Pred. No.: 2,15e-234 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 24 Gaps: 0
US-09-593-793a-113 (1-553) x ABL95412 (1-6976)
QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
Db 1202 GGCATTGGTCCAGTGGCTGGCTGTGTCTGTCCCGCTCCCTAGGCTCAGCCAGTGACCAC 1261
QY 78 TrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
Db 1262 TGGCTGGACGCTATGGCGCGCGCGCTTCATCTGGGCACCTCTCTGGGCATCTG 1321
QY 98 LeuSerLeuPheLeuIleProAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
Db 1322 CTGAGCCTCTTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTGCCGATCCC 1381
QY 118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
Db 1382 AGGCCCTGGAGCTGGCACTGCTCATCTGGCGGTGGGGCTGTGGACTTCTGTGGCCAG 1441
QY 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
Db 1442 GTGTGCTTCACTCCACTGGAGCCCTGCTCTCTGACCTCTTCCGGACCCGACCACTGT 1501
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
Db 1502 CGCCAGGCGCTACTGTCTATGCTTTCATGATCATGCTCTGGGGGTGCTGGGCTACCTC 1561
QY 178 LeuProAlaIleAspTTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGlu 197
Db 1562 CTGCTGCGCATGTGGACACAGTGCCTGGCGCCCTACCTGGGCACCCAGAGGAG 1621
QY 198 CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
Db 1622 TGCCTCTTTGGCGTCTCACCTCATCTCTCCTACCTGCGTAGCAGCCACACTGCTGGTG 1681
QY 218 AlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
Db 1682 GCTGAGGAGGCGCTGGGGCCCCACCGAGGCGAGAGGGCTGTGGCCCCCTCTCTTG 1741

QY 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
Db 1742 TCGCCCACTGCTGTCCATGCGGGCCGCTGGCTTCCGAACTGGGGCCCTGCTT 1801
QY 258 ProArgLeuHisGlnLeuLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277
Db 1802 CCGCGGCTGCACAGCTGTGCTGCGCATGCCCGCACCCCTGCGCGGCTCTTCGTGGCT 1861
QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
Db 1862 GAGCTGTGACGCTGGATGGCACTCATGACCTTCAGCTGTTTACACGATTTTCGTGGC 1921
QY 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
Db 1922 GAGGGCTGTACAGGGCGTGCACAGACTGAGCGGGCACCGAGGCCCGGAGACACTAT 1981
QY 318 AspGluGly 320
Db 1982 GATGAAGGT 1990
RESULT 30
AAC64928
ID AAC64928 standard; DNA; 2133 BP.
XX
XX AAC64928;
AC
XX
XX 07-FEB-2001 (first entry)
DT
XX
XX Human prostate-related PS108 partial coding sequence SEQ ID NO: 16.
DE
XX
XX Human; prostate cancer; PS108; antibody; tumour; metastasis; ds.
KW
XX
XX Homo sapiens.
OS
XX
XX US6130043-A.
PN
XX
XX 10-OCT-2000.
PD
XX
XX 01-MAY-1998; 98US-0071710.
PF
XX
XX 02-MAY-1997; 97US-0850713.
PR
XX
XX (ABBO) ABBOTT LAB.
PA
XX
XX Cohen M, Colpitts TL, Friedman PN, Gordon J, Granados EN;
PI Billing-Medel PA, Klass MR, Roberts-Rapp L, Stroupe SD, Yu H;
PI Kratochvil JD, Russell JC, Hodges SC;
PT
XX
XX WPI; 2000-655655/63.
DR
XX
XX Methods for detecting target prostate-specific polynucleotides or
PT diseases of the prostate (e.g. prostate cancer), comprising detecting
PT the presence of any of PS108 nucleic acid sequences in a test sample -
XX
XX
XX Claim 1; Column 77-80; 55pp; English.
PS
XX
XX The present invention is related to a number of partial coding and
CC protein sequences for the human prostate tissue protein PS108. These
CC sequences can be used in the diagnosis and prognosis of prostate
CC diseases, particularly prostate cancer. They can also be used to produce
CC antibodies which can be used in treatment. The present sequence is one
CC of the PS108 partial coding sequences.
XX
XX
SQ Sequence 2133 BP; 414 A; 618 C; 561 G; 540 T; 0 other;
Alignment Scores:
Pred. No.: 1,92e-227 Length: 2133
Score: 255.00 Matches: 255
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 46.11% Indels: 0
DB: 21 Gaps: 0

```
US-09-593-793A-113 (1-553) x AAC64928 (1-2133)
QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAsp 318
Db 2 GGGCTGTACACAGGGGTGCCAGAGCTGAGCCGGGACCGAGCGCGGAGACACTATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGCGTTTCGATGGCAGCGCTGGGCTGTTCTCCAGTGGCCATCTCCCTGGTCTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGGTCATGGACCGGTGTCAGCGATTCGGCACTTCGAGCAGTCTATTGGCCAGT 181
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 182 GTGGAGCTTTTCCCTGTGGCTGCCGTGCCACATGCTGCCACAGTGGCCGTGGTG 241
QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 242 ACAGCTTCAGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCTCGCCCTACACA 301
QY 399 LeuAlaSerLeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 302 CTGGCCTCCCTTACCACCGGAGAGCAGAGTGTCTCTGCCCAATACCGAGGGGACACT 361
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 362 GGAGGTGTAGCAGTAGAGACAGCTGTATGACACGCTTCTGCCAGGCCCTAAGCCTGGA 421
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 422 GCTCCCTCCCTTAATGGACACGTGGTGTGGAGCAGTGGCTGCTCCACCTCCACCC 481
QY 459 AlaLeuCysGlyAlaSerAlaCysaspValSerValArgValValValGlyGluProThr 478
Db 482 GCGCTCTGGGGGCTCTCCCTGTGTATGTCTCCGTACGTGTGGTGGTGGAGCCACC 541
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 542 GAGGCCAGGGTGTTCGGGGCGGGGCATCTGCTGGACCTCGCCATCTCGATAGTGCC 601
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 602 TTCTCTGCTGCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAG 661
QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 662 TCTGTCACTGCTATATGTGTCTGCCGAGGCCCTGGGTCTGTGCGCCATTTACTTTGCT 721
QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 722 ACACAGGTAGTATTGTGACAAAGACGACTTGGCCAAATACTCAGCG 766
RESULT 31
ID AAS07155
XX AAS07155 standard; cDNA; 2133 BP.
AC AAS07155;
XX
DT 23-OCT-2001 (first entry)
XX
DE Prostate gene PS108-specific cDNA (EST) consensus sequence.
XX
KW Prostate; PS108; immunogen; drug screening; image localisation;
KW diagnostic; therapeutic; prostate tissue disease; cancer; metastasis;
XX expressed sequence tag; EST; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS
FT 1..799

/*tag= a
/product= "Prostate-specific protein PS108"

US6252047-B1.
XX
XX
PD 26-JUN-2001.
XX
XX 15-MAR-2000; 2000US-0525397.
XX
XX 01-MAY-1998; 98US-0071710.
XX
XX 02-MAY-1997; 97US-0850713.
XX
XX (ABBO ) ABBOTT LAB.
XX
XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
XX Russell JC, Stroupe SD, Yu H;
XX WPI; 2001-424488/45.
XX
XX P-PSDB; AAU04205.
XX
XX Novel PS108 polypeptide useful in assays for detecting antibodies to
XX prostate tissue, and as immunogens to produce PS108 antibodies
XX
XX Example 1; Fig 1; 55pp; English.
XX
XX The sequence represents the prostate gene PS108-specific expressed
XX sequence tag (EST) consensus sequence. The sequence was produced from
XX overlapping PS108 ESTs sequences to produce a full length consensus
XX sequence. This sequence was then used to produce PS108 polypeptides which
XX are useful in assays for detecting antibodies to prostate tissue, and as
XX immunogens to produce antibodies. The polypeptide is useful for screening
XX compounds which specifically bind to the polypeptide and for screening
XX for drugs, compounds, or any other agent which can be used to treat
XX diseases associated with PS108. The antibody is useful to detect, or for
XX image localisation of, PS108 antigen in a patient, for detecting or
XX diagnosing a disease or condition, as delivery agents for therapeutic
XX agents as well as for diagnostic tests and for screening for diseases or
XX conditions associated with PS108, especially cancer. The antibody is also
XX useful for generating chimeric antibodies for therapeutic use, for
XX inhibiting the biological activity of PS108, in therapy (for e.g. to
XX treat prostate tissue disease including prostate cancer and its
XX metastases), and to detect the presence of any polypeptide in a test
XX sample which shares one or more antigenic determinants with the PS108
XX polypeptide.
XX
XX Sequence 2133 BP; 414 A; 618 C; 561 G; 540 T; 0 other;

Alignment Scores:
Pred. No.: 1,92e-227 Length: 2133
Score: 255.00 Matches: 255
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 46.11% Indels: 0
DB: 22 Gaps: 0

US-09-593-793A-113 (1-553) x AAS07155 (1-2133)
QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAsp 318
Db 2 GGGCTGTACACAGGGGTGCCAGAGCTGAGCCGGGACCGAGCGCGGAGACACTATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGCGTTTCGATGGCAGCGCTGGGCTGTTCTCCAGTGGCCATCTCCCTGGTCTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGGTCATGGACCGGTGTCAGCGATTCGGCACTTCGAGCAGTCTATTGGCCAGT 181
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 182 GTGGAGCTTTTCCCTGTGGCTGCCGTGCCACATGCTGCCACAGTGGCCGTGGTG 241
```

QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
|||||
Db 242 ACAGCTTCAGCGCCCTCACCAGGTTACCTTCTCAGCCCTCAGATCTGCCCTACACA 301
QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
|||||
Db 302 CTGGCTCCCTCTACCACCGGAGAGACAGAGTGTCTCTGCCCAATACCGAGGGACACT 361
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
|||||
Db 362 GGAGGTGCTAGCAGTGAGGACACCCCTGATGACACAGCTTCTGCCAGGCCCTAAGCCCTGGA 421
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyLysGlySerGlyLeuLeuProProPro 458
Db 422 GCTCCCTCCCTAAATGACACAGCTGGGTGCTGGAGGAGTGGCTGCTCCCACTCCACCC 481
QY 459 AlaLeuGlyGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
Db 482 GCGCTCTGGGGGCTCTGCTGTGATGTCCTCGTACGTGTGGTGGGTGAGCCACCC 541
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 542 GAGGCCAGGGTGTCTCCGGCGGGGCATCTGCCTGGACCTCGCCATCTGGATAGTGC 601
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 602 TTCTCTGCTGCCAGTGCCCGCCCATCCCTGTTATGGGCTCCATGTCCAGCTCAGCCAG 661
QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 662 TCTGTCACTGCTATATGTGTCTGCCGAGGCTGGGTGCTGCTGCCATTTACTTTGCT 721
QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 722 ACACAGGTAGTATTGACAAGACGACTTGGCCAAATACTCAGCG 766
RESULT 32
AAV71181
ID AAV71181 standard; cDNA; 2152 BP.
XX
AC AAV71181;
XX
DT 12-FEB-1999 (first entry)
XX
DE Consensus sequence of the PS108 gene derived from overlapping clones.
XX
KW PS108 gene; prostate disease; benign prostatic hyperplasia; BPH;
KW prostatitis; prostatic intraepithelial neoplasia; PIN; cancer;
KW drug screening; gene therapy; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 2..769
FT /*tag= a
XX
PN W098050567-A1.
XX
PD 12-NOV-1998.
XX
PF 01-MAY-1998; 98WO-US08930.
XX
PR 02-MAY-1997; 97US-0850713.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Billings-Medel PA, Cohen M, Colpitts TL, Friedman PN;
PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX
DR WPI; 1999-034731/03.

DR P-PSDB; AAW85068.
XX
PT New isolated prostate-specific polynucleotides - used to develop
PT products for the diagnosis and treatment of prostate diseases, e.g.
PT benign hyperplasia, prostatic or prostate cancer
XX
PS Claim 1; Fig 1A-E; 122pp; English.
XX
CC The present sequence represents the consensus sequence for a PS108
CC gene. The sequence is derived from overlapping clones AAV71166-79. The
CC clone sequences are PS108 gene-specific. They are used in the method
CC of the invention. The specification describes a method for detecting the
CC presence of a target PS108 polynucleotide in a test sample. The method
CC comprises contacting the test sample with at least 1 PS108-specific
CC polynucleotide or complement, and detecting the presence of the target
CC PS108 polynucleotide. The products can be used for detecting,
CC diagnosing, staging, monitoring, prognosticating, in vivo imaging,
CC preventing or treating, or determining predisposition to diseases or
CC conditions of the prostate such as benign prostatic hyperplasia (BPH),
CC prostatitis, prostatic intraepithelial neoplasia (PIN) and cancer. In
CC particular the products can be used in drug screening and gene therapy.
XX
SQ Sequence 2152 BP; 419 A; 622 C; 569 G; 542 T; 0 other;
Alignment Scores:
Pred. No.: 1.93e-227 Length: 2152
Score: 255.00 Matches: 255
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 46.11% Indels: 0
DB: 20 Gaps: 0
US-09-593-793a-113 (1-553) x AAV71181 (1-2152)
QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAsp 318
Db 2 GGGCTGTACACGGGCTGCCAGAGCTGAGCGGGACCGAGCGCCGGAGACACTATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGCGGTTCGGATGGGACGCTGGGGCTGTTCTTCGACGTGCCCATCTCCCTGCTTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGGTTCATGACCGGCTGGTGCGAGCATTCGGACACTCGAGCAGTCTATTGGCCACT 181
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 182 GTGGCAGCTTTCCTGTGGCTGCCGTGCCACATGCTCTCCACAGTGTGGCCGTGTG 241
QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 242 ACAGCTTCAGCGCCCTCACCAGGTTACCTTCTCAGCCCTCAGATCTGCCCTACACA 301
QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 302 CTGGCTCCCTCTACCACCGGAGAGCAGGTGTCTCTGCCCAATACCGAGGGACACT 361
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 362 GGAGGTGCTAGCAGTGAGGACACCTGATGACACAGTCTCTGCCAGGCCCTAAGCCCTGGA 421
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyLysGlySerGlyLeuLeuProProPro 458
Db 422 GCTCCCTCCCTAAATGACACAGCTGGGTGCTGGAGGAGTGGCTGCTCCCACTCCACCC 481
QY 459 AlaLeuGlyGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
Db 482 GCGCTCTGGGGGCTCTGCTGTGATGTCCTCGTACGTGTGGTGGGTGAGCCACCC 541
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 542 GAGGCCAGGGTGTCTCCGGCGGGGCATCTGCCTGGACCTCGCCATCTGGATAGTGC 601

QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
|||||
Db 602 TTCTCTGCTGCCAGGTGGCCCATCCCTGTTTATGGCTCCATTGTCCAGCTCAGCCAG 661
QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
|||||
Db 662 TCCTGTCACTCCCTATATGTTGTCTGCCAGGCTGGTCTGGTCTGCCCATTTACTTTGCT 721
QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||
Db 722 ACACAGGTAGTATTTGACAAAGCGACTTGGCCAAATACTACGCG 766
RESULT 33
AAC64927
ID AAC64927 standard; DNA; 2124 BP.
XX
AC AAC64927;
XX
DT 07-FEB-2001 (first entry)
XX
XX Human prostate-related PS108 partial coding sequence SEQ ID NO: 15.
DE Human prostate cancer; PS108; antibody; tumour; metastasis; ds.
XX
KW Human; prostate cancer; PS108; antibody; tumour; metastasis; ds.
XX
OS Homo sapiens.
XX
XX US6130043-A.
XX
XX 10-OCT-2000.
PD
XX
XX 01-MAY-1998; 98US-0071710.
XX
XX 02-MAY-1997; 97US-0850713.
XX
XX (ABBO) ABBOTT LAB.
XX
XX Cohen M, Colpitts TL, Friedman PN, Gordon J, Granados EN;
PI Billings-Medel PA, Klass MR, Roberts-Rapp L, Stroupe SD, Yu H;
PI Kratochvil JD, Russell JC, Hodges SC;
XX
XX WPI; 2000-655655/63.
DR
XX
XX Methods for detecting target prostate-specific polynucleotides or
PT diseases of the prostate (e.g. prostate cancer), comprising detecting
PT the presence of any of PS108 nucleic acid sequences in a test sample -
XX
XX Claim 1; Column 75-78; 55pp; English.
PS
XX
CC The present invention is related to a number of partial coding and
CC protein sequences for the human prostate tissue protein PS108. These
CC sequences can be used in the diagnosis and prognosis of prostate
CC diseases, particularly prostate cancer. They can also be used to produce
CC antibodies which can be used in treatment. The present sequence is one
CC of the PS108 partial coding sequences.
XX
SQ Sequence 2124 BP; 411 A; 616 C; 558 G; 539 T; 0 other;

Alignment Scores:
Pred. No.: 1.19e-224 Length: 2124
Score: 252.00 Matches: 252
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.57% Indels: 0
DB: 21 Gaps: 0

US-09-593-793A-113 (1-553) x AAC64927 (1-2124)

QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGlyVal 321
|||||
Db 3 CAGGGCGTCCCGACAGCTGAGCGGGCCAGCGAGGCCGCGAGACACTATGATGAGCGCTT 62
QY 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
|||||

Db 63 CGGATGGCAGCCCTGGGGCTGTTCCTCGAGTGGCCATCTCCCTGGTCTTCTCTGGTC 122
QY 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
|||||
Db 123 ATGGACCGGCTGGTGGCAGGATTCGGCACTCGGAGAGTCTATTGGCCAGTGGGAGCT 182
QY 362 PheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSer 381
|||||
Db 183 TTCCCTGTGGCTGCCGTGCCACATGCCGTGCCACAGTGTGGCCGTGGTGACAGCTTCA 242
QY 382 AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401
|||||
Db 243 GCGGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCCTGACACACTGGGCTCC 302
QY 402 LeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAla 421
|||||
Db 303 CTCTACACCGGAGAGAGAGGTGTTCTCGCCCAATATCCGAGGGGACACTGGAGGTCT 362
QY 422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
|||||
Db 363 AGCAGTGAGGACAGCCTGATGACACAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTC 422
QY 442 ProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCys 461
|||||
Db 423 CCTAATGGACACGTGGGTGCTGGAGGACGTGGCTGCTCCACCTCCACCCGCGCTGTC 482
QY 462 GlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAlaArg 481
|||||
Db 483 GGGGCTCTGCCCTGTGATGTCTCCGTACGTGTGGTGGGTGAGCCACCGAGGCGCAGG 542
QY 482 ValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501
|||||
Db 543 GTGTTCCGGCGGGGCGCATCTGCTGGACCTGCCCATCCTCGCATAGTGCTTCTGCTG 602
QY 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521
|||||
Db 603 TCCAGAGTGGCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGCACT 662
QY 522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 541
|||||
Db 663 GCCTATATGTGTCTGCCGAGGCGCTGGGTCTGTCGCCCATTTACTTTGCTACAGGTA 722
QY 542 ValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||
Db 723 GTATTTGACAAGAGCGACTTGGCCAAATACTACGCG 758
RESULT 34
AAS07601
ID AAS07601 standard; cDNA; 2124 BP.
XX
AC AAS07601;
XX
DT 23-OCT-2001 (first entry)
XX
DE Prostate gene PS108-specific cDNA clone 17113461H.
XX
KW Prostate; PS108; immunogen; drug screening; image localisation;
KW diagnostic; therapeutic; prostate tissue disease; cancer; metastasis;
KW expressed sequence tag; EST; ss.
OS Homo sapiens.
XX
PN US6252047-B1.
XX
XX 26-JUN-2001.
PD
XX
XX 15-MAR-2000; 2000US-0525397.
XX
PR 01-MAY-1998; 98US-0071710.
PR 02-MAY-1997; 97US-0850713.
XX
XX (ABBO) ABBOTT LAB.

CC prostatic intraepithelial neoplasia (PIN) and cancer. In particular the
CC products can be used in drug screening and gene therapy.

XX
SQ Sequence 2143 BP; 418 A; 621 C; 563 G; 541 T; 0 other;

Alignment Scores:

Pred. No.: 1.2e-224 Length: 2143
Score: 252.00 Matches: 252
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.57% Indels: 0
DB: 20 Gaps: 0

US-09-593-793A-113 (1-553) x AAV711180 (1-2143)

QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal 321
DB 3 CAGGGCGTCCAGAGCTGAGCGCGGACCGAGCGCGGAGACATATGATGAAGCGTT 62
QY 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
DB 63 CGGATGGGAGCGCTGGGCTGTCTCGAGTGCAGTCGCATCTCCTGCTCTCTGCTG 122
QY 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
DB 123 ATGGACCGGCTGGTGCAGCGATTTCGACATTCGAGCAGTCTATTGGCCAGTGGCAGCT 182
QY 362 PheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSer 381
DB 183 TTCCTGTGGCTGCGCGGCCACATGCTTCCTCCAGTGTGGCGTGGTGCAGCTTCA 242
QY 382 AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401
DB 243 GCGCGCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCTCCCTACACACTGGCCCTCC 302
QY 402 LeuTyrHisArgGluGlnValPheLeuProLysTyrArgGlyAspThrGlyAla 421
DB 303 CTCTACCAACGGGAGAGCAGGTGTCTCTGCCCAATACCGAGGGACACTGGAGGTGCT 362
QY 422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
DB 363 AGCAGTGGAGCAGCTGATGACAGCTTCTCCAGCGCCCTTAAGCCCTGAGCTCCCTTC 422
QY 442 ProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeuCys 461
DB 423 CCTAATGGACACGTGGTGTCTGGAGCAGTGCCTGCTCCCACTCCACCGCGCTCTGC 482
QY 462 GlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAlaArg 481
DB 483 GGGGCTCTGCTGTGATGTCTCCGTAGCTGTGTGGTGGTGGTGGTGGTGGTGGTGGT 542
QY 482 ValValProGlyArgGlyTleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501
DB 543 GTGGTTCGGGCGGGGATCTGCTGGACCTTCGCATCTCGGATGAGTGTCTCTGCTG 602
QY 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521
DB 603 TCCAGGTGGCCCATCTCTGTTATGGCTCCATTTGCTCCAGCTCAGCCAGCTGTCTACT 662
QY 522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 541
DB 663 GCCTATATGGTGTCTGCGCGAGCGCTGGGCTGTGGTGGTGGTGGTGGTGGTGGTGGT 722
QY 542 ValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 723 GTATTTGACAGAGCGACTTGGCCAAATACTCAGCG 758

RESULT 36

AAS64039
ID AAS64039 standard; cDNA: 2904 BP.

XX
AC AAS64039;

XX

DT 29-JAN-2002 (first entry)
XX Human prostate cDNA P553S splice variant #2.
XX Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.

XX Homo sapiens.

PN WO200173032-A2.

PD 04-OCT-2001.

PF 27-MAR-2001; 2001WO-US09919.

PR 27-MAR-2000; 2000US-0536857.

PR 09-MAY-2000; 2000US-0568100.

PR 12-MAY-2000; 2000US-0570737.

PR 13-JUN-2000; 2000US-0593793.

PR 27-JUN-2000; 2000US-0605783.

PR 10-AUG-2000; 2000US-0636215.

PR 26-SEP-2000; 2000US-0651236.

PR 02-OCT-2000; 2000US-0679426.

PR 10-OCT-2000; 2000US-0685166.

PA (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

PI Fangder GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;

PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;

XX WPI; 2001-639232/73.

PT New human prostate-specific polypeptides and polynucleotides useful for
the diagnosis and treatment of cancer, especially prostate cancer -
XX Claim 1; Page 482-483; 579pp; English.
CC The invention relates to isolated prostate-specific
polynucleotides, polypeptides, fusion proteins of the polypeptides,
antibodies raised against the polypeptides (or antigenic epitopes
derived from them) and antigen-presenting cells expressing the
polypeptides. The antibodies are useful for detecting the presence of
cancer, especially prostate cancer. The polypeptides, polynucleotides and
the antigen-presenting cells are useful for stimulating and/or expanding
T cells specific for a tumour protein, and for inhibiting the development
of cancer especially prostate cancer. Compositions comprising the
polynucleotide and/or polypeptide are useful for stimulating an immune
response, and for treating cancer. The oligonucleotide is useful for
detecting cancer. The present sequence is a prostate specific
polynucleotide of the invention.

XX SQ Sequence 2904 BP; 542 A; 875 C; 773 G; 714 T; 0 other;

Alignment Scores:

Pred. No.: 1.12e-208 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
DB: 22 Gaps: 0

US-09-593-793A-113 (1-553) x AAS64039 (1-2904)

QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338

DB 810 GAGGCGGTTCGATGGCAGCTGGGGCTGTCTGTGAGTGGCATCTCCTGTGCTTC 869

QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358

DB 870 TCTCTGGTATGGACCGGCTGGTGGCAGCATTCGGCATCTGAGCAGTCTATTTGGCCAGT 929

QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378

```
Db 930 GTGGCAGCTTCCCTGTGGCTCCGGTGCCACATGCTCTCCACAGTGTGGCCGTGGTG 989
Qy 379 ThrAlaSerAlaLeuThrGlyPheThrPheSerAlaLeuGlnLeuProTyrThr 398
Db 990 ACAGCTTACGGCGCCCTCACCGGGTTCACCTTCTCAGCCCTCAGATCTGCCCTACACA 1049
Qy 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 1050 CTGGCTCCCTCTACCACCGGAGAGCAGGTGTTCTTCCCAATACCGAGGGGACACT 1109
Qy 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 1110 GGAGGTGCTAGCAGTACGAGACACCTGTATGACAGCTTCTGCCAGCGCCCTAAGCCTGA 1169
Qy 439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProPro 458
Db 1170 GTCCTCTCCCTTAATGGACACGTGGGTGCTGGAGCAGTGGCTGCTCCACCTCCACCC 1229
Qy 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
Db 1230 GCGCTCTGGGGGCTCTGCTGCTGATGTCCTCGTACGTGTGTGGTGGTGAGCCACCC 1289
Qy 479 GluAlaArgValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 1290 GAGGCCAGGGTGTTCCTGGGGCGGGGCATCTGCTGGACCTGCGCATCTCGATAGTGCC 1349
Qy 499 PheLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 1350 TTCTCTGCTGCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTTGTCAGCTCAGCCAG 1409
Qy 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 1410 TCTGTCACTGCCTATATGTTGCTGCTCCGAGGCCCTGGGTCTGGTGGCCATTACTTGTCT 1469

RESULT 37
AAH93867
ID AAH93867 standard; cDNA; 2904 BP.
XX AC AAH93867;
XX DT 04-OCT-2001 (first entry)
XX DE P553S cDNA splice variant p553S-12.
XX KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
XX KW cytostatic; gene therapy; metastasis; ss.
XX OS Homo sapiens.
XX PN WO200151633-A2.
XX PD 19-JUL-2001.
XX PF 16-JAN-2001; 2001WO-US01574.
XX PR 14-JAN-2000; 2000US-0483672.
XX PA (CORI-) CORIXA CORP.
XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
XX PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
XX PI Wang A, Meagher MJ;
XX DR WPI; 2001-425873/45.
XX PT New polynucleotide encoding a prostate-specific protein, for
XX PT diagnosing, monitoring and treating prostate cancer in a patient and
XX PT for use in vaccines -
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XX Claim 1; Page 459-460; 543pp; English.
XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used to treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX SQ Sequence 2904 BP; 542 A; 875 C; 773 G; 714 T; 0 other;

Alignment Scores:
Pred. No.: 1,12e-208 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
DB: 22 Gaps: 0

US-09-593-793a-113 (1-553) x AAH93867 (1-2904)
Qy 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 810 GAGGCGCTTCGGATGGCAGCCTGGGGCTGTTCCTGTCAGTGGCCATCTCCCTGCTCTC 869
Qy 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 870 TCTCTGGTCATGGACCGGCTGGTGCAGCGATTTCGGCAGCTCGAGCAGTCTATTGGCCAGT 929
Qy 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 930 GTGGCAGCTTCCCTGTGGCTGCCGTGCCATGCTCTCCACAGTGTGCCCTGGTG 989
Qy 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 990 ACAGCTTACGGCGCCCTCACCGGGTTCACCTTCTCAGCCCTCAGATCTGCCCTACACA 1049
Qy 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 1050 CTGGCTCCCTCTACCACCGGAGAGCAGGTGTTCTTCCCAATACCGAGGGGACACT 1109
Qy 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 1110 GGAGGTGCTAGCAGTACGAGACACCTGTATGACAGCTTCTGCCAGCGCCCTAAGCCTGA 1169
Qy 439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProPro 458
Db 1170 GTCCTCTCCCTTAATGGACACGTGGGTGCTGGAGCAGTGGCTGCTCCACCTCCACCC 1229
Qy 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
Db 1230 GCGCTCTGGGGGCTCTGCTGCTGATGTCCTCGTACGTGTGTGGTGGTGAGCCACCC 1289
Qy 479 GluAlaArgValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 1290 GAGGCCAGGGTGTTCCTGGGGCGGGGCATCTGCTGGACCTGCGCATCTCGATAGTGCC 1349
Qy 499 PheLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 1350 TTCTCTGCTGCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTTGTCAGCTCAGCCAG 1409
Qy 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 1410 TCTGTCACTGCCTATATGTTGCTGCTCCGAGGCCCTGGGTCTGGTGGCCATTACTTGTCT 1469
```

QY 539 ThrGlnValPheAspTyrSerLeuAlaLysTyrSerAla 553
|||||
Db 1470 ACACAGGTAGTATTGACAAAGCGACTTGGCCAAATACTACGCG 1514

RESULT 38

ABL95410
ID ABL95410 standard; cDNA; 2904 BP.

AC ABL95410;

DT 19-JUL-2002 (first entry)

XX Human P553S splice variant SEQ ID NO 703.

XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;

KW gene therapy; gene; ss.

XX Homo sapiens.

OS US200202248-A1.

PN 21-FEB-2002.

XX 12-JAN-2001; 2001US-0759143.

XX 25-FEB-1997; 97US-0806099.

PR 01-AUG-1997; 97US-0904804.

PR 09-FEB-1998; 98US-0020956.

PR 23-FEB-1998; 98US-0030607.

PR 14-JUL-1998; 98US-0115453.

PR 23-SEP-1998; 98US-0159812.

PR 15-JAN-1999; 99US-0232149.

PR 09-APR-1999; 99US-0288946.

PR 13-JUL-1999; 99US-0352616.

PR 18-NOV-1999; 99US-0439313.

PR 12-NOV-1999; 99US-0443686.

PR 14-JAN-2000; 2000US-0483672.

PR 27-MAR-2000; 2000US-0536857.

PR 09-MAY-2000; 2000US-0568100.

PR 12-MAY-2000; 2000US-0570737.

PR 13-JUN-2000; 2000US-0593793.

PR 27-JUN-2000; 2000US-0605783.

PR 10-AUG-2000; 2000US-0636215.

PR 29-AUG-2000; 2000US-0651236.

PR 06-SEP-2000; 2000US-0657279.

PR 02-OCT-2000; 2000US-0679426.

PR 10-OCT-2000; 2000US-0685166.

XX (XUJ/) XU J.

PA (DILL/) DILLON D C.

PA (MITC/) MITCHAM J L.

PA (HARL/) HARLOCKER S L.

PA (JIAN/) JIANG Y.

PA (KALO/) KALOS M D.

PA (FANG/) FANGER G R.

PA (RETT/) RETTER M W.

PA (STOL/) STOLK J A.

PA (DAYC/) DAY C H.

PA (VEDV/) VEDVICK T S.

PA (CART/) CARTER D.

PA (LISX/) LI S X.

PA (WANG/) WANG A.

PA (SKEI/) SKEIKY Y A W.

PA (HEPL/) HEPLER W T.

PA (HEND/) HENDERSON R A.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;

PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;

XX WPI; 2002-255649/30.

XX

PT New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer
XX
XX
PS Claim 1; SEQ ID NO 703; 87pp; English.
XX
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
SQ Sequence 2904 BP; 542 A; 875 C; 773 G; 714 T; 0 other;

Alignment Scores:

Pred. No.: 1-12e-208 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
DB: 24 Gaps: 0

US-09-593-793A-113 (1-553) x ABL95410 (1-2904)

QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
|||||
Db 810 GAGGGCGTTCCGATGGCAGCGCTGGGCTGTTCTCGAGTGGCCATCTCCCTGGTCTTC 869
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
|||||
Db 870 TCTCTGGTCATGACCGCTGGTGGCAGCATTCGGCAGCTCGAGCAGCTATTATGGCCAGT 929
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
|||||
Db 930 GTGGCAGCTTCCCTGTGGCTGCCGTGCCACATGCTGCTCCACAGTGTGGCCGTGGTG 989
QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
|||||
Db 990 ACAGCTTTCAGCGCCCTACCCTCCGCTTCTCAGCTTCTCAGCTTCTGCGCTTACACA 1049
QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
|||||
Db 1050 CTGGCCCTCCCTTACCACCGGAGAGCAGGTGTTCTCCCAAAATACCGAGGGGACACT 1109
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
|||||
Db 1110 GGAGGTGCTAGCAGTGGAGCAGCAGCTGATGACAGCTTCTGCCAGGCCCTAAGCCTGGA 1169
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
|||||
Db 1170 GCTCCCTTCCCTAAATGGACACGTTGGTGTGGAGGAGTGGCTGCTCCACCTCCACCC 1229
QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr 478
|||||
Db 1230 GCGCTCTGCGGGGCTCTGCTGCTGATGCTCCGTACGTGTGGTGGGTGGGTGAGCCACC 1289
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
|||||
Db 1290 GAGGCCAGGGTGGTCCGGCCGGGGCATCTGCTGGACCTGCCATCTCGCATAGTGGC 1349
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
|||||
Db 1350 TTCTCTGCTGTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTTGCCAGCTCAGCCAG 1409
QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
|||||
Db 1410 TCTGTACCTGCTATATGTTGTTCTGCCGAGGCGCTGGTGTGGTGGTGGTGGTGGTGGT 1469
QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||
Db 1470 ACACAGGTAGTATTGACAAAGCGACTTGGCCAAATACTACGCG 1514
RESULT 39
AAZ45677

ID AA245677 standard; cDNA; 2462 BP.
XX AA245677;
XX
XX 06-APR-2000 (first entry)
XX cDNA sequence of a novel prostate cancer-associated gene.
XX
XX prostate cancer-associated gene; Incyte clone 1864683; bone cancer;
KW cell proliferation; cancer; adrenal gland cancer; bladder cancer;
KW prostate cancer; ss.
XX Homo sapiens.
XX
XX Location/Qualifiers
FH 376..1071
FT /*tag= a
FT /product= "prostate cancer-associated protein"
FT sig_peptide 376..516
FT /*tag= b
XX
XX W09967384-A2.
XX
XX 29-DEC-1999.
XX
XX 15-JUN-1999; 99WO-US13524.
XX
XX 22-JUN-1998; 98US-0102615.
XX (INCY-) INCYTE PHARM INC.
XX
XX Walker MG, Volkmath W, Klingler TM, Sprinzak EA;
XX
XX WPI: 2000-126631/11.
DR P-PSDB; AAY54369.
XX
XX Identifying biomolecules for the diagnosis and treatment of diseases
PT associated with cell-proliferation -
XX
XX Claim 8; Page 47-48; 52pp; English.
XX
XX The present sequence is derived from a prostate cancer-associated
CC gene, and is represented by Incyte clone number 1864683. The sequence
CC is used in the method of the invention. The specification
CC describes a method for identifying biomolecules for the diagnosis or
CC treatment of diseases associated with cell proliferation. The method
CC comprises examining polynucleotides, consisting of prostate cancer-
CC specific genes, and genes of unknown function, expressed in cDNA
CC libraries. The patterns of both gene sets are compared to identify
CC genes of unknown function with similar expression patterns to the
CC prostate cancer-specific genes. The biomolecules identified by the
CC method form pharmaceutical compositions useful for the diagnosis and
CC treatment of diseases associated with cell proliferation. Such diseases
CC include cancer of the adrenal gland, bladder and bone, but especially
CC prostate cancer. The method may also be applied using other disease-
CC specific genes. The prostate cancer-specific genes facilitate the
CC diagnosis and treatment of cell proliferation disorders.
XX
SQ Sequence 2462 BP; 483 A; 726 C; 632 G; 621 T; 0 other;

Alignment Scores:
Pred. No.: 1-6e-184 Length: 2462
Score: 209.00 Matches: 209
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 37.79% Indels: 0
DB: 21 Gaps: 0

US-09-593-793A-113 (1-553) x AA245677 (1-2462)

Qy 320 GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSer 339
Db 367 GCGGTTCGATGGGCGAGCTGGGGCTGTCTCTGCAGTGGCCATCTCCCTGGTCTCTCT 426

Qy 340 LeuValMetAspArgLeuValGlnArgPheGlyThrAspAlaValThrLeuAlaSerVal 359
|||||
Db 427 CTGGTCATGGACCGCTGGTGCAGCGATTGGCACTCAGCAGTCTATTGGCCAGTGTG 486
|||||
Qy 360 AlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThr 379
|||||
Db 487 GCAGCTTTCCCTGTGGCTGCCGTGCCACATGCCCTGTCCACAGTGTGCCGTGTGTGACA 546
|||||
Qy 380 AlaSerAlaIleLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeu 399
|||||
Db 547 GCTTCAGCGCGCCCTCACCGGTTTCACTTCTCAGCCCTGCAGATCCTCCCTACACACTG 606
|||||
Qy 400 AlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGly 419
|||||
Db 607 GCCTCCCTCTACCACCGGAGAGCAGGTGTCTCTGCCCAATACCGAGGGGACACTGGA 666
|||||
Qy 420 GlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAla 439
|||||
Db 667 GGTGCTAGCAGTAGGACAGCCTGATGACAGCTTCTCTGCCAGGCCCTTAAGCCTGGAGCT 726
|||||
Qy 440 ProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAla 459
|||||
Db 727 CCTTCCCTAATGGACACGTGGTGTCTGGAGGCAAGTGCCCTGCTCCACCTCCACCCCGC 786
|||||
Qy 460 LeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGlu 479
|||||
Db 787 CTCTCGGGGGCTCTGCTGTGTGTCTCCGTACGTGTGGTGGTGGTGGTGGTGGTGGTGG 846
|||||
Qy 480 AlaArgValValProGlyValArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPhe 499
|||||
Db 847 GCCAGGGTGGTTCGGGGCGGGGCATCTGCCTGGACCTGCCATCCTGGATAGTGCCTTC 906
|||||
Qy 500 LeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSer 519
|||||
Db 907 CTGCTGTCCAGTGGCCCATCCCTGTTTATGGCTCCTATGTGGCTCCTATGTCCAGCTCAGCAGCTCT 966
|||||
Qy 520 ValThrAlaTyrMetValSerAlaAla 528
|||||
Db 967 GTCACCTGCTATATGGTGTGTGCTGCCGCA 993
|||||
RESULT 40
ABN81320
ID ABN81320 standard; cDNA; 3663 BP.
XX
AC ABN81320;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human mast cell related gene MC14 SEQ ID NO 3.
XX
KW Human; mast cell; MC; antiallergic; antiinflammatory; antiasthmatic;
KW vasotrophic; dermatological; allergy; hypersensitivity; rhinitis; asthma;
KW gene; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 294..746
FT CDS /*tag= a
FT /*product= "MC14-1"
FT 1238..2218
FT /*tag= a
FT /*product= "MC14-2"
XX
XX W0200246389-A2.
XX
XX 13-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US46180.
XX
XX 08-DEC-2000; 2000US-251835P.
PR 14-MAR-2001; 2001US-275479P.
PR

Db 12 GCACGTGGCAGCTTCCCTGTGGCTGGCGGTGCCACATGCTGTCCACACAGTGTGGCC 71
QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396
Db 72 GTGGTGACAGCTTCAGCCGCCCTCACCAGGGTTCACCTTCTCAGCCCTGCAGATCCTGCC 131
QY 397 TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly 416
Db 132 TACACACTGGCCTCCCTCTACACCGGGAGAGCAGGTCTTCTGCCCAAATACCGAGGG 191
QY 417 AspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
Db 192 GACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACACAGCTTCTGCGCAGGCCCTAAG 251
QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro 456
Db 252 CCTGGAGCTCCCTTCCCTAATGACACGTGGGTGCTGGAGGAGTGGCTGTCCACCT 311
QY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476
Db 312 CCACCGCGCTCTGGGGGCTCTGCCTGTGATGCTCCGTACGTGTGGTGGGTGAG 371
QY 477 ProThr 478
Db 372 CCCACC 377
RESULT 42
AAV58487
ID AAV58487 standard; cDNA; 789 BP.
XX
AC AAV58487;
XX
DT 08-DEC-1998 (first entry)
XX
DE 3' fragment of prostate tumour specific gene L1-12.
XX
KW Prostate tumour specific gene; human; prostate cancer; detection;
KW therapy; ss.
XX
OS Homo sapiens.
XX
PN WO9837418-A2.
XX
PD 27-AUG-1998.
XX
PF 25-FEB-1998; 98WO-US03690.
XX
PR 09-FEB-1998; 98US-0904809.
PR 25-FEB-1997; 97US-080596.
PR 01-AUG-1997; 97US-0904809.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Xu J;
XX
DR WPI; 1998-480805/41.
XX
PT Novel human prostate specific tumour protein and fragments - useful
PT for detecting and treating prostate cancers
XX
PS Claim 1; Page 39; 141pp; English.
XX
CC This sequence represents a human prostate tumour specific gene, and can
CC be used in the method of the invention. The method is for detecting
CC prostate cancer comprises contacting a biological sample with an agent
CC able to bind an immunogenic portion of a prostate protein (such as
CC encoded by this sequence). An antibody which binds to an immunogenic
CC portion of the prostate protein, and the method can be used to detect,
CC monitor progression of, or treat prostate cancers. The antibody may
CC also be conjugated to a therapeutic agent for use in therapy of prostate
XX cancers.

SQ Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;
Alignment Scores:
Pred. No.: 6.07e-104 Length: 789
Score: 122.00 Matches: 122
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 22.06% Indels: 0
DB: 19 Gaps: 0
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QY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376
Db 12 GCACGTGGCAGCTTCCCTGTGGCTGGCGGTGCCACATGCTGTCCACACAGTGTGGCC 71
QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396
Db 72 GTGGTGACAGCTTCAGCCGCCCTCACCAGGGTTCACCTTCTCAGCCCTGCAGATCCTGCC 131
QY 397 TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly 416
Db 132 TACACACTGGCCTCCCTCTACACCGGGAGAGCAGGTGTCTGCCCAAATACCGAGGG 191
QY 417 AspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
Db 192 GACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACACAGCTTCTGCGCAGGCCCTAAG 251
QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro 456
Db 252 CCTGGAGCTCCCTTCCCTAATGACACGTGGGTGCTGGAGGAGTGGCTGTCCACCT 311
QY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476
Db 312 CCACCGCGCTCTGGGGGCTCTGCCTGTGATGCTCCGTACGTGTGGTGGGTGAG 371
QY 477 ProThr 478
Db 372 CCCACC 377
RESULT 43
AAA06250
ID AAA06250 standard; cDNA; 789 BP.
XX
AC AAA06250;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:10.
XX
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200004149-A2.
XX
PD 27-JAN-2000.
XX
PF 14-JUL-1999; 99WO-US15838.
XX
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 98US-0159822.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Harlocker SL, Yuqiu J, Xu J, Mitcham JL;
XX

DR WPI; 2000-171268/15.
 XX
 PT New polypeptide useful for treating and diagnosing prostate cancer
 PT comprises an immunogenic portion of prostate tumor protein
 XX
 PS Claim 1; Page 99; 263pp; English.
 XX
 CC The present invention describes isolated polypeptides, comprising an
 CC immunogenic portion of a prostate tumor protein (PTP). The polypeptides
 CC and polynucleotides encoding them have cytostatic activity and can be
 CC used in vaccines and in gene therapy. The polypeptides and
 CC polynucleotides encoding them, antigen presenting cells which express
 CC the polypeptides, antibodies against the polypeptides and vaccines
 CC comprising them can be used for inhibiting the development of prostate
 CC cancer in a patient. The polypeptides can be used to generate antibodies
 CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
 CC the polynucleotides encoding the polypeptides can be used as a probe or
 CC to modulate the expression of the polypeptides. AA06241 to AA06691 and
 CC AA082000 to AA082020 represent sequences used in the exemplification of
 CC the present invention.
 XX
 SQ Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;
 Alignment Scores:
 Pred. No.: 6,07e-104 Length: 789
 Score: 122.00 Matches: 122
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 22.06% Indels: 0
 DB: 21 Gaps:
 US-09-593-793a-113 (1-553) x AA06250 (1-789)
 QY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376
 DB 12 GCCAGTGTGGCAGCTTCCCTGTCGCTGCCGGTGCCACATGCTGTCCACAGTGTGGCC 71
 QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnLeuPro 396
 DB 72 GTGGTGACAGCTTCACGCCCTCACCGGGTTCACCTTCAGCCCTGCAGATCCTGCC 131
 QY 397 TyrThrLeuAlaSerLeuTyHisArgGluLysGlnValPheLeuProLysTyArgGly 416
 DB 132 TACACACTGGCTCCCTCTACCCACCGGGAGACAGAGTGTCTCTGCCCAATACCGAGG 191
 QY 417 AspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
 DB 192 GACACTGGAGGTGCTAGCAGTACGACACCTGTGATGATGCTCCGTACGTGTGGTGGTGAG 251
 QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro 456
 DB 252 CCTGGAGCTCCCTTCCTAATGGACACGTGGTGTGGAGGAGTGGCTGTCCACCT 311
 QY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476
 DB 312 CCACCGCGCTCTGGGGGCTCTGCTGTGATGCTCCGTGTGATGCTCCGTGTGGTGGTGAG 371
 QY 477 ProThr 478
 DB 372 CCCACC 377
 RESULT 44
 ID AAS63458
 XX AAS63458 standard; cDNA; 789 BP.
 XX
 AC AAS63458;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Human prostate cDNA sequence #10.
 XX
 KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
 XX

OS Homo sapiens.
 XX
 PN WO200173032-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US09919.
 XX
 PR 27-MAR-2000; 2000US-0536857.
 PR 09-MAY-2000; 2000US-0568100.
 PR 12-MAY-2000; 2000US-0570737.
 PR 13-JUN-2000; 2000US-0593793.
 PR 27-JUN-2000; 2000US-0605783.
 PR 10-AUG-2000; 2000US-0636215.
 PR 29-AUG-2000; 2000US-0651236.
 PR 06-SEP-2000; 2000US-0657279.
 PR 02-OCT-2000; 2000US-0679426.
 PR 10-OCT-2000; 2000US-0685166.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
 XX
 DR WPI; 2001-639232/73.
 XX
 PT New human prostate-specific polypeptides and polynucleotides useful for
 PT the diagnosis and treatment of cancer, especially prostate cancer -
 XX
 PS Claim 1; Page 232-233; 579pp; English.
 XX
 CC The invention relates to isolated prostate-specific
 CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
 CC antibodies raised against the polypeptides (or antigenic epitopes
 CC derived from them) and antigen-presenting cells expressing the
 CC polypeptides. The antibodies are useful for detecting the presence of
 CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
 CC the antigen-presenting cells are useful for stimulating and/or expanding
 CC T cells specific for a tumour protein, and for inhibiting the development
 CC of cancer especially prostate cancer. Compositions comprising the
 CC polynucleotide and/or polypeptide are useful for stimulating an immune
 CC response, and for treating cancer. The oligonucleotide is useful for
 CC detecting cancer. The present sequence is a prostate specific
 CC polynucleotide of the invention.
 SQ Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;
 Alignment Scores:
 Pred. No.: 6,07e-104 Length: 789
 Score: 122.00 Matches: 122
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 22.06% Indels: 0
 DB: 22 Gaps:
 US-09-593-793a-113 (1-553) x AAS63458 (1-789)
 QY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376
 DB 12 GCCAGTGTGGCAGCTTCCCTGTCGCTGCCGGTGCCACATGCTGTCCACAGTGTGGCC 71
 QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnLeuPro 396
 DB 72 GTGGTGACAGCTTCACGCCCTCACCGGGTTCACCTTCAGCCCTGCAGATCCTGCC 131
 QY 397 TyrThrLeuAlaSerLeuTyHisArgGluLysGlnValPheLeuProLysTyArgGly 416
 DB 132 TACACACTGGCTCCCTCTACCCACCGGGAGACAGAGTGTCTCTGCCCAATACCGAGG 191
 QY 417 AspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
 DB 192 GACACTGGAGGTGCTAGCAGTACGACACCTGTGATGATGCTCCGTACGTGTGGTGGTGAG 251


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OY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProPro 456
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Db 252 CCTGGAGCTCCCTTCCCTAATGGACACGCTGGGTGCTGGAGGAGTGGCTGCCACCT 311
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OY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476
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Db 312 CCACCCGGGCTCTGGGGGCTCTCCCTGTGATGTCCTCGGTACGTTGGTGGGTGAG 371
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OY 477 ProThr 478
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Db 372 CCCACC 377

RESULT 45
AAS10009
ID AAS10009 standard; cDNA; 789 Bp.
XX
AC AAS10009;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human prostate tumour cDNA L1-12 #1.
XX
KW Human; prostate tumour protein; prostate cancer; ss.
XX
OS Homo sapiens.
XX
PN US6262245-B1.
XX
PD 17-JUL-2001.
XX
PF 25-FEB-1998; 98US-0030607.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC;
XX
DR WPI; 2001-440862/47.
XX
PT Novel polynucleotide encoding polypeptide comprising a portion of
PT prostate tumour protein useful for inhibiting development of prostate
PT cancer or for treating prostate cancer in a patient
XX
PS Example 1; Column 32-33; 105pp; English.
XX
CC The sequence is a human prostate tumour cDNA which encodes a
CC partial tumour protein. The DNA is useful for inhibiting the development
CC of prostate cancer or for treating prostate cancer in a patient.
XX
SQ Sequence 789 Bp; 122 A; 250 C; 221 G; 182 T; 14 other;

Alignment Scores:
Pred. No.: 6.07e-104 Length: 789
Score: 122.00 Matches: 122
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.06% Indels: 0
DB: 22 Gaps: 0

US-09-593-793a-113 (1-553) x AAS10009 (1-789)

OY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376
|||||
Db 12 GCCAGTGTGGCAGCTTTCCTGTGGCTGCCGTGCCACATGCGCTGCCACAGTGTGGCC 71
|||||
OY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396
|||||
Db 72 GTGGTGACAGCTTACGCCGCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCC 131
|||||
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```
OY 397 TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly 416
|||||
Db 132 TACACACTGGCCTCCCTCTATCCACCGGGAGAGCAGGTGTTCTGCCCAATAACCGAGGG 191
|||||
OY 417 AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
|||||
Db 192 GACACTGGAGGTGCTAGCAGTGAAGACAGCCTGATGACAGCTTCTGCCAGGCCCTAAG 251
|||||
OY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProPro 456
|||||
Db 252 CCTGGAGCTCCCTTCCCTAATGGACACGCTGGGTGCTGGAGGAGTGGCTGCCACCT 311
|||||
OY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476
|||||
Db 312 CCACCCGGGCTCTGGGGGCTCTCCCTGTGATGTCCTCGGTACGTTGGTGGGTGAG 371
|||||
OY 477 ProThr 478
|||||
Db 372 CCCACC 377
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Search completed: February 19, 2003, 05:19:27
Job time : 306 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 05:11:24 ; Search time 53 Seconds

(without alignments)

3199.854 Million cell updates/sec

Title: US-09-593-793A-113

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Yqapop 60.0 , Yqapext 60.0

Fgapop 6.0 , Fgapext 7.0

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Searched: 441362 seqs, 153338381 residues

Word size: 3

Total number of hits satisfying chosen parameters: 706526

Minimum DB seq length: 0

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Post-processing: Listing first 100 summaries

Command line parameters:

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-NO_XIPYX -NO_MMAB -IABCFQUERY -NEC_SCORES=0 -WAIT -LONGCOC -DEV_TIMECOUT=120
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	553	100.0	3410	4	US-09-030-607-110	Sequence 110, App
3	553	100.0	3410	4	US-09-605-785-110	Sequence 110, App
4	553	100.0	3410	4	US-09-439-313-110	Sequence 110, App
5	553	100.0	3410	4	US-09-352-616A-110	Sequence 110, App
6	553	100.0	3410	4	US-09-602-877A-100	Sequence 100, App
7	553	100.0	3410	4	US-09-233-149A-110	Sequence 110, App
8	320	57.9	4034	4	US-09-605-785-704	Sequence 704, App
9	263	47.6	4894	4	US-09-605-785-702	Sequence 702, App
10	283	47.6	6976	4	US-09-603-785-705	Sequence 705, App
11	255	46.1	2152	3	US-09-071-710-16	Sequence 16, Appl
12	255	46.1	2152	4	US-09-525-397-16	Sequence 16, Appl

Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 2, Appli
Sequence 1, Appli
Sequence 36, Appl
Sequence 485, App
Sequence 485, App
Sequence 20, Appl
Sequence 20, Appl

100 7 1.3 46 1 US-08-794-153-20

ALIGNMENTS

RESULT 1

US-09-020-956-110

: Sequence 110, Application US/09020956

: Patent No 6261562

: GENERAL INFORMATION:

: APPLICANT: Xu, Jiangchun

: APPLICANT: Dilllin, Davin C.

: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO

: NUMBER OF SEQUENCES: 178

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: SEED AND BERRY LLP

: STREET: 6300 Columbia Center, 701 Fifth Avenue

: CITY: Seattle

: STATE: WA

: COUNTRY: USA

: ZIP: 98104

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patentin Release #1.0, Version #1.30

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/09/020,956

: FILING DATE: 09-FEB-1998

: CLASSIFICATION:

: ATTORNEY/AGENT INFORMATION:

: NAME: Maki, David J.

: REGISTRATION NUMBER: 31,392

: REFERENCE/DOCKET NUMBER: 210121.427C2

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (206) 622-4900

: TELEFAX: (206) 682-6031

: INFORMATION FOR SEQ ID NO: 110:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 3410 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: single

: TOPOLOGY: linear

: MOLECULE TYPE: cDNA

: ORIGINAL SOURCE:

: ORGANISM: Homo sapiens

US-09-020-956-110

Alignment Scores:

Pred. No.: 0 Length: 3410

Score: 553.00 Matches: 553

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-020-956-110 (1-3410)

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284 ATGGTCCAGAGCTGTGGGTGAGCGCCCTGCTGCGGCACCGGAAAGCCAGCTCTTGTGCG 343

Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40

344 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTGGCCGAGGCATCACCTATGTGCGG 403

Qy 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60

404 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGCTGTGGCATTTGCT 463

Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80

464 CCAAGTCTGGGGCTGTGCTGCTCCGCTCCTAGAGCTCAGCCAGTGCACCATGGGGTGA 523

Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100

524 CGCTATGGCCCGCCCGCCCTTCATCTGGGCACCTGCTCTGGGCATCTCTGCTGAGCCCTC 583

Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120

584 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGCTGCTGTGCCGATCCAGGCCCTG 643

Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140

644 GAGCTGGCACTGCTCATCTCTGGGCGCTGGGCTGCTGGACTTCTGTGCCAGGTGTCTTC 703

Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160

704 ACTCACCTGGAGGCTGCTCTGCTGACCTTCCGGGACCCGACACCTGTGCCAGGCT 763

Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180

764 TACTCTGCTATGCTTCATGATCAGTCTTGGGGCTGCTGGGTACCTCTGCTGCTGCC 823

Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200

824 ATTGACTGGGACACCAAGTGGCTTGGCCCTTACCTGGGCACCCAGGAGGTGCTCTTT 883

Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220

884 GGCTGCTCACCTCATCTTCTCCTCCTGCTGAGCAGCCACCTGCTGTGGTGGCTGAGGAG 943

Qy 221 AlaAlaLeuGlyProThrGluProAlaGluLeuSerAlaProSerLeuSerProHis 240

944 GCAGCCTGGGCCCCCACCAGCAGCAGAGAGGCTGTGCGCCCCCTCTCTGTGCGCCAC 1003

Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260

1004 TGCTGTCCATGCGCGCCGCTTGGCTTTCGGGAACCTGGGCGCCCTGCTTCCCGGCTG 1063

Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280

1064 CACCACTGTGCTGCGCATGCCCGCACCTGCGCGCGGCTCTCTGTGGCTGAGCTGTGC 1123

Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300

1124 AGCTGATGGCACTCATGACCTTACGCTGTTTACACGATTTCTGTGGCGAGGGGCTG 1183

Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320

1184 TACCAGGGCGTGGCAGAGCTGAGCGGCGACCCGAGGCCGCGGACACTATGATGAAGGC 1243

Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340

1244 GTTCGATGGGCGAGCTGGGGCTGTTCCTGAGCTGCGGCATCTCCCTGCTCTCTCTG 1303

Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360

1304 GTCATGGACCGCTGGTGCAGCGATTTCGCACTCGAGCAGTCTATTTGGCCAGTGTGGCA 1363

Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380

Db 1364 GCTTTCCCTGTGGCTGCCGATGCCATGCTGTCCACAGTGTGGCGTGTGCAGAGCT 1423
Qy 381 SerAlaLeuThrGlyPheThrPheSerAlaLeuGlnLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCCCTCACCGGTTACCTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1483
Qy 401 SerLeuTyrHisArgGlyLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCCTCTACCAACCGGAGAGCAGGTGTCTGTGCCCAATACCGAGGGGACACTGGAGT 1543
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTACAGTGGAGCAGCCTGTATGACCACTCTCCCTGCCAGGCCCTAAGCCTGGAGCTCC 1603
Qy 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCTATATGGACAGTGGGTGCTGGAGCAGTGGCTGTCTCCACCTCCACCCGGCTC 1663
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480
Db 1664 TGCGGGGCTCTGCCTGTGTATGCTCCGTACGTGTGGTGGTGAGCCACCGAGGCC 1723
Qy 481 ArgValValProGlyArgGlyLysCysLeuAspLeuAlaLeuAspSerAlaPheLeu 500
Db 1724 AGGCTGGTTCGGGGCGGGGCACTCTCCCTGGACCTCGCCATCCTGGATAGTGCCTTC 1783
Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCCAAGTGGCCCACTCCCTGTATATGGGCTCCATGTCCAGCTCAGCCAGTCTGTC 1843
Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGTGTCTGCCCGAGCCCTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1903
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTGTACAGAGCGACTTGGCCAAATACTCAGCG 1942

RESULT 2

US-09-030-607-110
; Sequence 110, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030.607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3410 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-607-110
Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-593-793a-113 (1-553) x US-09-030-607-110 (1-3410)
Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 284 ATGGTCCAGAGGCTGTGGGTGAGCCGCTGTCTGCGCACCGGAAAGCCAGCTCTTGCTG 343
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCGCAGGCATCACCTATGTGCG 403
Qy 41 ProLeuLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGTCTGGAAGTGGGGGTAGAGGAAAGTTTCATGACCATGGTGTGGGCATGTGT 463
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGGCTGTGTGTCTGCCGCTCTAGGCTCAGCCAGTACCACCTGGCGTGGA 523
Qy 81 ArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCCGCGCGGCGCTTCATCTGTGGCACTGTCTTGGGCACTCTCTGTGAGCCCTC 583
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGGCGGCTGGCTAGCAGGGCTGTGTGCGCGATCCAGGCCCTTG 643
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTCGGCGCTGGGGCTGTGGACTTCTGTGGCCAGGTGTCTTC 703
Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCGCTGCTCTTGACCTCTTCCGGGACCCGAGCACTGTGCCAGGCC 763
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTATATGCTTCATGATCAGTCTTGGGGGCTGTCTGGGCTTACCTCTGTGCTGCC 823
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 824 ATTGACTGGACACAGTGCCTTGGCCCTTACCTGGGACCCAGAGAGTGCCTCTTT 883
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGCTGTCTCACCTCATCTTCTCCTACCTGGGTAGCAGGCACACTGTGTGCTGAGGAG 943
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGCGCTGGGCCCCACCGAGCCAGCAAGGGCTGTGGGCCCCCTCTCTTGTGCGCCCCAC 1003
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATGCGGGCGCGCTTGGCTTCCGGAACTTGGGCGCCCTGCTTCCCGGGCTG 1063
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAAGTGTGTGCGCATGCCCCGACCCCTGCGCGGCTCTTCTGTGCTGAGCTGTGC 1123

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QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPheValGlyGluGlyLeu 300
DB 1124 AGCTGGATGGCACTCATGACCTTCAGCTGTTTACAGGATTCGTGGCGGAGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
DB 1184 TACCAGGGCGTCCAGAGCTGAGCCGGGACACGAGGGCCGGAGACACTATGATGAAGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
DB 1244 GTTCGGATGGCAGCTGGGGCTGTCTCCAGTGCGCCACTCTCCCTGGCTCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
DB 1304 GTCATGCGCGCTGTGCGAGGATTCGCGACCTCGAGCAGTCTATTTGGCCAGTGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
DB 1364 GCTTTCCCTGTGGCTGCCGGTGCACATGCCTGCCACAGTGTGCCGCTGGTGACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
DB 1424 TCAGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
DB 1484 TCCTCTACACACGGGAGAGCAGGTGTTCTCGCCCAATACGAGGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
DB 1544 GCTAGCAGTGAGACAGCTGATGACAGCTTCTGCCAGGCCCTAAGCCTGGAGCTCCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeu 460
DB 1604 TTTCCCTAATGGACACGTGGGTGCTGGAGCAGTGGGCTGCTCCACCTCCACCGCGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
DB 1664 TCGCGGGCTCTGCTGCTGATGTCCTCGTACGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
DB 1724 AGGGTGGTTCGGGGCGGGGATCTGCCCTGGACCTCGCCATCTGGATAGTGCCTTCCCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
DB 1784 CTGTCCAGGTGGCCCATCCCTGTTTATGGGTCCATTTGTCAGCTCAGCCAGTCTGTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
DB 1844 ACTGCCTATATGTGTCTGCCAGGCCCTGGGTCTGTGGTGGCCATTTACTTTGCTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 1904 GTAGTATTTGACAAGAGCAGCTTGGCCAAATACTCAGCG 1942

RESULT 3
US-09-605-785-110
: Sequence 110, Application US/09605785
: Patent No. 6321716
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yuqi
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
```

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: APPLICANT: Vedwick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.427C16
: CURRENT APPLICATION NUMBER: US/09/605,785
: CURRENT FILING DATE: 2000-06-27
: NUMBER OF SEQ ID NOS: 835
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 110
: LENGTH: 3410
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-605-785-110

Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-605-785-110 (1-3410)
QY 1 MetValGlnArgLeuTrpValSerArgLeuArgHisArgLysAlaGlnLeuLeu 20
DB 284 ATGGTCCAGAGGCTGTGGGTGAGCGCCCTGCTGGCGCACCGGAAAGCCAGCTCTTGCCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrValPro 40
DB 344 GTCAACCTCTAACCTTTGGCCTGGAGGTGTGTTGGCCGAGGCATCACCTATGTGCGG 403
QY 41 ProLeuLeuGluValGlyValGluLysPheMetThrMetValLeuGlyIleGly 60
DB 404 CTCTGCTGCTCGAAGTGGGGGTAGAGAGAGTTTCATCACCATGGTGTGGCATGTGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
DB 464 CCAGTGTCTGGCGTGTGTGTGTCGCCGCTCCCTAGGCTCAGCCAGTGCACCTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
DB 524 CGCTATGGCGCGCGCGCCCTTCATCTGGGCACTGTCTTGGGCATCTCTGTGACGCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
DB 584 TTTCTCATCCCAAGCGCGCTGGCTAGCAGGGCTGTCTGTCCCGGATCCAGGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
DB 644 GAGCTGGCACTGCTCATCTCTGGCGCTGGGCTGCTGGACTTCTGTGGCAGGTGTGCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
DB 704 ACTCAGCTGGAGGCCCTGTCTGTGACCTTCTCCGGGACCCGACACCTGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
DB 764 TACTCTGCTATGCCTTCATGATCAGTCTTGGGGCTGCTGGGTACCTCTGCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
DB 824 ATTGACTGGGACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
DB 884 GGCTGCTCACCTCATCTTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 943
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QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGGCGCTGGGCCCCACCAGGAGCAGAGAGGCTGTGCGCCCTCTCTGCGCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATGCGGGCGCGCTGTGCTTTCGGAAACCTGGGGCGCTCTCCCGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGCGCATGCGCCGACCTTGCAGCCCTTGCAGCGCTCTTGTGCTGAGTGGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrArgPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGATTTCTGCGGCGAGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCGTCCAGAGCTGAGCGGCGCACCGAGGCGCGGAGACACTATGATGAAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGCGAGCTGGGGCTGTCTCTGCGAGTGGCCATCTCCTGTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGGACCGCTGTGCGAGGATTCGGACACTCGAGCAGTCTATTGGCCAGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCCTGTGGCTGCGGGTGCACATGCTGTCTCCACAGTGTGGCGGTGACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCTCTACCAACCGGAGAGCAGGTGTCTCTGCCAAATACCGAGGGGACACTGGAGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProGlyAlaPro 440
Db 1544 GCTACAGTGGAGCAGCCTGTATGACCATCTCTCTGCCAGGCGCTTAAGCCTGGAGCTGCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProProAlaLeu 460
Db 1604 TTCCTATATGGACACTGGGTGCTGGAGCAGTGGCTGTCTCCACCTCCACCCCGGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480
Db 1664 TCGGGGCTCTGCGCTGTGATGCTCCGTACGTGTGGTGGTGAGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGGTGGTTCGGCGGCGGCGCATCGCTGGACCTTCGCCATCTCGGATAGTGCCTTCCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCCCCCATCTCTTTATGGCTCCATGTGCCAGTCCAGCCAGTCTGTG 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGTTGCTGCGCAGCGCTGGTCTGGTCTGGTCCGATTTACTTTGCTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTGTACAGAGGCACTTGGCCAAATACTCAGCG 1942
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RESULT 4

US-09-439-313-110

; Sequence 110, Application US/09439313

; Patent No. 6329505

; GENERAL INFORMATION:

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; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-110
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Alignment Scores:

Pred. No.:	0	Length:	3410
Score:	553.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-593-793A-113 (1-553) x US-09-439-313-110 (1-3410)

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QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
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QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGTCTAACCTTTGGCCTGGAGGTGTGTTGGCCGCGAGGCATCACCTATGTGCG 403
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAAGTTCATCACCATGGTGTCTGGCATTTGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGGCTGTGTGTCTGCCGCTCCTAGGCTCAGCCAGTGCAGCTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CCGTATGGCGCGCGCGCGCTTTCATCTGGGCACATGTCTTGGGCATCCTGCTGAGCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGCGCGCTGAGTGGCTAGCAGGCTGTCTGCCCGGATCCCGAGGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
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QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCGCTCTCTGACCTTTCGGGGACCGGACCTGTCTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
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QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
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QY 201 GlyLeuLeuThrLeuLeuLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
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Db 884 GGCTGCTGCACCTCATCTTCCCTACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
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Db 1064 CACCAGCTGTGCTGCCGATGCCCGCACCTTGGCGCGCTCTTCGTGGCTGAGCTGTGC 1123
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Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCTGTGGCGGAGGGCTG 1183
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Db 1184 TACCAGGGCTGCCAGAGCTGAGCGCGGACCGAGCCCGGAGACACTATGATGAAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
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QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValThrLeuAlaSerValAla 360
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Db 1304 GTCATGGACGGCTGTGTCAGCGATTTCGGCAGCTCGACAGCTATTTGGCCAGTGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
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Db 1364 GCTTTCCTGTGCTGCCGGTGCACATGCTGTGCCAGAGTGTGCCCGTGTGACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
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Db 1424 TCAGCGCGCTCACCGGGTTACCTTCTCAGCGCTGCAGATCTGCGCTTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
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Db 1484 TCCTCTACACCGGAGAGAGAGGTGTTCTCTGCCAAATACCGAGGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
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Db 1544 GCTAGCAGTGGAGACAGCTGATGACACAGCTTCTCTGCCAGGCGCTTAAGCTGGAGCTCC 1603
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QY 461 CysGlyAlaSerAlaCysaspValSerValArgValValValGlyGluProThrGluAla 480
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Db 1664 TCGGGGCTCTGCTGCTGTATGCTCTCCGTACGTGTGGTGTGGTGGAGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
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Db 1724 AGGGTGTTCGGGGCGGGGCATCTGCCCTGGACCTCGCCATCTCTGGATAGTGCCTTCCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
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Db 1784 CTGTCCAGGTGCCCCCATCTCTGTTTATGGGCTCCATGTTCCAGCTCAGCCAGTCTGTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
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Db 1844 ACTGCCATATGCTGTCTGCCGAGCCCTGGGTCTGGTGCCTTACTTTTGTCTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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Db 1904 GTAGTATTTGACAAGAGCAGCTTGGCCAAATACTACGC 1942
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RESULT 5
US-09-352-616A-110
: Sequence 110, Application US/09352616A
: Patent No. 6395278
: GENERAL INFORMATION:
: APPLICANT: Dillon, Davin C.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang, Yuhui
: APPLICANT: Xu, Jiangchun
: APPLICANT: Mitcham, Jennifer Lynn
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
: FILE REFERENCE: 210121.427CB
: CURRENT APPLICATION NUMBER: US/09/352,616A
: CURRENT FILING DATE: 1999-07-13
: NUMBER OF SEQ ID NOS: 472
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 110
: LENGTH: 3410
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-352-616A-110
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Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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US-09-593-793A-113 (1-553) x US-09-352-616A-110 (1-3410)

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QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
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Db 344 GTCAACCTCTTAACCTTTGGCCTGGAGGTGTGTTTGGCCGACAGCATCACCTATGTGCGG 403
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
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Db 404 CCTCTGCTGCTGGAAGTGGGGTGTAGAGAGAAATTCATGACCATGCTGTGGGCATTGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
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Db 464 CCAGTGTCTGGGCTGTGCTGTGTCCCGCTCTAGGCTCAGCCAGTACACACTGGCGGTGGA 523
QY 81 ArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
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Db 524 CGCTATGGCGCGCGCGCGCTTTCATCTGGGCACCTGCTTGGGCATCTGCTGAGCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
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Db 584 TTTCTCATCCCAAGCGCGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCGAGGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
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Db 644 GAGCTGGGCACTGCTCATCTGGCGGTGGGCTGTGAGACTTCTGTGGCCAGGTGTGCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
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Db 704 ACTCCACTGAGGCGCTGCTCTGACCTTTCGCGGACCCCGACCACTGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
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Db 764 TACTCTGTCTATGCTTTCATGATCATGCTGTGGGGGTGCTGTGGGTACCTCTGCTGCTGC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
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Db 824 ATTGACTGGGACACCACTGCTGCTTACCTGGCCCTTACCTGGGCGACCCAGGAGGTCTCTTT 883
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QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHIs 240
Db 944 GCAGCCTGGGCCCCACCAGGACGAGAGGCTGTCGGCCCTTCTTGGCCCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATCGCGGCCCGCTGGCTTCCGGAACCTGGCGCCCTGCTTCCCGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGTCGCGCATGCCCGCACCCCTGCGCGGCTCTTCTGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrArgPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTTCAGCTGTGTTTACACGGATTTCGTGGCCGAGGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGGTGCCAGAGCTGAGCGGACCGGAGCCCGGAGACACTATCATGAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGATGGGAGCCCTGGGGCTGTTCCTGCAGTGGCCCATCTCCCTGGCTTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGGACCGGCTGGTGCAGCGATTTCGGCACTCGAGCAGTCTATTGCGCCAGTGTGGA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCCTGTGGTCCCGGTCGCACATGCCCTGTCCACAGTGTGGCCGTGGTACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTFACACACTGGGC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCTCTACCAACCGGAGAGAGGTGTTCCTGCCCAATACCGAGGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
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QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TCGGGGCTCTGCTGTGATGTCCTGCTACGTGTGGTGTGGTGGTGGAGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGTGGTTCCGGGGCGGGGCACTGCTGGACCTTCTTCCAGCCATCTGGATAGTCCCTTC 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGCTGTGTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGGCTATATGCTGCTCCCGAGCCCTGGGTCTGGTGGCATTTACTTTCTCTACACAG 1903
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Db 1904 GTAGTATTTCACAGAGCCACTTGGCCAAATFACCTCAGCG 1942
RESULT 6
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US-09-602-877A-100
; Sequence 100, Application US/09602877A
; Patent No. 6432707
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.446C5
; CURRENT APPLICATION NUMBER: US/09/602,877A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-602-877A-100
Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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US-09-593-793A-113 (1-553) x US-09-602-877A-100 (1-3410)
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QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCGCGCAGGACATCACCTATGTGCG 403
QY 41 ProLeuLeuGluValGlyValGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGTAGAGAGAAGTTCAATGACCATGGTGTGGCGCATTTGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGGCTGTGCTGTCTCCGCTCTAGCTCAGCCAGTGACCCAGTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCCCTTCATCTGGGCACCTGTCTTGGGCATCTCTGTGAGCCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCATATCCCAAGGCGCGCTGGCTAGCAGGCTGTGTGCCCGGATCCCAGGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTCTCATCTCGGCGCTGGGGCTGTGGACTTCTGTGGCGAGGTGTCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
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QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
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QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 824 ATTGACTGGACACAGTGCCTTCCCTTACCTTGGGCACCCAGGAGGAGTGCCTCTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
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QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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Db 1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
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RESULT 7

US-09-232-149A-110

; Sequence 110, Application US/09232149A

; Patent No. 6465611

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; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-110
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Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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US-09-593-793A-113 (1-553) x US-09-232-149A-110 (1-3410)

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QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
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Db 344 GTCAACCTGCTAACCTTTGCGCTGGAGGTGTGTTGGCCGCGAGGCATCACCATTGTGCGG 403
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QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
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Db 404 CCTCTGCTGCTGAAGTGGGGTAGAGGAGAAGTTTCATGACCATGCTGCTGGGCATTGCT 463
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QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
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Db 464 CCAGTGTCTGGGCTGTGCTGTCCGCTCCTAGGCTCAGCCAGTACCATGGCGTGA 523
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QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
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Db 524 CGCTATGGCGCGCGCGCGCTTCATCTGGGCACACTGTCTTGGGCATCTCTGTGACCTC 583
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QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
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QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
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QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
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Db 704 ACTCCACTGGAGCGCTGCTCTTCACCTTTCGGGACCCCGAGCACACTGTGCCAGGCC 763
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QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
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QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
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Db 1004 TGCTGTCCATGCGGGCGCGCTTGCTTTCCGGAACCTTGGGCGCCCTGCTCCCGGCTG 1063
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGTGCGCATGCGCCGCCACCCCTGCGCGCTCTTCTGCTGAGCTGTC 1123
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrArgPheValGlyGluLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTCTTTACAGGATTCGTGGCGAGGGCTG 1183
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCGTCCAGAGCTGAGCGGGCCAGCGAGGCGGAGACATATGATGAAGC 1243
Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGCAGCTGGGGCTGTCTGTCAGTGGCCATCTCCCTGCTCTCTCTG 1303
Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGGACCGGCTGGTCACGCGATTCGCGACTCGAGCAGTCTATTGGCCAGTGGCA 1363
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
Db 1364 GCTTTCCTGTGGCTGCGGTCGCACATGCCCTGTCCACAGTGGCGGTGTGACAGCT 1423
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCCCTCACCGGCTTCACCTTCTCAGCCCTGCAGATCTTCCCTACACATGGCC 1483
Qy 401 SerLeuTyrHisArgGluGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCCTCTACCAACCGGAGAGAGAGGTGTCTCTGCCAAATACCGAGGGGACACTGGAGGT 1543
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
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Qy 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProProAlaLeu 460
Db 1604 TTCCCTAATGACACAGCTGGGTGCTGAGGACAGTGGCCCTGCCACCTCCACCCCGCTC 1663
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TCGGGGGCTCTGCGCTGTGATGTCCTCGTACGTGTGGTGGTGGTGGAGCCACCGAGGCC 1723
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Db 1724 AGGGTGGTTCGGGGCGGGGATCTGCTGACCTGCGCATCTCGGATAGTGGCTTCTCTG 1783
Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGGCCCATCCCTGTTTATGGCTCCATTGTCAGCTCAGCCAGCTCTCTC 1843
Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGGTGTCTGCGCGCAGGCTGGGTCTGTGGTGGCATTTACTTTGCTACACAG 1903
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTTGACAGAGCAGCTTGGCCAAATACTCAGCG 1942
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RESULT 8

US-09-605-785-704

; Sequence 704, Application US/09605785

; Patent No. 6321716

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

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; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605.785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-605-785-704
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Alignment Scores:
Pred. No.: 1.53e-300 Length: 4034
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 4 Gaps: 0
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US-09-593-793A-113 (1-553) x US-09-605-785-704 (1-4034)

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Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 281 ATGGTCCAGAGCTGTGGGTGAGCGCGCTGCTGGCGCACCGGAAAGCCAGCTCTTGCTG 340
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 341 GTCAACCTGCTAACCTTTGGCTGGAGCTGTCTTTGGCGCGAGGCATCACCTATGTGCGC 400
Qy 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 401 CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAAGTTTCATGACCATGTGTGCTGGGCATTGGT 460
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 461 CCAGTGTGGGCTGGTCTGTGTCCCGCTCTAGGCTCAGCAGTACCATCTGCGCTGGA 520
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 521 CGCTATGSCCGCGCGCGCCCTTCATCTGGCACCTGTCTTGGGCATCTCTGCTGAGCCTC 580
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTCTCATCCCAAGGGCGGCTGGCTAGCAGGGCTGTCTGTGCCCGGATCCCGAGGCCCTG 640
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 641 GAGCTGGCACCTGCTCATCTGGGCTGGGCTGTCTGGGACTTCTGTGGCCAGGTGTGCTTC 700
Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGACCGGACCACCTGTCTGCCAGCC 760
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 761 TACTCTGTCTATGCTTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCTGCTGCTGCC 820
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; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-605-785-705

Alignment Scores:
Pred. No.: 5,22e-245 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 4 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-605-785-705 (1-6976)

QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
DB 1202 GGCATTGGTCCAGTGTGGCGCTGTCTGTCTCCCGCTCAGTGGCTCAGCCAGTACCAC 1261

QY 78 TrpArgGlyArgTrpGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
DB 1262 TGGGTGGACGATGGCGCGCCGCCGCTTCATCTGGGCACGTCTTGGGCATCCTG 1321

QY 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
DB 1322 CTGAGCCTCTTCTCATCCCAAGGCGCGCTGGCTAGCAGCGCTGCTGCCGGATCCC 1381

QY 118 ArgProLeuLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
DB 1382 AGGCCCTCGAGCTGGCACTGCTCATCTCTGGCGTGGCGCTGCTGAGCTCTCTGGCCAG 1441

QY 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
DB 1442 GTGTGCTTCACCTCCACTGGAGGCGCTGCTCTGACCTCTCCGGGACCCGGACCACTGT 1501

QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
DB 1502 CGCCAGGCTACTCTCTATGCCCTCATGATCAGTCTTGGGGCTGCTGGGCTACCTC 1561

QY 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
DB 1562 CTGCGCTGCATTGACTGGGACACCACTGCTGCTGGCGCTGGCGCTGCTGGCAGGAG 1621

QY 198 CysLeuPheGlyLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
DB 1622 TGCCCTTTGGGCTGCTCACCCTCATCTTCTCACCCTGCGTAGCAGCCACACTGCTGGTG 1681

QY 218 AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
DB 1682 GCTGAGGAGCAGCGCTGGGCCCCCAGCAGCAGCAGAGGGCTGTGCGCCCCCTCTTG 1741

QY 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
DB 1742 TCGCCCCACTGTGTCCATGCGGGCGCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTT 1801

QY 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277
DB 1802 CCGCGGCTGCACAGCTGTGCTGCGGCATGCCCCCAGCCACCTGCGCGGCTCTTCGTGGCT 1861
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QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
DB 1862 GAGCTGTGCAGCTGGATGCGCACTCATGACCTTCACGCTGTTTTACACGAGATTCGTGGGC 1921

QY 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
DB 1922 GAGGCGCTGTACAGGGCGTGGCCAGAGCTGAGCGCGCACCGAGCGCCGAGACACTAT 1981

QY 318 AspGluGly 320
DB 1982 GATGAAGGT 1990

RESULT 11
US-09-071-710-16
; Sequence 16, Application US/09071710
; Patent No. 6130043
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/850,713
; FILING DATE: 02-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2152 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-710-16

Alignment Scores:
Pred. No.: 9,36e-238 Length: 2152
Score: 255.00 Matches: 255
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 46.11% Indels: 0
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DB: 3 Gaps: 0
US-09-593-793a-113 (1-553) x US-09-071-710-16 (1-2152)
QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrCluAlaArgHisTyrAsp 318
Db 2 GGGCTGTACAGGGCGTGGCCAGAGTGGAGCGGGGACCGAGCGCCGAGACACTATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGGGCTTCGGATGGGCGGTTCCTCGAGTGGCCCATCTCCCTGGTCTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGTGTATGACCGGCTGGTGCAGCGATTCCGACATCGGCGGCGGAGTATTTGGCCAGT 181
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 182 GTGGCAGCTTCCTCTGGCTGGCGGTGCACATGCTGCCACAGTGTGGCGGTGGTG 241
QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 242 ACAGCTTACAGCGCCCTCAGCGGTTCCACTTCTCAGCGCTGCAGATCTCGCCCTACACA 301
QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 302 CTGGCCTCCCTCTACCCACCGGAGAGCAGGTGTCTGCCAAATACCGAGGGGACACT 361
QY 419 GlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 362 GGAGGTGCTAGCAGTGGAGACGCTGATGACAGCTTCTGCCAGCGCCCTAAGCCTGGA 421
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 422 GCTCCCTTCCCTAATGGACAGTGGGTGCTGGAGGAGTGGCTGTCCACCTCCACCC 481
QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValGlyValValGlyGluProThr 478
Db 482 GCCTCTGCGGGGCTCTGCTGTGTATGCTCGGTACGTGTGGTGGGTGAGCCACC 541
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 542 GAGCGCAGGTGTGTCGGGCGGGGATCTGCTCGGAGCTCGCCATCTCGGATAGTGC 601
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetClySerIleValGlnLeuSerGln 518
Db 602 TTCTGCTGCTCCAGGTGGCCCATCCCTGTTATGGGCTCCATTGTCCAGCTCAGCCAG 661
QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 662 TCTGTCACTGCCCTATATGTTGTCTGCGGAGGCTGGGTCTGGTCTGGTCTGGTCTGGT 721
QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 722 ACAGGTAGTATTGACAGAGCGACTTGGCCAAATACTACGCG 766
RESULT 12
US-09-525-397-16
; Sequence 16, Application US/09525397
; Patent No. 6252047
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.

; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/525,397
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/071,710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2152 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-525-397-16
Alignment Scores:
Pred. No.: 9,36E-238 Length: 2152
Score: 255.00 Matches: 255
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 46.11% Indels: 0
DB: 4 Gaps: 0
US-09-593-793a-113 (1-553) x US-09-525-397-16 (1-2152)
QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAsp 318
Db 2 GGGCTGTACAGGGCGTGGCCAGAGTGGAGCGGGGACCGAGCGCCGAGACACTATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGGGCTTCGGATGGGCGGTTCCTCGAGTGGCCCATCTCCCTGGTCTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGTGTATGACCGGCTGGTGCAGCGATTCCGACATCGGCGGCGGAGTATTTGGCCAGT 181
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 182 GTGGCAGCTTCCTCTGGCTGGCGGTGCACATGCTGCCACAGTGTGGCGGTGGTG 241
QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 242 ACAGCTTACAGCGCCCTCAGCGGTTCCACTTCTCAGCGCTGCAGATCTCGCCCTACACA 301
QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 302 CTGGCCTCCCTCTACCCACCGGAGAGCAGGTGTCTGCCAAATACCGAGGGGACACT 361
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438

Db 362 GGAGTGTAGCAGTACGACAGCTGATGACACAGCTTCTCCAGGCGCTAAGCCTGGA 421
Qy 439 AlaProPheProAspGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 422 GTCCTTCCCTAAAGGACAGCTGGGTGCTGGAGGAGTGGCTGCTCCACCTCCACCC 481
Qy 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
Db 482 GCGCTCTCGGGGCTCTGCTGTGATGCTCCGTACGTGTGGTGGTGGTGGTGGTGGT 541
Qy 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 542 GAGGACAGGTGGTTCGGGGCGGGGCGATCTCCCTGGACCTCGCCATCTGGATAGTGC 601
Qy 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 602 TTCCTGTCTGCCAGTGGCCGCCATCCCTGTTATGGGCTCCATGTCCAGCTACGCCAG 661
Qy 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 662 TCTGTCACTGCTATATGTGTGCTCCGCGAGGCTGGGTCTGGTCCCATTTTACTTTGCT 721
Qy 539 ThrGlnValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 722 ACACAGGTAGTATTGACAAGAGCGACTTGGCCAAATACTACGCG 766

RESULT 13

US-09-071-710-15
; Sequence 15, Application US/09071710
; Patent No. 6130043
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071.710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/850,713
; FILING DATE: 02-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083-US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623

; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2143 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-710-15
Alignment Scores:
Pred. No.: 7,58e-235 Length: 2143
Score: 252.000 Matches: 252
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.57% Indels: 0
DB: 3 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-071-710-15 (1-2143)
Qy 302 GlnGlyValProArgAlaGluProGlyThrGluAlaAArgHisTyrAspGluGlyVal 321
Db 3 CAGGCGGTGCCAGAGCTGAGCGGCGACCGAGGCGCGGAGACATATGATGAAGGCGTT 62
Qy 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
Db 63 CGGATGGCGAGCTGGGGCTGTTCCTGCGAGTGGCGCATCTCCCTGGTCTCTCTCTGCTC 122
Qy 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
Db 123 ATGGACCGGCTGGTGCAGCGATTGCGCATCTGAGCAGTCTATTGGCCAGTGTGGCAGCT 182
Qy 362 PheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSer 381
Db 183 TTCCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 242
Qy 382 AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401
Db 243 GCGCGCTTCCAGCGGTTCACCTTCTCAGCCCTGCAGATCTCCTCCCTACACACTGGCCTCC 302
Qy 402 LeuTyrHisArgGluGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyAlaAla 421
Db 303 CTCCTACCGCGGAGAGCAGGTGTTCCTGCCCAATACCGAGGGGACACTGGAGGTGCT 362
Qy 422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
Db 363 AGCAGTGGAGGACAGCTGATGACAGCTTCTGCCAGGCCCTAAGCCTGGAGCTCCCTTC 422
Qy 442 ProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProProAlaLeuCys 461
Db 423 CCTAATGGACAGCTGGGTGCTGGAGGAGTGGCTTCCACCTCCACCTCCACCTCCCTCTGC 482
Qy 462 GlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAlaArg 481
Db 483 GGGGCTCTGCTGTGATGCTCCGTAGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 542
Qy 482 ValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501
Db 543 GTGGTTCGGGCGGGGCGATCTGCTGACCTGCGCATCTCCGTAGTAGGCTTCCTGCTG 602
Qy 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521
Db 603 TCCAGGTGGGCCCATCTCTTTATGGCTCCATTTGCGCTCAGCTCAGCAGCTCTGCTACT 662
Qy 522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 541
Db 663 GCCTATATGGTCTCTGCGCGAGGCTGGGTCTCTGGTGGCATTTTACTTTGCTACAGGTA 722
Qy 542 ValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 723 GTATTTGACAAGAGCGACTTGGCCAAATACTACGCG 758
RESULT 14
US-09-525-397-15

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: Sequence 15, Application US/09525397
: Patent No. 6252047
: GENERAL INFORMATION:
: APPLICANT: BILLING-MEDEL, PATRICIA
: APPLICANT: COHEN, MAURICE
: APPLICANT: COLPITTS, TRACEY L.
: APPLICANT: FRIEDMAN, PAULA N.
: APPLICANT: GORDON, JULIAN
: APPLICANT: GRANADOS, EDWARD N.
: APPLICANT: HODGES, STEVEN C.
: APPLICANT: KLASS, MICHAEL R.
: APPLICANT: KRATOCHVIL, JON D.
: APPLICANT: ROBERTS-RAPP, LISA
: APPLICANT: RUSSELE, JOHN C.
: APPLICANT: STROUPE, STEPHEN D.
: TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
: TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Abbott Laboratories
: STREET: 100 Abbott Park Road
: CITY: Abbott Park
: STATE: IL
: COUNTRY: USA
: ZIP: 60064-3500
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/525,397
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/071,710
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Becker, Cheryl L.
: REGISTRATION NUMBER: 35,441
: REFERENCE/DOCKET NUMBER: 6083.US.P1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 847/935-1729
: TELEFAX: 847/938-2623
: TELEX:
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2143 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-09-525-397-15

Alignment Scores:
Pred. No.: 7.58e-235 Length: 2143
Score: 252.00 Matches: 252
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.57% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-525-397-15 (1-2143)

Qy 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGlu
Db 3 CAGGCGCTGCCAGAGCTGTAGCCGGGACCACCGAGGCCGAGACACTATGATGA
Qy 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSer
Db 63 CGGATGGCACCCTGGGGGCTGTCTCGAGTCGCCGCACTCCCTGGTCTCTCT
Qy 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerVal

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-605-785-703

Alignment Scores:
Pred. No.: 3,19e-218 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
DB: 4 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-605-785-703 (1-2904)

QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
DB 810 GAGGCGTTCGATGGCAGCCTGGGCTGTCTTCAGTGGCCATCTCCCTGGTCTTC 869
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
DB 870 TCTCTGGTCATGACCGGCTGTGCGAGGATTTCGGCAGTTCGAGCAGTCTATTGGCCAGT 929
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
DB 930 GTGGCAGCTTTCCTGTGGCTGCCGCTGCACATGCTGTCCACAGTGTGGCCGTGGTG 989
QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
DB 990 ACAGCTTCAGCGCCCTCACCGGGTTCACCTTCTCAGCCCTCAGATCTGCGCCCTACACA 1049
QY 399 LeuAlaSerLeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGlyAspThr 418
DB 1050 CTGGCTCCTCTACACCGGAGAGCAGGTGTCTTCCGCCAAATACCGAGGGACACT 1109
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
DB 1110 GGAGGTGTAGCAGTTCAGGACAGCCTGATGACACAGCTTCTCCAGGCGCTTAAGCCTGGA 1169
QY 439 AlaProPheProAspGlyHisValGlyAlaGlySerGlyLeuLeuProProProPro 458
DB 1170 GTCCTCTCCCTAATGGACACGTGGGTGCTGGAGCAGTGGGCTGCTCCACCTCCACCC 1229
QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr 478
DB 1230 GCGCTCTCGGGGCTCTGCTGCTGATGCTCCGTACGTGTGGTGGTGGAGCCACC 1289
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
DB 1290 GAGGCCAGGGTGTTCGGGCGGGGCGCATCTGCCTGGACCTCGCCATCTGATAGTGCC 1349
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
DB 1350 TTCCTGCTGTCCAGTGGCCCATCCCTGTTATTAGGGCTCCATGTCCAGCTCAGCCAG 1409
QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
DB 1410 TCTGTCACTGCCTATATGTGTCTCGGCGAGCCCTGGGTCTGGTGGCATTACTTTGCT 1469
QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 1470 ACACAGGTAGTATTGACAAGAGCAGCTTGGCCAAATACTCAGCG 1514

RESULT 16

US-09-020-956-10
; Sequence 10, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaqun
; APPLICANT: Dillin, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-020-956-10

Alignment Scores:
Pred. No.: 3,67e-109 Length: 789
Score: 122.00 Matches: 122
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.06% Indels: 0
DB: 4 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-020-956-10 (1-789)

QY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376
DB 12 GCAGTGTGGCAGCTTTCCTGTGGCTGCCGCTGCACATGCTTCCACAGTGTGGCC 71
QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396
DB 72 GTGGTGACAGCTTCAGCGCCCTCACCGGTTTCACTTCTCAGCCCTGCAGATCTCGCC 131
QY 397 TyrThrLeuAlaSerLeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGly 416
DB 132 TACACACTGGCTCCTCTACCCACCGGAGAGCAGGTGTTCTCCCAAAATACCGAGGG 191
QY 417 AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
DB 192 GACACTGGAGGTGCTAGCAGTGCAGCAGCCCTGATGACAGCTTCTCCAGGCGCTAAG 251
QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro 456
DB 252 CCTGGAGTCCCTTCCCTAATGGACACGCTGGGTGGAGGAGTGGCTGCTCCACCT 311
QY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476
DB 312 CCACCCGCGCTCTGGGGGCGCTCTGCCTGTGATGCTCCGTACGTGTGGTGGTGGTGAG 371
QY 477 ProThr 478
DB 372 CCCACC 377

RESULT 17
US-09-030-607-10
; Sequence 10, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR
 NUMBER OF SEQUENCES: 224
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/030,607
 FILING DATE: 25-FEB-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Makl, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.427C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 789 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-09-030-607-10

Alignment Scores:		
Pred. No.:	3.67e-109	Length:
Score:	122.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	22.06%	Indels:
DB:	4	Gaps:

US-09-593-793A-113 (1-553) x US-09-030-607-10 (1-789)

Qy	357	AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla	376
Db	12	GCCAGTGTGGCAGCTTTCCCTGTGGCTGGCGGTGCCACATGCTGTCCACACAGTGTGGCC	71
Qy	377	ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro	396
Db	72	GTGGTGACAGCTTCAGCGCGCCCTCACCGGGTTCCACCTCTCACGCCGTGCAGATCCTGGCC	131
Qy	397	TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly	416
Db	132	TACACATGGCCCTCCCTCTACCAACCGGGAGACAGGTGTCTCGCCAAATACCGAGGG	191
Qy	417	AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys	436
Db	192	GACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCACGGCCCTTAG	251
Qy	437	ProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProPro	456
Db	252	CCTGGAGCTCCCTTCCCTAATGACACAGCTGGGTGCTGGAGGAGTGGCGTCTCCACCT	311
Qy	457	ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu	476
Db	312	CCACCCCGCTCTGCGGGGCTCTGCTGTGATGTCCTGATGTCCTGACGTGTGGTGGGTGAG	371

RESULT 18	
US-09-605-785-10	
Sequence 10, Application US/09605785	
Patent No. 6321716	
GENERAL INFORMATION:	
APPLICANT: Xu, Jiangchun	
APPLICANT: Dillon, Davin C.	
APPLICANT: Mitcham, Jennifer L.	
APPLICANT: Harlocker, Susan L.	
APPLICANT: Jiang, Yuqi	
APPLICANT: Henderson, Robert A.	
APPLICANT: Kalos, Michael D.	
APPLICANT: Fanger, Gary R.	
APPLICANT: Retter, Marc W.	
APPLICANT: Stolk, John A.	
APPLICANT: Day, Craig H.	
APPLICANT: Vedvick, Thomas S.	
APPLICANT: Carter, Darrick	
APPLICANT: Li, Samuel	
APPLICANT: Wang, AiJun	
APPLICANT: Skeiky, Yasir A.W.	
APPLICANT: Hepler, William	
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND	
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER	
FILE REFERENCE: 210121.427C16	
CURRENT APPLICATION NUMBER: US/09/605,785	
CURRENT FILING DATE: 2000-06-27	
NUMBER OF SEQ ID NOS: 835	
SOFTWARE: FastSeq for Windows Version 3.0	
SEQ ID NO 10	
LENGTH: 789	
TYPE: DNA	
ORGANISM: Homo sapien	
FEATURE:	
NAME/KEY: misc_feature	
LOCATION: (1)...(789)	
OTHER INFORMATION: n = A,T,C or G	
US-09-605-785-10	
Alignment Scores:	
Pred. No.:	3.67e-109
Score:	122.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	22.06%
DB:	4
	Length: 789
	Matches: 122
	Conservative: 0
	Mismatches: 0
	Indels: 0
	Gaps: 0

US-09-593-793A-113	(1-553) x US-09-605-785-10	(1-789)	
Qy	357	AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla	376
Db	12	GCCAGTGTGGCAGCTTTCCCTGTGGCGTCGGGTGCCACATGCCTGTCCACACAGTGtggcc	71
Qy	377	ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro	396
Db	72	GTGGTAGACgTTCAGCGCGCTCACCGGGTTCACCTTCTCAGCCCTCGAGATCCTGCC	131
Qy	397	TyrThrLeuAlaSerLeuTyrHisArgGluLySglNValPheLeuProLysTyrArgGly	416
Db	132	TACACATGGcCTCCCTCTACACCcGGGAGAGAGGTGTTCTGTGCCAAATACCGAGGG	191
Qy	417	AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys	436
Db	192	GACTCGAGGTGCTAGCASTAGGACAGGCTCATCACCAGCTTCTCGCCAGGCCCTAAG	251
Qy	437	ProGlyAlaProPheProAsnGlyHisValGlyAlaGlyLysSerGlyLeuLeuProPro	456
Db	252	CCTGGACCTCCCTCCCTAATGCACACGTGGGTGCTGGAGGCAGTGCCTGCCACCT	311
Qy	457	ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu	476
Db	312	CCACCcGGCTCTgcggggccttgctgtgatgtctcgatcgctgtggTGGGTGAG	371

QY 477 ProThr 478
|||||
Db 372 CCCACC 377

RESULT 19

US-09-439-313-10
; Sequence 10, Application US/09439313
; Patent No. 6329505

; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi

; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael

; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark

; APPLICANT: Solk, John
; APPLICANT: Day, Craig

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313

; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10

; LENGTH: 789
; TYPE: DNA

; ORGANISM: Homo sapien
; FEATURE:

; NAME/KEY: misc_feature
; LOCATION: (1)...(789)

; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-10

Alignment Scores:

Pred. No.: 3,67e-109 Length: 789
Score: 122.00 Matches: 122
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.06% Indels: 0
DB: 4 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-439-313-10 (1-789)

QY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376

Db 12 GCCAGTGTGGCAGCTTCCCTGTGGCTGCCGTGCCACATGCTCTCCACAGTGTGGCC 71

QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396

Db 72 GTGGTGACAGCTTCACCGCCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCCTGCC 131

QY 397 TyrThrLeuAlaSerLeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGly 416

Db 132 TACACACTGGCCCTCCCTCTACCCACCGGAGAGCAGGTGTTCTCCCAAAATACCGAGGG 191

QY 417 AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436

Db 192 GACACTGGAGGTGCTAGCAGTGCAGACAGCCTGATGACAGCTTCTCCAGCCCTTAAG 251

QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProPro 456

Db 252 CCTGAGCTCCCTCCCTTAATGGACACGTGGGTGCTGGAGGAGTGTCTCCAGCCCTTAAG 311

QY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476

Db 312 CCACCCGGCGCTCTGGGGCCCTCTCCCTGTGTGATGCTCCGTACGTGTGGTGGGTGAG 371

QY 477 ProThr 478
|||||

Db 372 CCCACC 377
|||||

RESULT 20

US-09-352-616A-10
; Sequence 10, Application US/09352616A
; Patent No. 6395278

; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.

; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi

; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A

; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10

; LENGTH: 789
; TYPE: DNA

; ORGANISM: Homo sapien
; FEATURE:

; NAME/KEY: misc_feature
; LOCATION: (1)...(789)

; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-10

Alignment Scores:

Pred. No.: 3,67e-109 Length: 789
Score: 122.00 Matches: 122
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.06% Indels: 0
DB: 4 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-352-616A-10 (1-789)

QY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376

Db 12 GCCAGTGTGGCAGCTTCCCTGTGGCTGCCGTGCCACATGCTCTCCACAGTGTGGCC 71

QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396

Db 72 GTGGTGACAGCTTCACCGCCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCCTGCC 131

QY 397 TyrThrLeuAlaSerLeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGly 416

Db 132 TACACACTGGCCCTCCCTCTACCCACCGGAGAGCAGGTGTTCTCCCAAAATACCGAGGG 191

QY 417 AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436

Db 192 GACACTGGAGGTGCTAGCAGTGCAGACAGCCTGATGACAGCTTCTCCAGCCCTTAAG 251

QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProPro 456

Db 252 CCTGAGCTCCCTCCCTTAATGGACACGTGGGTGCTGGAGGAGTGTCTCCAGCCCTTAAG 311

QY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476

Db 312 CCACCCGGCGCTCTGGGGCCCTCTCCCTGTGTGATGCTCCGTACGTGTGGTGGGTGAG 371

QY 477 ProThr 478
|||||

Db 372 CCCACC 377

RESULT 21

US-09-232-149A-10
; Sequence 10, Application US/09232149A
; Patent No. 6465611

; GENERAL INFORMATION:
; APPLICANT: Harlocker, Susan Louise

APPLICANT: Xu, Jlangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C6
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 789
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(789)
OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-10

Alignment Scores:
Pred. No.: 3 67e-109 Length: 789
Score: 122.00 Matches: 122
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.06% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-232-149A-10 (1-789)

Qy 357 AlaserValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376
Db 12 GCCAGTGTGGCAGCTTCCTCCCTGTGGCTGCCGTGCCACATGCTGTCCACAGTGTGGCC 71
Qy 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnLeuPro 396
Db 72 GTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCC 131
Qy 397 TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly 416
Db 132 TACACACTGGCTCCCTCTACCCACCGGAGACAGGTGTTCTGCCCAATACCGAGGG 191
Qy 417 AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
Db 192 GACACTGGAGGTGCTAGCAGTGCAGACAGCCTGATGACCAGCTTCTGCCAGGCCCTAAG 251
Qy 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProPro 456
Db 252 CTGGAGCTCCCTTCCTTAATGGACACAGTGGGTGCTGGAGGAGTGGCTGTCCACCT 311
Qy 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476
Db 312 CCACCGCGCTCTGGGGGCCCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGGTGAG 371
Qy 477 ProThr 478
Db 372 CCCACC 377

RESULT 22

US-09-071-710-1
; Sequence 1, Application US/09071710
; Patent No. 6130043

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA

APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,710
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,713
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-710-1

Alignment Scores:
Pred. No.: 9 47e-74 Length: 258
Score: 85.00 Matches: 85
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.37% Indels: 0
DB: 3 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-071-710-1 (1-258)

Qy 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAsp 318
Db 2 GGCTGTACAGGGCGTGCACAGCTGAGCGCGGACCGAGCGCCGGAGACACTATGAT 61
Qy 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGCGTTCGATGGCAGCGCTGGGCTGTCTCTGCAGTGGCCATCTCCCTGGTCTTC 121
Qy 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGGTTCATGGACCGGCTGTGTCAGCATTCGGCACTTCGAGCAGCTATTTGGCCAGT 181
Qy 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal 378
Db 182 GTGGCAGCTTTCCCTGTGGCTGCCGTGCCCATGCTGTCCACAGTGTGGCCGTGGTG 241
Qy 379 ThrAlaSerAlaAla 383
Db 242 ACAGCTTCAGCGGCC 256
RESULT 23
US-09-525-397-1
; Sequence 1, Application US/09525397

Patent No. 6252047
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/525.397
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/071.710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 258 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-525-397-1

Alignment Scores:
Pred. No.: 9.47e-74 Length: 258
Score: 85.00 Matches: 85
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.37% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-525-397-1 (1-258)

QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAsp 318
Db 2 GGGCTGTACCGGGCGTGCACAGCTGAGCGGCGCCGAGCGGCGGAGACATATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGCGGTTCGATGGGAGCGCTGGGGCTGTCTTCAGTGGCCCATCTCCCTGGTCTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGGTCATGGACCGGCTGTGTGACGCGATTTCGCGCACTTCGAGCAGTCTATTGGCCAGT 181

QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 182 GTGGCAGCTTCCCTGTGGCTGCCGCGTGCACATGCCTGTCCACAGTGTGCCCGTGGTG 241
QY 379 ThrAlaSerAlaAla 383
Db 242 ACAGCTTCAGCGCC 256
RESULT 24
US-09-071-710-4
; Sequence 4, Application US/09071710
; Patent No. 6130043
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071.710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/850.713
; FILING DATE: 02-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-710-4
Alignment Scores:
Pred. No.: 7.38e-71 Length: 247
Score: 82.00 Matches: 82
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.83% Indels: 0
DB: 3 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-071-710-4 (1-247)

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QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 1 GCTCCCTTCCCTAATGACACAGTGGGTGCTGGAGGAGTGGCTGCTCCACCTCCACCC 60
QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr 478
Db 61 GCCTCTGCGGGGCCCTCTGCTGTGATGCTCCGTACGTGTGGTGGGTGAGCCACCC 120
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 121 GAGCCAGGTGGTTCGGGGCCGGGCATCTGCTGGACCTCCCATCTCTGGATAGTGCC 180
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 181 TTCCTGCTGCCAGGTGGGCCCATCCCTGTTTATGGGCTCCATTGTCACAGTCACGCCAG 240
QY 519 SerVal 520
Db 241 TCTGTC 246
RESULT 26
US-09-525-397-4
; Sequence 4, Application US/09525397
; Patent No. 6252047
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/525,397
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/071,710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

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; TOPOLOGY: linear
US-09-525-397-4
Alignment Scores:
Pred. No.: 7.38e-71 Length: 247
Score: 82.00 Matches: 82
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.83% Indels: 0
DB: 4 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-525-397-4 (1-247)
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
... Db 1 GCTCCCTTCCCTAATGACACAGTGGGTGCTGGAGGAGTGGCTGCTCCACCTCCACCC 60
QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr 478
Db 61 GCCTCTGCGGGGCCCTCTGCTGTGATGCTCCGTACGTGTGGTGGGTGAGCCACCC 120
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 121 GAGCCAGGTGGTTCGGGGCCGGGCATCTGCTGGACCTCCCATCTCTGGATAGTGCC 180
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 181 TTCCTGCTGCCAGGTGGGCCCATCCCTGTTTATGGGCTCCATTGTCACAGTCACGCCAG 240
QY 519 SerVal 520
Db 241 TCTGTC 246
RESULT 26
US-09-071-710-2
; Sequence 2, Application US/09071710
; Patent No. 6130043
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/850,713
; FILING DATE: 02-MAY-1997
; ATTORNEY/AGENT INFORMATION:
```



```
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 217 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-710-2

Alignment Scores:
Pred. No.: 3,04e-60 Length: 217
Score: 71.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.84% Indels: 0
DB: 3 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-071-710-2 (1-217)
QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGlyVal 321
Db 3 CAGGGCGTCCAGAGCTGAGCGGGCCAGGCGGAGACACTATGATGAAGCGGT 62
QY 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
Db 63 CGGATGGGCGAGCTGGGGCTGTTCCTGCAGTGGCCATCTCCCTGGTCTCTCTGTC 122
QY 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
Db 123 ATGGACCGGCTGGTGCAGCGATTTCGCACTCGAGCAGTCTATTGGCCAGTGTGGCAGCT 182
QY 362 PheProValAlaAlaGlyAlaThrCysLeuSer 372
Db 183 TTCCCTGTGGCTGGCGTGCCACATGCCCTGTCC 215

RESULT 27
US-09-525-397-2
; Sequence 2, Application US/09525397
; Patent No. 6252047
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/525,397
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/071,710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 217 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-525-397-2

Alignment Scores:
Pred. No.: 3,04e-60 Length: 217
Score: 71.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.84% Indels: 0
DB: 4 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-525-397-2 (1-217)
QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGlyVal 321
Db 3 CAGGGCGTCCAGAGCTGAGCGGGCCAGGCGGAGACACTATGATGAAGCGGT 62
QY 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
Db 63 CGGATGGGCGAGCTGGGGCTGTTCCTGCAGTGGCCATCTCCCTGGTCTCTCTGTC 122
QY 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
Db 123 ATGGACCGGCTGGTGCAGCGATTTCGCACTCGAGCAGTCTATTGGCCAGTGTGGCAGCT 182
QY 362 PheProValAlaAlaGlyAlaThrCysLeuSer 372
Db 183 TTCCCTGTGGCTGGCGTGCCACATGCCCTGTCC 215

RESULT 28
US-09-071-710-3
; Sequence 3, Application US/09071710
; Patent No. 6130043
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
```

STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,710
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,713
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083.US.P1
TELEPHONE: 847/935-1729
TELEFAX: 847/938-3623
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: base_polymorphism
LOCATION: 215
OTHER INFORMATION: /note= " N' represents an A or G or
OTHER INFORMATION: T or C polymorphism at this position"
US-09-071-710-3

Alignment Scores:
Pred. No.: 3.57e-60 Length: 255
Score: 71.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.84% Indels: 0
DB: 3 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-071-710-3 (1-255)

QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
|||||
Db 2 ACAGCTTCAGCGCCCTCACCGGGTTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACA 61

QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
|||||
Db 62 CTGGCTCCCTCTACACCGGGAGAGCAGGTGTCTCTGCCAAATACCGAGGGGACACT 121

QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
|||||
Db 122 GGAGGTGCTAGCAGTGCAGGACGCTGATGACCAGCTTCTGTCCAGGCCCTTAAGCCTGGA 181

QY 439 AlaProPheProAsnGlyHisValGlyAlaGly 449
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Db 182 GCTCCCTTCCCTAATGACACAGTGGGTGCTGGA 214

RESULT 29

US-09-525-397-3
Sequence 3, Application US/09525397
Patent No. 6252047

GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.

APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/525,397
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/071,710
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083.US.P1
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: base_polymorphism
LOCATION: 215
OTHER INFORMATION: /note= " N' represents an A or G or
OTHER INFORMATION: T or C polymorphism at this position"
US-09-525-397-3

Alignment Scores:
Pred. No.: 3.57e-60 Length: 255
Score: 71.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.84% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-525-397-3 (1-255)

QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
|||||
Db 2 ACAGCTTCAGCGCCCTCACCGGGTTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACA 61

QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
|||||
Db 62 CTGGCTCCCTCTACACCGGGAGAGCAGGTGTCTCTGCCAAATACCGAGGGGACACT 121

QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
|||||
Db 122 GGAGGTGCTAGCAGTGCAGGACGCTGATGACCAGCTTCTGTCCAGGCCCTTAAGCCTGGA 181

QY 439 AlaProPheProAsnGlyHisValGlyAlaGly 449
|||||

Db 182 GCTCCCTTCCTAATGGACACGCTGGGTGCTGGA 214

RESULT 30
US-09-071-710-5
; Sequence 5, Application US/09071710
; Patent No. 6130043
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/850,713
; FILING DATE: 02-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-710-5

Alignment Scores:
Pred. No.: 2.54e-24 Length: 231
Score: 34.00 Matches: 57
Percent Similarity: 98.28% Conservative: 0
Best Local Similarity: 98.28% Mismatches: 1
Query Match: 6.15% Indels: 1
DB: 3 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-071-710-5 (1-231)

Qy 496 AspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGln 515

Db 3 GATAGTGCCTTCTGCTGCCAGGTGGCCCATCCCTGTTATGGGCTCCATTGTCAG 62

Qy 516 LeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIle 535

|||||

Db 63 CTCAGCCAGTCTGCTCACTGCCTATATGGTGTCTGCGCGCAGG-CTGGGTCTGGTCGCCATT 121

Qy 536 TyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||

Db 122 TACTTTGCTACACAGGTAGTATTGACAGAGCGACTTGCCCAATACTCAGCG 175

RESULT 31
US-09-525-397-5
; Sequence 5, Application US/09525397
; Patent No. 6252047
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/525,397
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/071,710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-525-397-5

Alignment Scores:
Pred. No.: 2.54e-24 Length: 231
Score: 34.00 Matches: 57
Percent Similarity: 98.28% Conservative: 0
Best Local Similarity: 98.28% Mismatches: 1
Query Match: 6.15% Indels: 1
DB: 4 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-525-397-5 (1-231)

Qy 496 AspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGln 515

|||||

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; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 488
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-439-313-488

Alignment Scores:
Pred. No.: 0.658 Length: 33
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.63% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-439-313-488 (1-33)

Qy 256 LeuLeuProArgLeuHisGlnLeuCys 264
|||||
Db 7 CTTCTCCCGGCTGCACGAGCTGTC 33

RESULT 34
US-09-397-787-331
; Sequence 331, Application US/09397787
; Patent No. 6468758
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
; TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.466C2
; CURRENT APPLICATION NUMBER: US/09/397,787
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 331
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-397-787-331

Alignment Scores:
Pred. No.: 3.47 Length: 176
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.63% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-397-787-331 (1-176)

Qy 227 GluProAlaGluGlyLeuSerAlaPro 235
|||||
Db 76 GAACCTGCGGAGGACTGAGTGCCCT 102

RESULT 35
US-08-658-639-11
; Sequence 11, Application US/08658639
; Patent No. 5914238

```

;; GENERAL INFORMATION:
;; APPLICANT: KEESEE, SUSAN
;; APPLICANT: OBAR, ROBERT
;; APPLICANT: WU, YING-JYE
;; TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Testa, Hurwitz & Thibault
;; STREET: 125 High St.
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02110
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/658,639
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MEYERS, THOMAS C
;; REGISTRATION NUMBER: 36,989
;; REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 248-7000
;; TELEFAX: (617) 248-7100
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 613 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..519
US-08-658-639-11

Alignment Scores:
Pred. No.: 12 Length: 613
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.63% Indels: 0
DB: 2 Gaps: 0

US-09-593-793A-113 (1-553) x US-08-658-639-11 (1-613)

Qy 227 GluProAlaGluGlyLeuSerAlapro 235
Db 504 GAACCTGCGGAGGACTGAGTGCCT 530

RESULT 36
US-08-944-604-11
; Sequence 11 Application US/08944604
; Patent No. 6218131
; GENERAL INFORMATION:
; APPLICANT: KEESEE, SUSAN
; APPLICANT: OBAR, ROBERT
; APPLICANT: WU, YING-JYE
; TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,604
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, THOMAS C
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 613 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..519

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/944,604
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MEYERS, THOMAS C
;; REGISTRATION NUMBER: 36,989
;; REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 248-7000
;; TELEFAX: (617) 248-7100
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 613 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..519
US-08-944-604-11

Alignment Scores:
Pred. No.: 12 Length: 613
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.63% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-08-944-604-11 (1-613)

Qy 227 GluProAlaGluGlyLeuSerAlapro 235
Db 504 GAACCTGCGGAGGACTGAGTGCCT 530

RESULT 37
US-08-944-604-15
; Sequence 15 Application US/08944604
; Patent No. 6218131
; GENERAL INFORMATION:
; APPLICANT: KEESEE, SUSAN
; APPLICANT: OBAR, ROBERT
; APPLICANT: WU, YING-JYE
; TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,604
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, THOMAS C
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 613 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..519

```
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 903 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 130..795
; OTHER INFORMATION: /product= "BC-2"
US-08-944-604-15

Alignment Scores:
Pred. No.: 17.7 Length: 903
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.63% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-08-944-604-15 (1-903)

QY 227 GluProAlaGluGlyLeuSerAlaPro 235
|||||
DB 780 GAACCTCGGGAGGACTGAGTGCCT 806

RESULT 38
US-09-729-995-3/c
; Sequence 3, Application US/09729995
; Patent No. 6426206
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO00904
; CURRENT APPLICATION NUMBER: US/09/729,995
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 29629
; TYPE: DNA
; ORGANISM: Human
US-09-729-995-3

Alignment Scores:
Pred. No.: 568 Length: 29629
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.63% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-729-995-3 (1-29629)

QY 231 GlyLeuSerAlaProSerLeuSerPro 239
|||||
DB 26382 GGTCTCTCAGCCGCCAGTCTCAGCCG 26356

RESULT 39
US-09-605-785-487/c
; Sequence 487, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui

; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 487
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-605-785-487

Alignment Scores:
Pred. No.: 6.7 Length: 36
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.45% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-605-785-487 (1-36)

QY 318 AspGluGlyValArgMetGlySer 325
|||||
DB 36 GATGAGCGCTCGATGGCAGC 13

RESULT 40
US-09-439-313-487/c
; Sequence 487, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 487
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-439-313-487

Alignment Scores:
```

Pred. No.: 6.7 Length: 36
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.45% Indels: 0
DB: 4 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-439-313-487 (1-36)

Qy 318 AspGluGlyValArgMetGlySer 325

Db 36 GATGAGGCGTTCGGATGGCGAC 13

RESULT 41

US-08-673-190A-6
Sequence 6, Application US/08673190A
Patent No. 5985668
GENERAL INFORMATION:
APPLICANT: Mattes, Ralf
APPLICANT: Klein, Kathrin
APPLICANT: Stegmaier, Sabine
TITLE OF INVENTION: Sucrose Metabolism Mutants.
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,190A
FILING DATE: 27-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 06473.0001-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Enterobacter species

US-08-673-190A-6
Alignment Scores:
Pred. No.: 65.5 Length: 357
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.45% Indels: 0
DB: 2 Gaps: 0

US-09-593-793a-113 (1-553) x US-08-673-190A-6 (1-357)

Qy 106 AlaGlyTrpLeuAlaGlyLeuLeu 113

Db 312 GCCGCGTGGCTGGCGGCGCTGCTG 335

RESULT 42

US-09-593-793a-113 (1-553) x US-09-328-111-46 (1-633)
Qy 231 GlyLeuSerAlaProSerLeuSer 238
Db 116 GGCCTAAGTGACCGTCTCTGAGC 93
RESULT 43
US-09-345-882-3
Sequence 3, Application US/09345882
Patent No. 6399373
GENERAL INFORMATION:
APPLICANT: Bouquellet, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP - ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.pm
SEQ ID NO 3
LENGTH: 999
TYPE: DNA
ORGANISM: Homo sapiens
US-09-345-882-3
Alignment Scores:
Pred. No.: 182 Length: 999

Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.45% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-345-882-3 (1-999)

QY 93 SerLeuGlyIleLeuLeuSerLeu 100
|||||
Db 484 AGCCTAGGCACTCTTTTAICTTG 507

RESULT 44

US-09-020-956-175/c
; Sequence 175, Application US/09020956
; Patent No. 6261562

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 175:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1167 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cdna

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

US-09-020-956-175

Alignment Scores:

Pred. No.: 213 Length: 1167
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.45% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-020-956-175 (1-1167)

QY 447 GlyAlaGlySerGlyLeuLeu 454
|||||
Db 836 GGGGCTGGGGGTCTGGACTCCTG 813

RESULT 45

US-09-030-607-175/c
; Sequence 175, Application US/09030607
; Patent No. 6262245

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 175:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1167 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cdna

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

US-09-030-607-175

Alignment Scores:

Pred. No.: 213 Length: 1167
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.45% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-030-607-175 (1-1167)

QY 447 GlyAlaGlySerGlyLeuLeu 454
|||||
Db 836 GGGGCTGGGGGTCTGGACTCCTG 813

Search completed: February 19, 2003, 06:36:44

Job time : 106 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 05:09:05 ; Search time 1653 Seconds
(without alignments)
5418.091 Million cell updates/sec

Title: US-09-593-793a-113

Perfect score: 553

Sequence: 1 MVQRLWVSRLHRKAQLL.....AIYEATQVVFCKSLAKYSA 553

Scoring table:

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Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 3

Total number of hits satisfying chosen parameters: 32278190

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Command line parameters:
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-DB=EST -QFMT=fastcap -SUFFIX=olig.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=100
-DOALIGN=200 -THR_SCORE=quality -THR_MIN=3 -ALIGN=45 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09593793.ecgn_1_1_959_@runat_13022003_161426_21829 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_WMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THRGRADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

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2: em_esthum.*
3: em_estlin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_estl.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pin.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_Other.*
26: em_gss_pro.*
27: em_gss_rod.*

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	180	32.5	718	12	BE867241
3	136	24.6	885	14	BQ948390
4	135	24.4	1060	14	BM914562
5	108	19.5	959	14	BQ950805
6	99	17.9	894	12	BG469520
7	86	15.6	850	12	BF972601
8	76	13.7	228	9	AA112574
9	76	13.7	482	9	AF109299
10	72	13.0	800	12	BG469487
11	69	12.5	418	12	BF922335
12	69	12.5	1035	12	BG828841
13	63	11.4	342	9	AA112573
14	60	10.8	265	12	BF371417
15	59	10.7	523	10	AW822644
16	59	10.7	537	10	AW878124
17	59	10.7	592	10	AW412402
18	59	10.7	630	13	BI145201
19	59	10.7	650	10	BB627844
20	59	10.7	692	10	BB627667
21	59	10.7	759	12	BF789072
22	59	10.7	858	13	BI107873
23	59	10.7	901	13	BI650119
24	59	10.7	929	12	BF785813
25	59	10.7	1116	12	BG242597
26	57	10.3	348	9	AA984323
27	51	9.2	934	14	BQ934815
28	48	8.7	322	12	BF854825
29	48	8.7	412	10	AW175665
30	48	8.7	1025	14	BM915082
31	47	8.5	1667	14	BM912193
32	46	8.3	1063	14	BM915527
33	45	8.1	341	13	BI045233
34	45	8.1	428	12	BF854834
35	44	8.0	242	9	AA647708
36	43	7.8	1037	12	BE914848
37	41	7.4	549	12	BG081576
38	41	7.4	700	12	BF581244
39	41	7.4	969	12	BG173136
40	39	7.1	786	12	BG174399
41	37	6.7	317	10	BB707065
42	37	6.7	844	12	BG246497
43	34	6.1	430	9	AF109303
44	33	6.0	466	12	BG086547
45	33	6.0	564	13	BG964810
46	33	6.0	578	17	AZ418156
47	33	6.0	700	10	BB610495
48	33	6.0	717	12	BG745565
49	33	6.0	872	12	BG846609
50	33	6.0	963	12	BF233285
51	32	5.8	416	12	BF454698
52	30	5.4	468	10	BB852004
53	29	5.2	509	10	BB701488
54	28	5.1	748	12	BF232636
55	27	4.9	363	9	AU023209
56	24	4.3	75	17	AZ601104
57	21	3.8	572	13	BI345407
58	20	3.6	277	10	AW346593
59	18	3.3	669	10	BB113685
60	16	2.9	518	10	BB853288
61	16	2.9	906	12	BF680993
62	15	2.7	414	10	BB850079
63	15	2.7	520	12	BG364300
64	15	2.7	946	13	BI144556

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65 13 2.4 565 13 BM192568
66 13 2.4 865 17 CNS03VMF
67 12 2.2 441 10 BB48279
68 12 2.2 744 17 CNS04J40
69 10 1.8 262 12 BG221458
70 10 1.8 323 12 BG193546
71 10 1.8 431 10 AW022261
72 10 1.8 450 10 AW185227
73 10 1.8 455 10 BE137141
74 10 1.8 458 10 BE590088
75 10 1.8 549 14 R50985
76 10 1.8 557 9 AL707231
77 10 1.8 622 14 BM725284
78 10 1.8 715 14 BM677725
79 10 1.8 826 12 BG214056
80 10 1.8 989 12 BE893061
81 10 1.8 1220 17 AG044788
82 9 1.6 173 9 AI335878
83 9 1.6 205 9 AI650487
84 9 1.6 219 9 AI753410
85 9 1.6 229 12 BF808211
86 9 1.6 230 17 AQ892511
87 9 1.6 259 9 AV162773
88 9 1.6 268 9 AI868949
89 9 1.6 271 9 AI632739
90 9 1.6 272 9 AA036979
91 9 1.6 281 9 AI918017
92 9 1.6 283 9 AI826425
93 9 1.6 284 12 BE762324
94 9 1.6 285 10 AW104168
95 9 1.6 287 14 D24129
96 9 1.6 289 10 BE241795
97 9 1.6 293 12 BE762344
98 9 1.6 293 17 BH867320
99 9 1.6 305 9 AI650794
100 9 1.6 310 13 BI491393

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ALIGNMENTS

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LOCUS 602533345F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4661075 5',
DEFINITION mRNA sequence.
ACCESSION BG469889
VERSION BG469889.1 GI:13402164
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 946)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM1459 row: i column: 12
High quality sequence stop: 798.
Location/Qualifiers
1..946
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:4661075"
/clone_lib="NIH_MGC_15"
FEATURES
source

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/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT 120 a 331 c 296 g 199 t
ORIGIN
Alignment Scores:
Pred. No.: 1,26e-164 Length: 946
Score: 192.00 Matches: 192
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 34.72% Gaps: 0
DB: 12
US-09-593-793a-113 (1-553) x BG469889 (1-946)
QY 27 GlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValProLeuLeuLeuGluVal 46
DB 1 GGCCTGGAGGTGTGTTGGCCGAGCATCATATGTGCCCTCTGCTGCTGAAGTG 60
QY 47 GlyValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66
DB 61 GGGGTAGAGAGAGAGATTCATGACCATGTTGGGCAATGGTCCAGTGTGGCCCTGGTC 120
QY 67 CysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArg 86
DB 121 TGTGTCCCGCTCCTAGGCTCAGCCAGTACCAGTGGCGTGGAGCTATGSCGCCCGCG 180
QY 87 ProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuLeuProArgAla 106
DB 181 CCCTTCATCTGGGCACCTGCTTGGGCATCCCTGCTGAGCCTCTTCTCATCCAGGGCC 240
QY 107 GlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeu 126
DB 241 GGCTGGCTAGCAGGGCTGCTGTGCCGATATCCAGGCCCTGGAGCTGGCAGTGCATC 300
QY 127 LeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeu 146
DB 301 CTGGGGCTGGGGCTGCTGGACTTCTGTGGCCAGGTGCTTCACTCCACTGGAGGCCCTG 360
QY 147 LeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPhe 166
DB 361 CTCTCTGACCTCTTCCGGGACCGGACCACCTGTGCGCAGGCTTACTCTCTATGCTTC 420
QY 167 MetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspThrSer 186
DB 421 ATGATCAGCTTTGGGGGCTGCTGGGCTACCTCCTCGCCATTCGACATGGGACACAGT 480
QY 187 AlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPheGlyLeuLeuLeuLeu 206
DB 481 GCCCTGGCCCCCTACCTGGGACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCTCATC 540
QY 207 PheLeuThrCysValAlaAlaThrLeuLeuValAla 218
DB 541 TTCTCCTACCTGGGTAGCAGCCACACTGCTGTGGTGGCT 576
RESULT 2
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LOCUS 601442309F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846411 5',
DEFINITION mRNA sequence.
ACCESSION BE867241
VERSION BE867241.1 GI:10316017
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9559 row: a column: 04
High quality sequence stop: 693.

FEATURES

source

Location/Qualifiers
1..718
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3846411"
/clone_lib="NIH_MGC_65"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies." 112 a 227 c 210 g 168 t 1 others

BASE COUNT 112 a 227 c 210 g 168 t 1 others

ORIGIN

Alignment Scores:
Pred. No.: 8 18e-154 Length: 718
Score: 180.00 Matches: 180
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 32.55% Indels: 0
DB: 12 Gaps: 0

US-09-593-793a-113 (1-553) x BE867241 (1-718)

Qy 340 LeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerVal 359
|||||
Db 2 CTGGTCATGGACGGCTGGTGCAGGATTCGGCACTCGCAGCAGTCTATTGGCCAGTGTG 61
Qy 360 AlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThr 379
|||||
Db 62 GCAGCTTTCCCTGTGGCTGCCGGTCCACATGCCTGTCCACAGTGGCGGTGTGACA 121
Qy 380 AlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeu 399
|||||
Db 122 GCTTCAGCGCGCTCACCGGGTTCACCTTCAGCCCTGCAGATCCTGCCCTACACACTG 181
Qy 400 AlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGly 419
|||||
Db 182 GCCTCCCTCTACCCACCGGAGAGCAGGTGTCTCTGCCCAATACCGAGGGACACTGGA 241
Qy 420 GlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAla 439
|||||
Db 242 GGTGTAGCAGTGGAGACAGCTGATGACCATGCTTCCTGCCAGGCCCTTAAGCCTGGAGCT 301
Qy 440 ProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAla 459
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Db 302 CCCTTCCTTATGGACAGTGGGTGCTGGAGCAGTGGCTGCTCCACCTCCACCCCGC 361
Qy 460 LeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGlu 479
|||||
Db 362 CTCCTCGGGGCTCTGCTCTGTGATCTCCGTACGTGTGGTGGTGGAGCCACCCAG 421
Qy 480 AlaArgValValProGlyArgGlyTleCysLeuAspLeuAlaIleLeuAspSerAlaPhe 499
|||||
Db 422 GCCAGGGTGGTTCGGGGCGGGGATCTGCCTGGACCTTCGCCATCCTGGATAGTGCCTC 481

Qy 500 LeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSer 519
|||||
Db 482 CTGCTGTCCAGGTGGCCCATCCCTCTGTATTGGGCTCCATTGTCACGCTCAGCAGTCT 541

RESULT 3

BQ948390

LOCUS

DEFINITION AGENCOURT_8803099 Lupski_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6198823 5', mRNA sequence.

ACCESSION

BQ948390

VERSION

BQ948390.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 885)

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13611 row: b column: 08
High quality sequence stop: 615.

FEATURES

source

Location/Qualifiers
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/clone_lib="Lupski_sciatic_nerve"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/note="vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTTCATGATCGGCGGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies." 129 a 286 c 294 g 176 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 1 72e-113 Length: 885
Score: 136.00 Matches: 136
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 24.59% Indels: 0
DB: 14 Gaps: 0

US-09-593-793a-113 (1-553) x BQ948390 (1-885)

Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
|||||
Db 259 ATGGTCCAGAGGCTGGGTGAGCGCTGCTGCGGACCGGAGCCAGCTTGTGCTG 318
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGlyTleThrTyrValPro 40
|||||
Db 319 GTCAACCTGCTTAACCTTTGGCTGGAGGTGTGTTGGCGCGCAGGCATCACCTATGTGCG 378

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QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 379 CCTCTGCTGCTGAAGTGGGGTAGAGAGAGATTTCATGACCATGGTGTGGGCTTGGT 438
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 439 CCAGTCTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 498
QY 81 AtgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 499 CGCTATGGCCGGCCGGCCCTTCATCTGGGCACTGCTTGGGCATCTGCTGAGCCTC 558
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 559 TTTCTCATCCCAAGGCCGGCTGGCTAGCAGGGCTGCTGTGCCGATCCAGGCCCTG 618
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGly 136
Db 619 GAGCTGGCACTGCTCATCTGGGCGTGGGCTGCTGGACTTCTGTGGC 666

RESULT 4
BM914562
LOCUS BM914562 1060 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT_6615475 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480245
ACCESSION BM914562
VERSION BM914562.1 GI:19364941
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL 1 (bases 1 to 1060)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2002 row: m column: 14
High quality sequence stop: 485.
FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5480245"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 282 a 294 c 314 g 169 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 1.78e-112 Length: 1060
Score: 135.00 Matches: 135
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 24.41% Indels: 0
DB: 14 Gaps: 0

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US-09-593-793a-113 (1-553) x BM914562 (1-1060)
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 3 GGAGGTGCTAGCAGTGGAGCAGCCCTGATGACAGCTTCTCCAGGCCCTAAGCCTGGA 62
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 63 GCTCCTCTCCCTTAATGGACACCTGGTGTGGAGGAGCTGGCTGCTCCACCTCCACCC 122
QY 459 AlaLeuCysGlyAlaSerAlaCysaspValSerValArgValValValGlyGluProThr 478
Db 123 GCGCTCTGCGGGGCTCTGCTGCTGATGCTCCGTACGTGTGTGTGTGTGTGTGTGTGT 182
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 183 GAGGCAAGGTGTGTTCGGGGCCGGGCACTGCTCCGTGGACCTGCCATCTCGATGATGTC 242
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 243 TTCTCTGCTGTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTTGCCAGCTCAGCCAG 302
QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 303 TCTGTCACTGCTATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 362
QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 363 ACACAGGTAGTATTTCACAGAGGACATTGGCCAAATACTCAGCG 407

RESULT 5
BM950805
LOCUS BM950805 959 bp mRNA linear EST 21-AUG-2002
DEFINITION AGENCOURT_8842232 Lupski_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6204253 5', mRNA sequence.
ACCESSION BM950805
VERSION BM950805.1 GI:22366283
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL 1 (bases 1 to 959)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13625 row: d column: 14
High quality sequence start: 2
High quality sequence stop: 490.
FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6204253"
/clone_lib="Lupski_sciatic_nerve"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/note="Vector: pCMV-SpOTr6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGGCTGCGG-3' and
5'-GACTAGTCTTAGATCGCGGCGGCGCT(15)-3'. Size selected >

```

1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life

technologies.			
BASE COUNT	139 a	312 c	308 g
ORIGIN			200 t

Alignment Scores:

Pred. No.:	7,34e-88	Length:	959
Score:	108.00%	Matches:	108
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	19.53%	Indels:	0
DB:	14	Gaps:	0

US-09-593-793A-113 (1-553) x BQ950805 (1-959)

QY	446	valGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAla	465
Db	8	GTGGGTGCTGGAGGAGTGGCTGTCTCCACCTCCACCGCGCTCTGCGGGGCTCTGGCC	67
QY	466	CysAspValSerValArgValValValGlyGluProThrGluAlaArgValValProGly	485
Db	68	TGTGATGTTCCGCTAGCTGTGGTGGTGGAGCCACCAGGCCAGGGTGGTTCGGGCG	127
QY	486	ArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAla	505
Db	128	CGGGGCAATCTGCCTGGACCTCGCCATCTGGATAGTGGCTTCTGCTGCTCCAGGTGGCC	187
QY	506	ProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVal	525
Db	188	CCATCCCTGTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCCTATATGGTG	247
QY	526	SerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLys	545
Db	248	TCTGCCCGAGGCTGGGTCTGTGCGCAATTACTTTGCTACAGGTAGTATTGACAAAG	307
QY	546	SerAspLeuAlaLysTyrSerAla	553
Db	308	AGCGACTTGGCCAAATACTCAGCG	331

RESULT 6

BG469520

LOCUS	BC469520	894 bp	linear	EST 21-MAR-2001
DEFINITION	602532833F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4660496 5', mRNA sequence.			

ACCESSION BG469520

VERSION BG469520.1 GI:13401795

KEYWORDS EST.

SOURCE	human
ORGANISM	human

ORGANISM	Homo	Euk
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96	1	1
97	1	1
98	1	1
99	1	1
100	1	1

Eukaryotes
Mammals

REFERENCE

AUTHORS
NIH - M(

TITLE	Nation
1. <i>Chlorophyll</i>	U.S.A.
2. <i>Chlorophyll</i>	U.S.A.
3. <i>Chlorophyll</i>	U.S.A.
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100. <i>Chlorophyll</i>	U.S.A.

JOURNAL Unpub.

COMMENT

Email

Tissue
CDNACDNA
CDNA

DNA :

Cloned

found

http://

Plate 1.

High α

FEATURES

SOURCE

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/clone="IMAGE:46G0496"
/clone_lib="NIH_MGC_15"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT      173 a      272 c      264 g      185 t
ORIGIN

Alignment Scores:
Pred. No.:      1.12e-79      Length:      894
Score:          99.00      Matches:      163
Percent Similarity: 97.60%      Conservative: 0
Best Local Similarity: 97.60%      Mismatches: 1
Query Match:      17.90%      Indels:      4
DB:              12      Gaps:      0

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US-09-593-793A-113 (1-553) x BG469520 (1-894)

QY	390	SerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLuysGlnVal	409
Db	3	TCAGCCCTGCAGATCCTGCCCTACACATGGCGCTCCCTCTACACC	CGGAGACGAGTG 62
QY	410	PheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThr	429

63	TTCTCTGCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGACAGCCTGATGACC	12
Db		
430	SerPheLeuProGlyProGlyAlaProPheProAsnGlyHisValGlyAlaGly	449
QY		
123	AGCTTCTGCGAGGCCCTAAGCCTGGAGCTCCCTCCCTAATGGACACAGTGGTGCTGGA	182
Db		
450	GlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSer	469
QY		
183	GGCAGTGGCCTGCTCCACCTCCACCCGGCTCTGCGGGGCCCTCTGCCTGTGATGTCCTC	242
Db		

490	--LeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeup	509
QY		
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501		
502	GCCTGACCTCGCCATCCCTGGATAGTCCTCTGCTGCCAGGTGGCCCATCCCTCT	361
Db		
503		
504		
505	heMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAla-	528
QY		
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529	GlyLeuGlyLeuValaIaIeIyrPheAlaThrGlnValValPheAspGlySerAspIeu	548
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542	GGCCTGGGCTGGTGGCCATTACTTTGCTACACAGGTAGTATTTCACAAGAGCGACTTG	481
549	AlaLysIyr-SerAla	553
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[illegible]

SOURCE	ORGANISM
human.	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE 1 (bases 1 to 850)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gcgaps-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1196 row: a column: 08
High quality sequence stop: 675.
FEATURES             Location/Qualifiers
     source
       1..850
         /organism="Homo sapiens"
         /db_xref="taxon:9606"
         /clone="IMAGE:431407"
         /clone_lib="NIH_MGC_46"
         /tissue_type="leiomyosarcoma cell line"
         /lab_host="DH10B (phage-resistant)"
         /note="Organ: uterus; Vector: pOT87; Site_1: XhoI; Site_2:
         EcoRI; cDNA made by oligo-dr priming. Directionally cloned
         into EcoRI/XhoI sites using the following 5' adaptor:
         GGCACGAG(G). Size-selected >500bp for average insert size
         1.8kb. Library constructed by Ling Hong in the laboratory
         of Gerald M. Rubin (University of California, Berkeley)
         using ZAP-cDNA synthesis kit (Stratagene) and Superscript
         II RT (Life Technologies). Note: this is a NIH_MGC
         Library."
BASE COUNT 128 a 266 c 261 g 195 t
ORIGIN

Alignment Scores:
Pred. No.: 7,966-68 Length: 850
Score: 86.00 Matches: 157
Percent Similarity: 99.37% Conservative: 0
Best Local Similarity: 99.37% Mismatches: 1
Query Match: 15.55% Indels: 1
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BF972601 (1-850)

Qy 396 ProTyThrLeuAlaSerLeuTyHisArgGluLysGlnValPheLeuProLysTyArg 415
Db 3 CCTACACACTGGCTCTCCCTACACCGGAGAGCAGGTGTTCTGCCCAATACCGA 62
Qy 416 GlyAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyPro 435
Db 63 GGGGACACTGGAGGTGTAGCAGTGCAGACAGCCTGATGACCAGCTTCTGCGAGGCCCT 122
Qy 436 LysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuPro 455
Db 123 AAGCTGGAGCTCCCTTCCCTAATGGACACAGTGGGTGTGGAGGAGTGGCTGCTCCCA 182
Qy 456 ProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGly 475
Db 183 CTTCCACCGCGCTCTGGGGGCTCTGCTGCTGATGTCTCGTACGTGTGGTGGGT 242
Qy 476 GluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeu 495
Db 243 GAGCCACCGAGGCCAG-GTGGTTCGGGGCGGGCATCTGCTGGACCTGCGCCATCTG 301
Qy 496 AspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGln 515
Db 302 GATAGTGGCTCTCTGCTGTCAGGTGGCCCATCCCTGTTATGGGTCCATGTCACG 361
Qy 516 LeuSerGlnSerValThrAlaTyMetValSerAlaAlaGlyLeuGlyLeuValAlaIle 535
Db 362 CTCACCCAGTCTGTCACGTATATGTTGTTCTGCGGAGGCGCTGGTCTGGTCCCAT 421

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Qy 536 TyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTySerAla 553
Db 422 TACTTTGTACACAGGTAGTATTTGACAAGACGACTTGGCCAAATACTACGCG 475
RESULT 8
AAL12574
LOCUS AAL12574 228 bp mRNA linear EST 23-DEC-1997
DEFINITION zm28c12.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone
IMAGE:526966 3', mRNA sequence.
ACCESSION AAL12574
VERSION AAL12574.1 GI:1665121
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 228)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissole, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore
, B., Morris, M., Parsons, J., Plante, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevasakis, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box, 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should be
kept in mind should you use this clone.
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham.
FEATURES             Location/Qualifiers
     source
       1..228
         /organism="Homo sapiens"
         /db_xref="GDB:3918395"
         /db_xref="taxon:9606"
         /clone="IMAGE:526966"
         /clone_lib="Stratagene pancreas (#937208)"
         /lab_host="SOLR cells (kanamycin resistant)"
         /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
         EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
         Oligo dt. Pancreatic adenocarcinoma cell line. Average
         insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
         sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequence: 5'
         CTCGACGTTTTTTTTTTTTTTT 3"
BASE COUNT 40 a 81 c 62 g 45 t
ORIGIN

Alignment Scores:
Pred. No.: 2,02e-59 Length: 228
Score: 76.00 Matches: 76
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.74% Indels: 0
DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x AAL12574 (1-228)

Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1 GCTTTCCCTGTGGCTGCGGTGCCACATGCTGTCCACAGTGTGCGCGTGTGACAGCT 60
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyThrLeuAla 400
Db 1

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Db	61	TCAGCGCCCTCACCGGGTTCACTTCTCAGCCCTGCAGATCTCGCCCTACACACTGGCC	120
Qy	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	420
Db	121	TCCCTCTACCCACCGGAGACAGGTGTTCTGCGCCAAATACCGAGGGACACTGGAGGT	180
Qy	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys	436
Db	181	GCTAGCAGTGGAGACAGCCTGATCACCAGCTTCTCGCAGGCCCTAAG	228
RESULT	9		
LOCUS	AF109299		
DEFINITION	AF109299 Homo sapiens prostate adult Homo sapiens cDNA clone IPCA-2	482 bp	linear
ACCESSION	AF109299		
VERSION	AF109299.1	GI:6782692	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 482)		
DESCRIPTION	Walker, M.G., Volkmut, W., Sprinzak, E., Hodgson, D. and Klingler, T.		
JOURNAL	Prediction of gene function by genome-scale expression analysis:		
MEDLINE	prostate cancer-associated genes		
COMMENT	Genome Res. 9 (12), 1198-1203 (1999)		
CONTACT	20082966		
FEATURES	Contact: Walker MG		
SOURCE	Incyte Pharmaceuticals		
	3174 Porter Drive, Palo Alto, CA 94304, USA		
	co-expressed with known prostate-cancer genes.		
	Location/Qualifiers		
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	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
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	/clone_lib="Homo sapiens prostate adult"		
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	/dev_stage="adult"		
	/note="multiple clone assembly from multiple libraries and donors"		
BASE COUNT	57 a 179 c 141 g 105 t		
ORIGIN			
Alignment Scores:			
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Score:	76.00	Matches:	151
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Best Local Similarity:	98.69%	Mismatches:	1
Query Match:	13.74%	Indels:	2
DB:	9	Gaps:	0
US-09-593-793A-113 (1-553) x AF109299 (1-482)			
Qy	136	GlyGlnValCysPheThrProLeuGluAlaLeuSerAspLeuPheArgAspProAsp	155
Db	26	GGCCAGGTGGCTTCACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCGGGACCCGGAC	85
Qy	156	HisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGly	175
Db	86	CACGTGCGCCAGGCGCTACTCTGTATGCCTCATGATTAGTCTTGGGGCTGCCTGGGC	145
Qy	176	TyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln	195
Db	146	TACCTCTGCGTGCATTTGACTGGGACACAGTGCCTGGCCCTACCTACCTGGGACCCAG	205
Qy	196	GluGluCysLeuPheGlyLeuLeuThrLeuPheLeuThrCysValAlaAla-ThrLe	215
Db	206	GAGGAGTGCCTCTTTGGCCTGCTCACCTCATCTTCTCACCTGCGTAGA-GCCACACT	264
Qy	215	uLeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaPr	235

(Stratagene) and Superscript II RT (Life Technologies)."

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BASE COUNT      227 a   273 c   341 g   194 t
ORIGIN

Alignment Scores:
Pred. No.:      3.51e-52      Length:      1035
Score:          69.00      Matches:      69
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      12.48%      Indels:      0
DB:              12      Gaps:      0

US-09-593-793A-113 (1-553) x BG828841 (1-1035)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
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Db 279 ATGGTCCAGAGCTGTGGGTGAGCCGCTGCGCACCGAAGCCAGCTCTTGCTG 338
|||||

QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||||
Db 339 GTCAACCTGCTAACTTTGGCCTGGAGGTGTGTTGGCGCAGGCATCACCTATGTGCGG 398
|||||

QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
|||||
Db 399 CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAAAGTTTCATGACCATGTGCTGGCATTTGGT 458
|||||

QY 61 ProValLeuGlyLeuValCysValPro 69
|||||
Db 459 CCAGTGTGGGCTGTGCTGTGTCCTCG 485

RESULT 13
AA112573/c
LOCUS          AA112573          342 bp      mRNA      linear      EST 23-DEC-1997
DEFINITION    zm28c12 r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone
IMAGE:526966 5', mRNA sequence.
ACCESSION     AA112573
VERSION       AA112573.1 GI:1665120
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 342)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins
, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
Underwood, K., Wohlmann, P., Wilson, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
9704478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should be
kept in mind should you use this clone.

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 307.
Location/Qualifiers
1. 342
/organism="Homo sapiens"
/db_xref="GDB:3918395"
/db_xref="taxon:9606"
/clone="IMAGE:526966"

FEATURES
source
```

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/clone.lib="Stratagene pancreas (#937208)"
/lab_host="SOLR cells (kanamycin resistant)"
/note="organ: pancreas; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Pancreatic adenocarcinoma cell line. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5'
CTCGAGTTTCTTTTCTTTTCTTTT 3'"

BASE COUNT      67 a   100 c   115 g   59 t
ORIGIN

Alignment Scores:
Pred. No.:      2.57e-47      Length:      342
Score:          63.00      Matches:      98
Percent Similarity: 98.00%      Conservative: 0
Best Local Similarity: 98.00%      Mismatches: 1
Query Match:      11.39%      Indels:      2
DB:              9      Gaps:      0

US-09-593-793A-113 (1-553) x AA112573 (1-342)

QY 383 AlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeu 402
|||||
Db 303 GCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGCCCTCCCTC 244
|||||

QY 403 TyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSer 422
|||||
Db 243 TACCACCGGGAGAACGAGGTGTCTGCCCAATACCAGGGGACACTGGAGTGCTAGC 184
|||||

QY 423 SerGluAspSerLeuMetThrSerPhe-LeuProGlyProLysProGlyAlaProPhePr 442
|||||
Db 183 AGTGAGGACAGCTGATGACCACTTCCTTGCAGGCCCTAAAGCTGGAGCTCCCTTCCC 124
|||||

QY 442 OAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeuCysG 462
|||||
Db 123 TAATGGACACGTGGGTGCTGGAGCAGTGGCTGTCCACCTCCACCGN-CTCTGCGG 65
|||||

QY 462 yAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAlaArg 481
|||||
Db 64 GGCCTCTGCTGTGATGTCTCCGTACGTGTGGTGGTGAGCCACCGAGGCCGCGG 7
|||||

RESULT 14
BF371417/c
LOCUS          BF371417          265 bp      mRNA      linear      EST 24-NOV-2000
DEFINITION    RCO-FN0140-040800-023-h03 FN0140 Homo sapiens cDNA, mRNA sequence.
ACCESSION     BF371417
VERSION       BF371417.1 GI:11333442
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 265)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Naqai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
```

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC0&t2=RC0-FN0140-040800-023-h03&t3=2000-08-04&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 265.

FEATURES

source
1. .265
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0140"
/dev_stage="Adult"
/note="Organ: prostate normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

BASE COUNT 68 a 72 c 94 g 31 t

Alignment Scores:
Pred. No.: 1.02e-44 Length: 265
Score: 60.00 Matches: 60
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.85% Indels: 0
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BF371417 (1-265)

QY 124 LeuLeuIleuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeu 143
|||||
Db 255 CTGCTCATCTGGCGTGGGCTGGACTTCTGTGGCCAGGTGTCTCACTCCACTA 196
QY 144 GluAlaLeuLeuSerAspLeuPheArgProAspHisCysArgGlnAlaTyrSerVal 163
|||||
Db 195 GAGGCCCTGCTCTGACTCTTCCGGGACCGGACCACTGCGCCAGCCCTACTCTGTC 136
QY 164 TyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrp 183
|||||
Db 135 TATGCCCTTCATGATCAGTCTTGGGGGCTGCTGGGTACTCTCTGCTGCCCACTGCTGG 76

RESULT 15
AW822644
LOCUS
DEFINITION
uq13q05.Y1 Ren Stubbs mouse thymus Mus musculus cDNA clone
IMAGE:2803292 5', mRNA sequence.
ACCESSION
AW822644
VERSION
AW822644.1 GI:7915661
KEYWORDS
EST.
SOURCE
house mouse.
MUS MUSCULUS

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 523)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Other ESTs: uq13q05.x1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.lbnl.gov) for further information.
MG1:1041916

TITLE
JOURNAL
COMMENT

Seq primer: Primer name ambiguous
High quality sequence stop: 474.
Location/Qualifiers

source

1. .523
/organism="Mus musculus"
/strain="C3H"
/db_xref="taxon:10090"
/clone="IMAGE:2803292"
/clone_lib="Ren Stubbs mouse thymus"
/sex="mixed"
/dev_stage="3 weeks"
/lab_host="DH10B"

/note="Organ: thymus; Vector: pT73D-Pac; Site_1: NotI;
Site_2: PacI; 1st strand cDNA was primed with an oligo(dT)
primer; double-stranded cDNA was ligated using 5' linker
ggcgctat and 3' linker aactggaagcttaatt. Library is
size-selected >2.5 kb and average insert size is 3.5 kb.
Clones were arrayed from primary plating; non-amplified.
Library constructed by X. Ren and L. Stubbs (Lawrence
Livermore National Laboratory and DOE Joint Genome
Institute, 7000 East Ave, L-453, Livermore, CA 94550)."

BASE COUNT 102 a 146 c 170 g 105 t

ORIGIN

Alignment Scores:
Pred. No.: 2.01e-43 Length: 523
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.67% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x AW822644 (1-523)

QY 8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGly 27
|||||
Db 294 AGCCCTGCTCTAGGCACCGGAAAGCTCAGCTCCTGCTGCTCAACCTGCTCACCCTTGGC 353
QY 28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProProLeuLeuGluValGly 47
|||||
Db 354 CTGGAGGTGTGCTGCTGGTGGCGGCATTACCTATGTGCGCACCCCTCTCTGCTGGAAGTCGGG 413
QY 48 ValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66
|||||
Db 414 GTGGAGGAGAAATTCATGACCATGCTGTGGGCAITGGCCCACTGCTAGCCTGGTT 470

RESULT 16
AW878124
LOCUS
DEFINITION
120845 MARC lPIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION
AW878124
VERSION
AW878124.1 GI:7843900
KEYWORDS
EST.
SOURCE
pig.
ORGANISM
Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 537)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

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PCR Primers
FORWARD: AGGAACACGATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 45 row: C column: 12
Seq primer: ATTTAGTCGACACTATAG.
Location/Qualifiers
1. .537
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC lpiG"
/tissue_type="pooled"
/lab_host="DH10B"
/Note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 96 a 161 c 186 g 94 t
ORIGIN
Alignment Scores:
Pred. No.: 2.07e-43 Length: 537
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.67% Indels: 0
DB: 10 Gaps: 0
US-09-593-793a-113 (1-553) x AW787124 (1-537)
QY 8 SerArgLeuAurghisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGly 27
Db 297 AGCCGCTCTCGGGCATCGGAAGCCAGCTCCTGCTGTTAACCTGCTGACGTTCCGC 356
QY 28 LeuGluValCysLeuAlaAlaGlyIleThrTyrrValProLeuLeuLeuGluValGly 47
Db 357 CTGGAGGTGCTGCTGGCCCGCAGCATCCTACGTGCCACCCCTGCTGTGAAGTGGG 416
QY 48 ValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66
Db 417 GTAGAGGAGAAGTTATGACCATGTTGCTGGGCATCGGTCCAGTCTGGGCTGGTGC 473
RESULT 17
LOCUS AW412402 592 bp mRNA linear EST 08-FEB-2000
DEFINITION u078h02.y1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:2648691 5',
similar to TR:Q39231 Q39231 SUCROSE-PROTON SYMPORTER. [1] ; , mRNA
sequence.
ACCESSION AW412402
VERSION AW412402.1 GI:6938274
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 592)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Other_ESTs: u078h02.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1137 row: n column: 24
High quality sequence start: 2
High quality sequence stop: 630.
Location/Qualifiers
1. .630
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="IMAGE:5050583"
/clone_lib="NCI_CGAP_L19"
FEATURES
source
1. .592
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="IMAGE:2648691"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/Note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 91 a 193 c 168 g 140 t
ORIGIN
Alignment Scores:
Pred. No.: 2.35e-43 Length: 592
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.67% Indels: 0
DB: 10 Gaps: 0
US-09-593-793a-113 (1-553) x AW412402 (1-592)
QY 262 GlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSer 281
Db 341 CAGCTGTGTCGGCATGCTCGACCCCTACGCCACACTCTTTGTGGCTGAGCTGTGCAGC 400
QY 282 TrpMetAlaLeuMetThrPheThrLeuPheTyrrThrAspPheValGlyGlyLeuTyr 301
Db 401 TGGATGGCACTTATGACTTTCACACTGTTCTACACGGACTTCCTGGGAGAGGGCTGTAC 460
QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrrAspGluGly 320
Db 461 CAGGTTGTACCCAGAGCCGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 517
RESULT 18
LOCUS B1145201 630 bp mRNA linear EST 05-JUL-2001
DEFINITION 602909395F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:5050583 5',
mRNA sequence.
ACCESSION B1145201
VERSION B1145201.1 GI:14605202
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 630)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL NIH-MGC http://mgc.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1137 row: n column: 24
High quality sequence start: 2
High quality sequence stop: 630.
Location/Qualifiers
1. .630
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="IMAGE:5050583"
/clone_lib="NCI_CGAP_L19"
FEATURES
source
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/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.9 Kb. Constructed by Life
Technologies. Note: this is a NCI-CGP Library."
BASE COUNT 114 a 180 c 199 g 137 t
ORIGIN
Alignment Scores:
Pred. No.: 2,55e-43 Length: 630
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.67% Indels: 0
DB: 13 Gaps: 0
US-09-593-793A-113 (1-553) x BI145201 (1-630)
QY 8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGly 27
|||||
Db 272 AGCGGTCTGCTACGGCACCAGCAAGCTCAGCTCTGCTGTCACACCTGCTCAGCTTTGGC 331
QY 28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProLeuLeuLeuGluValGly 47
|||||
Db 332 CTGGAGGTGTGCTGCTGCTGCCGCGCATTACCTATGTGCCACCCCTTCTGCTGGAAGTCGGG 391
QY 48 ValGluGlyLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66
|||||
Db 392 CTGGAGGAGAAATTCATGACCATGCTGGTGGGCGATTTGGCCAGTGTAGCCCTGGTT 448
RESULT 19
BB627844 650 bp mRNA linear EST 26-OCT-2001
LOCUS BB627844 RIKEN full-length enriched, adult male urinary bladder Mus
DEFINITION musculus cDNA clone 9530042D02 5', mRNA sequence.
VERSION BB627844.1 GI:16465416
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okada
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
Tagami,M., Tagawa,A., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
```

```

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
FEATURES
Location/Qualifiers
1..650
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="9530042D02"
/clone_lib="RIKEN full-length enriched, adult male urinary
bladder"
/sex="male"
/tissue_type="urinary bladder"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAAGGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 370.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCGAGTTAAATTAATCCGCCCCGCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from
Lambda FLC I."
BASE COUNT 120 a 182 c 214 g 134 t
ORIGIN
Alignment Scores:
Pred. No.: 2,65e-43 Length: 650
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.67% Indels: 0
DB: 10 Gaps: 0
US-09-593-793A-113 (1-553) x BB627844 (1-650)
QY 8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGly 27
|||||
Db 333 AGCGGTCTGCTACGGCACCAGCAAGCTCAGCTCTGCTGTCACACCTGCTCAGCTTTGGC 392
QY 28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProLeuLeuLeuGluValGly 47
|||||
Db 393 CTGGAGGTGTGCTGCTGCTGCCGCGCATTACCTATGTGCCACCCCTTCTGCTGGAAGTCGGG 452
QY 48 ValGluGlyLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66
|||||
Db 453 GTGGAGGAGAAATTCATGACCATGCTGGTGGGCGATTTGGCCAGTGTAGCCCTGGTT 509
RESULT 20
BB627667 692 bp mRNA linear EST 26-OCT-2001
LOCUS BB627667 RIKEN full-length enriched, adult male urinary bladder Mus
DEFINITION musculus cDNA clone 9530024M01 5', mRNA sequence.
ACCESSION BB627667
VERSION BB627667.1 GI:16465271
```

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

EST.
house mouse.
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 692)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Kouda
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
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Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
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M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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prepare full-length cDNA libraries for rapid discovery of new
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S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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sequencing pipeline with 384 multicapillary sequencer. Genome Res.
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Y. and Hayashizaki,Y.
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nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

FEATURES

source

1. 692
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="9530024M01"
/clone_lib="RIKEN full-length enriched, adult male urinary
bladder"
/sex="male"
/tissue_type="urinary bladder"
/dev_stages="adult"
/lab_host="DH10B"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTTCTTTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 370.0. Second
strand cDNA was prepared with the primer adapter of

sequence [5' GAGAGAGATTCTCGAGTAAATTAATTAATCCCTCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from
Lambda FLC I."
BASE COUNT 127 a 197 c 224 g 143 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 2.87e-43 Length: 692
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.67% Indels: 0
DB: 10 Gaps: 0
US-09-593-793a-113 (1-553) x BB627667 (1-692)
Qy 8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGly 27
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Db 333 AGCCGCTGCTACGGCAGCGGAAAGCTACGCTCTGCTGGTCAACCTGCTCACCCTTGGC 392
Qy 28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProLeuLeuGluValGly 47
|||||
Db 393 CTGGAGGTGCTGCTGGCTGCCGCGCATACCTATGTGCCACCCCTTCTGCTGGAAGTCGGG 452
Qy 48 ValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66
|||||
Db 453 GTGGAGGAGAAATTCATGACCATGTGTGTGGGCATTTGCCCATGCTAGGCTGCTGTT 509
RESULT 21
BF789072 759 bp mRNA linear EST 12-JAN-2001
LOCUS 602104930F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4222998
DEFINITION 5', mRNA sequence.
ACCESSION BF789072
VERSION BF789072.1 GI:12094108
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 759)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM9810 row: 1 column: 07
High quality sequence start: 3
High quality sequence stop: 756.
Location/Qualifiers
1. 759
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4222998"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT 131 a 218 c 243 g 167 t
ORIGIN
Alignment Scores:

Pred. No.: 3.23e-43 Length: 759
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.67% Indels: 0
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BF789072 (1-759)

QY 8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGly 27

|||||

Db 303 AGCGGCTGTCAGCGCACCGAAGCTCAGCTCCTGCTGCTCAACCTGCTCAGCTTTGGC 362

QY 28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProProLeuLeuLeuGluValGly 47

|||||

Db 363 CTGAGGTGCTGCTGCTGCCGCGCATACCTATGTGCCACCCCTTCTGCTGGAAGTCGGG 422

QY 48 ValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66

|||||

Db 423 GTGGAGGAGAAATTCATGACCATGGTGTGGGCAATGGCCAGTGTAGCGCTGGTT 479

RESULT 22

BI107873

LOCUS 602901816F1 NCI_CGAP_Mam3 Mus musculus cdna clone IMAGE:5031771 5',

DEFINITION mRNA sequence.

ACCESSION BI107873 858 bp mRNA linear EST 26-JUN-2001

VERSION BI107873.1 GI:14558766

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1088 row: 0 column: 04

High quality sequence stop: 810.

FEATURES

source

1. .858

Location/Qualifiers

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/strain="129,C57BL/6J,FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5031771"

/clone_lib="NCI_CGAP_Mam3"

/tissue_type="tumor, gross tissue"

/dev_stage="10 months"

/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH

Reference for transgenic model: Xu et al., Nature Genetics

22, 37-43 (1999)."

BASE COUNT 133 a 265 c 245 g 215 t

ORIGIN

Alignment Scores:

Pred. No.: 3.79e-43 Length: 858

Score: 59.00 Matches: 59

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 10.67% Indels: 0

DB: 0 Gaps: 0

US-09-593-793A-113 (1-553) x BF789072 (1-759)

QY 8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGly 27

|||||

Db 303 AGCGGCTGTCAGCGCACCGAAGCTCAGCTCCTGCTGCTCAACCTGCTCAGCTTTGGC 362

QY 28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProProLeuLeuLeuGluValGly 47

|||||

Db 363 CTGAGGTGCTGCTGCTGCCGCGCATACCTATGTGCCACCCCTTCTGCTGGAAGTCGGG 422

QY 48 ValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66

|||||

Db 423 GTGGAGGAGAAATTCATGACCATGGTGTGGGCAATGGCCAGTGTAGCGCTGGTT 479

RESULT 22

BI107873

LOCUS 602901816F1 NCI_CGAP_Mam3 Mus musculus cdna clone IMAGE:5031771 5',

DEFINITION mRNA sequence.

ACCESSION BI107873 858 bp mRNA linear EST 26-JUN-2001

VERSION BI107873.1 GI:14558766

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1088 row: 0 column: 04

High quality sequence stop: 810.

FEATURES

source

1. .858

Location/Qualifiers

/organism="Mus musculus"

/strain="129,C57BL/6J,FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5031771"

/clone_lib="NCI_CGAP_Mam3"

/tissue_type="tumor, gross tissue"

/dev_stage="10 months"

/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH

Reference for transgenic model: Xu et al., Nature Genetics

22, 37-43 (1999)."

BASE COUNT 133 a 265 c 245 g 215 t

ORIGIN

Alignment Scores:

Pred. No.: 3.79e-43 Length: 858

Score: 59.00 Matches: 59

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 10.67% Indels: 0

DB: 0 Gaps: 0

US-09-593-793A-113 (1-553) x BF789072 (1-759)

QY 8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGly 27

|||||

Db 303 AGCGGCTGTCAGCGCACCGAAGCTCAGCTCCTGCTGCTCAACCTGCTCAGCTTTGGC 362

QY 28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProProLeuLeuLeuGluValGly 47

|||||

Db 363 CTGAGGTGCTGCTGCTGCCGCGCATACCTATGTGCCACCCCTTCTGCTGGAAGTCGGG 422

QY 48 ValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66

|||||

Db 423 GTGGAGGAGAAATTCATGACCATGGTGTGGGCAATGGCCAGTGTAGCGCTGGTT 479

RESULT 22

BI107873

LOCUS 602901816F1 NCI_CGAP_Mam3 Mus musculus cdna clone IMAGE:5031771 5',

DEFINITION mRNA sequence.

ACCESSION BI107873 858 bp mRNA linear EST 26-JUN-2001

VERSION BI107873.1 GI:14558766

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1088 row: 0 column: 04

High quality sequence stop: 810.

FEATURES

source

1. .858

Location/Qualifiers

/organism="Mus musculus"

/strain="129,C57BL/6J,FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5031771"

/clone_lib="NCI_CGAP_Mam3"

/tissue_type="tumor, gross tissue"

/dev_stage="10 months"

/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH

Reference for transgenic model: Xu et al., Nature Genetics

22, 37-43 (1999)."

BASE COUNT 133 a 265 c 245 g 215 t

ORIGIN

Alignment Scores:

Pred. No.: 3.79e-43 Length: 858

Score: 59.00 Matches: 59

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 10.67% Indels: 0

DB: 0 Gaps: 0

US-09-593-793A-113 (1-553) x BF789072 (1-759)

QY 8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGly 27

|||||

Db 303 AGCGGCTGTCAGCGCACCGAAGCTCAGCTCCTGCTGCTCAACCTGCTCAGCTTTGGC 362

QY 28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProProLeuLeuLeuGluValGly 47

|||||

Db 363 CTGAGGTGCTGCTGCTGCCGCGCATACCTATGTGCCACCCCTTCTGCTGGAAGTCGGG 422

QY 48 ValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66

|||||

Db 423 GTGGAGGAGAAATTCATGACCATGGTGTGGGCAATGGCCAGTGTAGCGCTGGTT 479

RESULT 22

BI107873

LOCUS 602901816F1 NCI_CGAP_Mam3 Mus musculus cdna clone IMAGE:5031771 5',

DEFINITION mRNA sequence.

ACCESSION BI107873 858 bp mRNA linear EST 26-JUN-2001

VERSION BI107873.1 GI:14558766

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1088 row: 0 column: 04

High quality sequence stop: 810.

FEATURES

source

1. .858

Location/Qualifiers

/organism="Mus musculus"

/strain="129,C57BL/6J,FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5031771"

/clone_lib="NCI_CGAP_Mam3"

/tissue_type="tumor, gross tissue"

/dev_stage="10 months"

/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH

Reference for transgenic model: Xu et al., Nature Genetics

22, 37-43 (1999)."

BASE COUNT 133 a 265 c 245 g 215 t

ORIGIN

Alignment Scores:

Pred. No.: 3.79e-43 Length: 858

Score: 59.00 Matches: 59

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 10.67% Indels: 0

DB: 0 Gaps: 0

US-09-593-793A-113 (1-553) x BF789072 (1-759)

QY 8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGly 27

|||||

Db 303 AGCGGCTGTCAGCGCACCGAAGCTCAGCTCCTGCTGCTCAACCTGCTCAGCTTTGGC 362


```
Db 339 AGCCGTCCTACGGCACCAGAAAGTCAGCTCCTGCTGCTCAACCTGCTCACCTTTGGC 398
|||||
QY 28 LeuGluValCysLeuAlaLaGlyIleThrTyrValProLeuLeuGluValGly 47
|||||
Db 399 CTGAGGTGTGCTGCTGCTGCCGCAATACCTATGTGCCACCCCTCTGCTGGAAGTCGGG 458
|||||
QY 48 ValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66
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Db 459 GTGGAGGAGAAATTCATGACCATGTGTGTGGCATTTGGCCAGTCGTAGGCTGGTT 515
|||||

RESULT 24
BF785813 929 bp mRNA linear EST 12-JAN-2001
LOCUS 602112437F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4240617
DEFINITION 5', mRNA sequence.
ACCESSION BF785813
VERSION BF785813.1 GI:12090849
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 929)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9855 row: j column: 10
High quality sequence stop: 610.
Location/Qualifiers
1..929
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4240617"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT 190 a 275 c 262 g 202 t
ORIGIN

Alignment Scores:
Pred. No.: 4,19e-43 Length: 929
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.67% Indels: 0
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BF785813 (1-929)

QY 262 GlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSer 281
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Db 267 CAGCTGTGTCGCGATGCTGCACCCCTACCGGACTCTTTGTGGCTGAGCTGTGCAGC 326
|||||
QY 282 TrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyr 301
|||||
Db 327 TGGATGGCACTTATGACTTTTCACATGTTCTACACGAGCTTCGTGGGAGGGGCTGTAC 386
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QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
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Db 387 CAGGGTGTACCCAGAGCCGAGCAGCAGCCGAGGCCGAGACACTATGATGAAGGC 443
|||||
RESULT 25
BG242597 1116 bp mRNA linear EST 13-FEB-2001
LOCUS 602354010F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4482362 5',
DEFINITION mRNA sequence.
ACCESSION BG242597
VERSION BG242597.1 GI:12752412
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1116)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10319 row: c column: 03
High quality sequence stop: 666.
Location/Qualifiers
1..1116
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4482362"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 209 a 349 c 314 g 244 t
ORIGIN

Alignment Scores:
Pred. No.: 5,3e-43 Length: 1116
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.67% Indels: 0
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BG242597 (1-1116)

QY 262 GlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSer 281
|||||
Db 53 CAGCTGTGTCGCGATGCTGCACCCCTACCGGACTCTTTGTGGCTGAGCTGTGCAGC 112
|||||
QY 282 TrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyr 301
|||||
Db 113 TGGATGGCACTTATGACTTTTCACATGTTCTACACGAGCTTCGTGGGAGGGGCTGTAC 172
|||||
QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
|||||
Db 173 CAGGGTGTACCCAGAGCCGAGCAGCCGAGGCCGAGACACTATGATGAAGGC 229
|||||

RESULT 26
AA984323 348 bp mRNA linear EST 27-MAY-1998
LOCUS am84a12.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone
DEFINITION IMAGE:1629790 3', mRNA sequence.
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ACCESSION   BF854825
VERSION     BF854825.1
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 322)
AUTHORS    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
            Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE       Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE    20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&t2=RC6-FN0202-
            271000-011-A03&t3=2000-10-27&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 12
            High quality sequence stop: 321.
FEATURES    Location/Qualifiers
             source
               1..322
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone_lib="FN0202"
               /dev_stage="Adult"
               /note="Organ: prostate.normal; Vector: puc18; Site_1: SmaI
               ; Site_2: SmaI; A mini-library was made by cloning
               products derived from ORESTES PCR (U.S. Letters Patent
               application No. 196,716 - Ludwig Institute for Cancer
               Research) profiles into the puc 18 vector. Reverse
               transcription of tissue mRNA and cDNA amplification were
               performed under low stringency conditions."
BASE COUNT  64 a 101 c 112 g 45 t
ORIGIN
Alignment Scores:
Pred. No.: 1.21e-33 Length: 322
Score: 48.00 Matches: 48
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.68% Indels: 0
DB: 12 Gaps: 0
US-09-593-793A-113 (1-553) x BF854825 (1-322)
Qy 430 SerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGly 449
Db 242 AGCTTCCTGCCAGGCCCTAAGCGCTGAGCTCCCTCCCTAATGGACACGTGGTGCTGGA 183
Qy 450 GlySerGlyLeuLeuProProProAlaLeuGlyAlaSerAlaCysAspValSer 469
Db 182 GCGAGTGGCGCTGCTCCACCTCCACCCGCGGCTCTCGCGGGGCTGTGCTGTGCTCC 123
Qy 470 ValArqValValValGlyGluPro 477
Db 122 GTACGTGTGGTGGTGGTGAGCCC 99
RESULT 29
AW175665/c

LOCUS       AW175665
DEFINITION  RC3-BT0046-310899-002-F07 BT0046 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW175665
VERSION     AW175665.1
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 412)
AUTHORS    HCCP http://www.ludwig.org.br/ORESTES.
            The FAPESP/LICR Human Cancer Genome Project
            Unpublished (1999)
JOURNAL
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-BT0046-
            310899-002-F07&t3=1999-08-31&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 411.
FEATURES    Location/Qualifiers
             source
               1..412
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone_lib="BT0046"
               /dev_stage="Adult"
               /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
               SmaI; A mini-library was made by cloning products derived
               from ORESTES PCR (U.S. Letters Patent application No. 196
               ,716 - Ludwig Institute for Cancer Research) profiles
               into the puc 18 vector. Reverse transcription of tissue
               mRNA and cDNA amplification were performed under low
               stringency conditions."
BASE COUNT  106 a 117 c 128 g 61 t
ORIGIN
Alignment Scores:
Pred. No.: 1.66e-33 Length: 412
Score: 48.00 Matches: 48
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.68% Indels: 0
DB: 10 Gaps: 0
US-09-593-793A-113 (1-553) x AW175665 (1-412)
Qy 506 ProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVal 525
Db 401 CCTTCCCTGTTTATGGGCTCCATTGTCAGCTCAGCCAGTCTGCTCAGCTATATGCTG 342
Qy 526 SerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLys 545
Db 341 TCTGCCGAGGCGCTGGGTCTGTCGCCATTTACTTTGTACACAGGTAGTATTTGACAAG 282
Qy 546 SerAspLeuAlaLysTyrSerAla 553
Db 281 ACCGACTTGGCCAAATACTACGCG 258
RESULT 30
BW915082
LOCUS       BW915082
DEFINITION  AGENCOURT_6702317 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5481218
            5', mRNA sequence.
ACCESSION   BW915082
VERSION     BW915082.1
KEYWORDS    EST.

```


Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/Drp

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LCM2006 row: j column: 22

High quality sequence start: 131

High quality sequence stop: 308.

Location/Qualifiers

FEATURES

source

1. .1063

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5481717"

/clone_lib="NIH_MGC_41"

/tissue_type="amelanotic melanoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site:2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGCAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

BASE COUNT 246 a 283 c 261 g 272 t 1 others

ORIGIN

Alignment Scores: 3.77e-31 Length: 1063

Pred. No.: 46.00 Matches: 46

Score: 100.00% Conservative: 0

Percent Similarity: 100.00% Mismatches: 0

Best Local Similarity: 100.00% Indels: 0

Query Match: 8.32% Gaps: 0

DB: 14

US-09-593-793A-113 (1-553) x BM915527 (1-1063)

QY 507 SerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSer 526

Db 1 TCCCTGTTATGGGCTCCATTGTCAGCTCAGCCAGTCTGTCACTGCCTATATGGTCT 60

QY 527 AlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSer 546

Db 61 GCCGAGGCCCTGGTCTGGTCCCACTTACTTGTCTACAGAGTAGTATTTGACAAGAGC 120

QY 547 AspLeuAlaLysTyrSer 552

Db 121 GACTTGGCCAAATACTCA 138

RESULT 33

B1045233

LOCUS B1045233 341 bp mRNA linear EST 14-JUN-2001

DEFINITION RC6-FN0202-080101-014-F01 FN0202 Homo sapiens cDNA, mRNA sequence.

ACCESSION B1045233

VERSION B1045233.1 GI:14451855

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 341)

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalheiro,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

TITLE Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

MEDLINE

COMMENT

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&t2=RC6-FN0202-

080101-014-F01&t3=2001-01-08&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 18

High quality sequence stop: 279.

Location/Qualifiers

1. .341

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="FN0202"

/dev_stage="Adult"

/note="Organ: prostate,normal; Vector: puc18; Site:1: SmaI

; Site:2: SmaI; A mini-library was made by cloning

products derived from ORESTES PCR (U.S. Letters Patent

application No. 196,716 - Ludwig Institute for Cancer

Research) profiles into the puc 18 vector. Reverse

transcription of tissue mRNA and cDNA amplification were

performed under low stringency conditions."

BASE COUNT 56 a 105 c 84 g 95 t 1 others

ORIGIN

Alignment Scores: 7.19e-31 Length: 341

Pred. No.: 45.00 Matches: 45

Score: 100.00% Conservative: 0

Percent Similarity: 100.00% Mismatches: 0

Best Local Similarity: 100.00% Indels: 0

Query Match: 8.14% Gaps: 0

DB: 13

US-09-593-793A-113 (1-553) x B1045233 (1-341)

QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77

Db 206 GCATGTGTCAGTGTGGGCTGTGTCTGTCTCCGCTCTAGGCTCAGCCAGTACCAC 265

QY 78 TrpArgGlyArgTyrGlyArgArgPropheIleTfpAlaLeuSerLeuGlyIleLeu 97

Db 266 TGGCGTGGACGCTATGGCGCGGCGGCTTCATCTGGCAGTGTCTTGGGCATCCTG 325

QY 98 LeuSerLeuPheLeu 102

Db 326 CTGAGCCTCTTCTC 340

RESULT 34

BF854834/c

LOCUS BF854834 428 bp mRNA linear EST 16-JAN-2001

DEFINITION RC6-FN0202-271000-011-E04 FN0202 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF854834

VERSION BF854834.1 GI:12242578

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 428)

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalheiro,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

TITLE

JOURNAL

JOURNAL
MEDLINE
COMMENT

sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6<2=RC6-FN0202-271000-011-E04&t3=2000-10-27&t4=1>)

Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence stop: 423.

FEATURES
source

1..428
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0202"
/dev_stage="Adult"

/note="organ: prostate_normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector; Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

BASE COUNT 111 a 111 c 137 g 68 t 1 others
ORIGIN

Alignment Scores:

Pred. No.: 9,62e-31 Length: 428
Score: 45.00 Matches: 45
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.14% Indels: 0
DB: 12 Gaps: 0

US-09-593-793a-113 (1-553) x BF854834 (1-428)

QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77

Db 218 GCGATTGGTCCAGTCTGGCGCTCTGTCTGTCCGCTCTTAGGCTCAGCCAGTACCAC 159

QY 78 TrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97

Db 158 TGGCGTGGAGCGTATGGCGCGCGCGCCCTTCATCTGGGCACCTGTCCTTGGGCATCCTG 99

QY 98 LeuSerLeuPheLeu 102

Db 98 CTGAGCCTCTTCTC 84

RESULT 35
AA647708

LOCUS AA647708 242 bp mRNA linear EST 28-OCT-1997
DEFINITION vq77h04.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone

IMAGE:1108375 5', mRNA sequence.

ACCESSION AA647708

VERSION AA647708.1 GI:2574137

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 242)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and

TITLE
JOURNAL
COMMENT

The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box #501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infoimage.llnl.gov) for further information.
MGI:60543

High quality sequence stop: 213.

FEATURES
source

1..242
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
/clone="IMAGE:1108375"
/clone_lib="Knowles Solter mouse 2 cell"
/tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH10B"

/note="organ: embryo; Vector: pBluescribe (modified);
Site_1: MluI; Site_2: SalI; Cloned unidirectionally from
mRNA prepared from 13,500 2-cell stage embryos. Primer:
SalI(dT): 5'-CGGTGACCGTCGACCGTGTGCTTTT-3', CDNAS
were cloned into the MluI/SalI sites of a modified
pBluescribe vector using commercial linkers (NEB).
Average insert size: 1.2 kb."

BASE COUNT 42 a 68 c 75 g 57 t

ORIGIN

Alignment Scores:

Pred. No.: 3,79e-30 Length: 242
Score: 44.00 Matches: 44
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.96% Indels: 0
DB: 9 Gaps: 0

US-09-593-793a-113 (1-553) x AA647708 (1-242)

QY 16 AlaGlnLeuLeuValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGly 35

Db 109 GTCAGCTCTGCTGGTCAACCTGCTACCTTGGCTGGAGGTGCTGCTGGCGCGC 168

QY 36 IleThrTyrValProLeuLeuGluValGlyValGluLysPheMetThrMet 55

Db 169 ATTACTATGTGCCACCCCTTCTGCTGGAAGTCGGGTGGAGAGAAATTCATGACCATG 228

QY 56 ValLeuGlyIle 59

Db 229 GTGTTGGGCATT 240

RESULT 36
BE914848

LOCUS BE914848 1037 bp mRNA linear EST 29-
DEFINITION 601667874F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3967,

ACCESSION BE914848

VERSION BE914848.1 GI:10413891

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 1037)
NIH-MGC <http://mgi.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM9143 row: C column: 19
 High quality sequence stop: 564.
 Location/Qualifiers
 1..1037
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:3967818"
 /clone_lib="NCI_CGAP_Maml"
 /tissue_type="tumor, biopsy sample"
 /dev_stage="10 months, virgin"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
 a 202 a 289 c 310 g 234 t 2 others

BASE COUNT

202 a 289 c 310 g 234 t

ORIGIN

Alignment Scores:
 Pred. No.: 2,01e-28 Length: 1037
 Score: 43.00 Matches: 43
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 7.78% Indels: 0
 DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BE914848 (1-1037)

QY 8 SerArgLeuAurHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGly 27
 |||||
 Db 280 AGCCGTCGTACGACCGGAAAGCTCAGCTCCTGCTGCTCACCCTTGCG 339

QY 28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProLeuLeuGluValGly 47
 |||||
 Db 340 CTGGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 399

QY 48 ValGluGlu 50
 |||||

Db 400 GTGGAGGAG 408

RESULT 37
 BG081576
 LOCUS H3066G04-5 NTA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
 DEFINITION H3066G04 5', mRNA sequence.
 ACCESSION BG081576
 VERSION BG081576.1 GI:12564144
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 AUTHORS Karul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka
 T.S., Carter,M.G. and Ko,M.S.H.
 TITLE Verification and initial annotation of NIA mouse 15K cDNA clone set
 JOURNAL Unpublished (2001)
 COMMENT Other_ESTS: H3066G04-3
 Contact: George J. Karul
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@lgsun.grc.nia.nih.gov
 This clone set has been freely distributed to the community. Please

visit <http://lgsun.grc.nia.nih.gov/cDNA/15k.html> for details.
 Plate: H3066 row: G column: 04
 Seq primer: -21M13 Reverse
 High quality sequence stop: 549
 POLYA-No.

FEATURES

source

Location/Qualifiers
 1..549
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="niaEST:H3066G04-5"
 /db_xref="taxon:10090"
 /clone="H3066G04"
 /clone_lib="NIA Mouse 15K cDNA Clone Set"
 /sex="Clones arrayed from a variety of cDNA libraries"
 /dev_stage="Clones arrayed from a variety of cDNA libraries"
 /lab_host="DH10B"
 /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT) primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U.S.A., 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

BASE COUNT 98 a 176 c 160 g 115 t

ORIGIN

Alignment Scores:
 Pred. No.: 5,98e-27 Length: 549
 Score: 41.00 Matches: 41
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 7.41% Indels: 0
 DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BG081576 (1-549)

QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396
 |||||
 Db 291 GTAGTGACAGCCTCAGCTGCGCTCACCAGGGTTCACCTCTCGGCGCTTCGAGATCTCGCT 350

QY 397 TyrThrLeuAlaSerLeuTyrHisArgGluTysGlnValPheLeuProLysTyrArgGly 416
 |||||
 Db 351 TACACGCTCGCTCCTCTTACCACCGTGAGAGCAGGTGTTCTCTCCCAATACCGAGG 410

QY 417 Asp 417
 |||

Db 411 GAC 413

RESULT 38

LOCUS

BF581244

DEFINITION

602100464F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4220415 5', mRNA sequence.

ACCESSION

BF581244

VERSION

BF581244.1 GI:11654956

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

REFERENCE 1 (bases 1 to 700)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9803 row: p column: 16
High quality sequence start: 2
High quality sequence stop: 680.
FEATURES
source
Location/Qualifiers
1..700
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4220415"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 110 a 227 c 197 g 166 t
ORIGIN
Alignment Scores:
Pred. No.: 8,17e-27 Length: 700
Score: 41.00 Matches: 41
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.41% Indels: 0
DB: 12 Gaps: 0
US-09-593-793a-113 (1-553) x BF581244 (1-700)
QY 262 GlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSer 281
Db 254 CAGCTGTGCTGCCGATGCTCGCACCTACGCCGACTTTTGTGGCTGAGCTGTGCAGC 313
QY 282 TrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyr 301
Db 314 TGGATGGCATTATGACTTTCACACTGTCTACACGGACTTCGTGGAGAGGGGCTGTAC 373
QY 302 Gln 302
Db 374 CAG 376
RESULT 39
BG173136 969 bp mRNA linear EST 06-FEB-2001
LOCUS 602335411F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4458602 5',
DEFINITION mRNA sequence.
ACCESSION BG173136
VERSION BG173136.1 GI:12679748
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 969)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10254 row: e column: 05
High quality sequence stop: 666.

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10257 row: e column: 03
High quality sequence stop: 608.
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Location/Qualifiers
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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4458602"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 199 a 289 c 287 g 194 t
ORIGIN
Alignment Scores:
Pred. No.: 1.24e-26 Length: 969
Score: 41.00 Matches: 41
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.41% Indels: 0
DB: 12 Gaps: 0
US-09-593-793a-113 (1-553) x BG173136 (1-969)
QY 262 GlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSer 281
Db 229 CAGCTGTGCTGCCGATGCTCGCACCTACGCCGACTTTTGTGGCTGAGCTGTGCAGC 288
QY 282 TrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyr 301
Db 289 TGGATGGCATTATGACTTTCACACTGTCTACACGGACTTCGTGGAGAGGGGCTGTAC 348
QY 302 Gln 302
Db 349 CAG 351
RESULT 40
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LOCUS 602334219F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4457452 5',
DEFINITION mRNA sequence.
ACCESSION BG174399
VERSION BG174399.1 GI:12681102
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 786)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10254 row: e column: 05
High quality sequence stop: 666.

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/lab_host="DH10B"
 /note="Vector: pSPOR1; Site_1: SalI; Site_2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT) primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U.S.A., 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

BASE COUNT 121 a 138 c 126 g 81 t
 ORIGIN

Alignment Scores:
 Pred. No.: 9.9e-20 Length: 466
 Score: 33.00 Matches: 60
 Percent Similarity: 96.77% Conservative: 0
 Best Local Similarity: 96.77% Mismatches: 1
 Query Match: 5.97% Indels: 2
 DB: 12 Gaps: 0

US-09-593-793a-113 (1-553) x BG068547 (1-466)

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 QY 505 AlaProSerLeuPheMetGlySerIleValGlnLeuSerGln-SerValThrAlaTyrMe 524
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 Db 303 GCTCCGCTCCCTGTTTCATGGCTCCATTGCCAGCTGAGCCA-CTCTGTCTACCTGCTATAT 245
 QY 524 tValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAs 544
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 QY 544 pLys 545
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 Db 184 CAAG 181

RESULT 45
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 LOCUS 602829364F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4984191 5',
 DEFINITION mRNA sequence.
 ACCESSION BG964810
 VERSION BG964810.1 GI:14352447
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 JOURNAL NIH-MGC http://mgi.nci.nih.gov/
 COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
 Plate: LLAM10989 row: p column: 16
 High quality sequence stop: 563.

FEATURES

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 /db_xref="taxon:10090"
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 /clone_lib="NCI_CGAP_Co24"
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 /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 95 a 156 c 168 g 143 t
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Alignment Scores:
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US-09-593-793a-113 (1-553) x BG964810 (1-564)

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 QY 505 AlaProSerLeuPheMetGlySerIleValGlnLeuSerGln-SerValThrAlaTyrMe 524
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 Db 189 GCTCCGCTCCCTGTTTCATGGCTCCATTGCCAGCTGAGCCA-CTCTGTCTACCTGCTATAT 247
 QY 524 tValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAs 544
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 Db 308 CAAG 311

Search completed: February 19, 2003, 06:34:54
 Job time : 1672 secs

Seq 16

2-7th

→ encodes 254 AA

AA 299-553

553

~~299~~
254

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79 10 1.8 30 10 US-09-822-827-856 Sequence 856, App
80 10 1.8 31 9 US-10-012-896-970 Sequence 970, App
81 10 1.8 31 9 US-09-895-814-970 Sequence 970, App
82 10 1.8 32 9 US-10-012-896-975 Sequence 975, App
83 10 1.8 32 9 US-09-895-814-975 Sequence 975, App
84 9 1.6 27 9 US-10-012-896-859 Sequence 859, App
85 9 1.6 27 9 US-09-895-793-859 Sequence 859, App
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87 9 1.6 27 10 US-09-838-785-f Sequence 6, Appli
88 9 1.6 27 10 US-09-759-143-859 Sequence 859, App
89 9 1.6 27 10 US-09-780-669-859 Sequence 859, App
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91 9 1.6 33 9 US-10-012-896-488 Sequence 488, App
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96 9 1.6 33 10 US-09-822-827-488 Sequence 850, App
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c 99 9 1.6 40 9 US-09-895-814-850 Sequence 850, App
c 100 9 1.6 40 10 US-09-759-143-850 Sequence 850, App

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09838785
; Patent No. US20020009455A1
; GENERAL INFORMATION:
; APPLICANT: Lau, Ted
; APPLICANT: Lin, Rick
; APPLICANT: Parkes, Debbie
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; APPLICANT: Van Heult, Pam T
; APPLICANT: Wu, John
; TITLE OF INVENTION: DNA Encoding a No. US20020009455A1e1 PROST 03
; FILE REFERENCE: 51831AUSM1
; CURRENT APPLICATION NUMBER: US/09/838,785
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/200,065
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3320
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (282)..(1943)
US-09-838-785-1

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Pred. No.: 0 Length: 3320
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

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Db 342 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTTGGCCGACGACATCATATGTGCGG 401
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Db 402 CCTCTGCTCTGGAAGTGGGGGTAGAGGAGATTTCATGACCATGCTGTGGCATTTGGT 461
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Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
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Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
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QY 481 ArgValValProGlyArgGlyLeuLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
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QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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RESULT 2
US-09-232-880-110
; Sequence 110, Application US/09232880
; Publication No. US20020182596A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C6
; CURRENT APPLICATION NUMBER: US/09/232,880
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-880-110

Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-232-880-110 (1-3410)

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QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrThrValPro 40
|||||
Db 344 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTGGCCGCGAGGCATCACCTATGTGGCG 403
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
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Db 404 CCTCTGCTCTGAAAGTGGGGTAGAGGAGAAGTTTCATGACCATGGTGTGGCGCATGGT 463
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|||||
Db 884 GGCCTGCTCACCTCATCTTCTCCTCAGTGGCTAGCAGCCACACTGCTGGTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
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QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
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Db 1424 TCAGCGCGCCTCACCAGGTTTCACTTCTCAGCCCTGCGAGTCTGCGCTTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
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Db 1484 TCCTCTACACCGGAGAGAGGTTGCTTCCGCCAATACCGAGGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProGlyProGlyAlaPro 440
Db 1544 GCTAGCAGTGGAGACAGCTGATGACACAGCTTCTGCCAGGCCCTAAGCTGGAGTCCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCCTAAATGGACACGTGGGTGCTGGAGGCAGTGGCTGTCTCCACCTCCACCGCGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TGGGGGCGCTCTCCCTGTGTATGTCCTCGTACGTGTGGTGGGTGAGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGTGGTTCGGGCGCGGGGCATCTGCTGGACCTGCCATCTCGATAGTGGCTTCCG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCCATATATGGTGTCTGCCGAGGCGCTGGGTCTGGTGGCCATTTACTTTGTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACCTACGCG 1942

RESULT 3

US-10-012-896-110
; Sequence 110, Application US/10012896
; Publication No. US20020183251A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-012-896-110

Alignment Scores:

Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGCTGTTGGCCGCGAGCATCACTATGTGCCG 403
QY 41 ProLeuLeuLeuGluValGlyValGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGTAGAGAGAGTTTCATGACCATGGTGTGGGCATTTGGT 463
QY 61 ProValLeuClyLeuValCysValProLeuLeuGlySerAlaSerAspHisTyrPheGly 80
Db 464 CCAGTCTGGCCGTGCTGTGTCCCGCTCCTAGGCTCAGCCAGTACCCAGCTGGCGTGA 523
QY 81 ArgTyrGlyArgArgPropheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCGCCCTTCATCTGGGCACCTGCTCTGGGCATCTCTGTGAGCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGCGCGGCTGGCTAGCAGGCTCTGTGCCCGCATCCAGGCCCTCG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTCTGGGCGTGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCCCTGCTCTGACCTTCTCCGGGACCCCGGACCACCTGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTCTATGCCCTTCATGATCAGTCTTGGGGGTGCTGGGCTACCTCTGCCCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
Db 824 ATTGACTGGGACACCACTAGTGGCTTGGCCCTCTACCTGGGCACCCAGGAGGAGTGCCTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGCTCTCACCCTCATCTTCCTCACCTGCTAGCAGCCACACTGCTGCTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGCGCTGGGCCCCACCGAGCCAGCAGAGGGCTGTGCGGCCCTCTCTGTGCGCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGTGTCCATAGCGGGCGCGCTTGGCTTTCGGGAACCTGGCGGCCCTGTCTTCCCCGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGTGCGCATGCCCGCACCTTGCAGCGGCTCTTCGTGGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTATACAGGATTTCTGTGGCGAGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCGTGGCCAGAGCTGAGCGGGGACCGAGGCCCGGAGACACTATGATGAAGGC 1243

[illegible]

364	11ACGATCCCAAGGGCGCCGCTGGCTATGCATACAGAGGCTGCTGTGTCGCCGACTTCTGTGCGCAGAGTGCTGTC		
Qy	121	GLULeuAlaLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe	140
Db	644	GAGCTGGCACTGCTCATCTCGGGCGTGGGGCTGCTGGCACTTCTGTGCGCAGAGTGCTGTC	703
Qy	141	ThrProLeuLalaLeuLeuSerAspLeuPheAtqAspProAspHisCysArgGlnAla	160
Db	704	ACTCCACTGGAGGCGCTGCTCTGACCTCTTCCGGGACCCGACCACCTGTGCCAGGGCC	763
Qy	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180
Db	764	TACTCTGCTATGCCCTCATGATCAGTCTTGGGGCTGCCTGGCTACCTCCTGCTGCC	823
Qy	181	IleAspTrpaspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe	200
Db	824	ATTGACTGGGACACCAAGTGGCCCTGGCCCCCTACTCTGGGCACCAGAGGAGTGCCTTT	883
Qy	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
Db	884	GGCTGCTCACCCCTCATCTTCTCACTCGGTAGACGCCACACTGCTGCTGGCTGAGGAG	943
Qy	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHls	240
Db	944	GCAGCGCTGGCCCCCACCGACGAGCAGAAGGGCTCTGGCCCCCTCTCTTGTGCGCCAC	1003

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Oy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATGCGGCGCGCTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCGCGCTC 1063
Oy 261 HisGlnLeuCysCysArgMetProArgThrLeuAtgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGTCGCGCATGCCCGCACCTTGCGCGCGCTCTTCGTGGCTGAGCTGTGC 1123
Oy 281 SerTrpMetAlaLeuMetThrPheThrLeuPhePheThrAspPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGAATTCGTGGCGGAGGGCTG 1183
Oy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
Db 1184 TACCAGGGGTGCCAGAGCTGAGCGGGCACCGAGCGCCGAGACACATATGATGAAGC 1243
Oy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGATGGCAGCGCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGCTCTCTCTCTG 1303
Oy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValIleLeuAlaSerValAla 360
Db 1304 GTCTGGACCGGCTGGTGCGAGCATTCGCGCACTCGAGCAGTCTATTGGCCAGTGTGGA 1363
Oy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
Db 1364 GCTTTCCCTGTGGCTGCCGTGCCACATGCCTGTCCACAGTGTGGCGCTGGTGACGCT 1423
Oy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProThrThrLeuAla 400
Db 1424 TCAGCGCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCTCCCTTACACACTGGCC 1483
Oy 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCTCTACACCGGAGAGCAGGTGTCTCGCCAAATACCGAGGGACACTGGAGT 1543
Oy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGAGACAGCGCTGATGACCACTTCCTGCCAGGCCCTAAGCCTGGAGCTCC 1603
Oy 441 PheProAspGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCTTAATGGACAGCTGGGTGCTGGAGCAGTGGCGCTCTCCACCTCCACCGCGCTC 1663
Oy 461 CysGlyAlaSerAlaCysAspValSerValArgValValValValValValValValVal 480
Db 1664 TCGGGGCGCTCTGCCTGTGATGCTCCGTACCTGTGGTGGTGAGCCACCGAGGCC 1723
Oy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGGTGGTTCCGGGCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG 1783
Oy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCCCAATCCCTGTTTATGGCTCCATTTGTCAGCTCAGCCAGCTGCTGC 1843
Oy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCCTATATGTGCTGCCCGCAGGCGCTGGGTCTGGTGGCCATTTACTTTGCTACAG 1903
Oy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTGTACAAGAGGCACTTGGCCAAATACTCAGCG 1942
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RESULT 5

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US-09-895-814-110
; Sequence 110, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
```

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; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-814-110

Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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Db 284 ATGGTCCAGAGGCTGTGGGTGAGCGCCCTGCTGCGGCACCGAAAGCCAGCTCTTTGCTG 343
Oy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCCCGCAGGCATCACCTATGTGCGC 403
Oy 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGAAAGTGGGGCTAGAGGAGAAGTTTCATCACCATGCTGTGGCATTGCT 463
Oy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGGCTGTGCTGTCTCCCGCTCCTAGGCTCAGCCAGTACACCATGGCGTGA 523
Oy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CCCTATGGCGCGCGCGCCCTTCATCTGGGCACATGCTCCTTGGGCATCTCTGTGACCCCT 583
Oy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCAGGCCCTG 643
Oy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCAGCTGCTCATCTCTGGGCGCTGGGCTGTGGACTTCTGTGGCCAGGTGTCTTC 703
Oy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCGGGACCCGAGCACCTGTGCCAGGCC 763
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Qy	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe	200
Db	824	ATTGACTGGGACACCACTGGCCCTTACCTGGGACCCAGGAGTGCTCTTT	883
Qy	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
Db	884	GGCTGTCTACCTCATCTTCTTCACCTCGTAGCAGCCACACTCTGCTGGCTGAGGAG	943
Qy	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
Db	944	GCAGCGTGGGCCCCACCGAGCCAGAAAGGGCTGTGGGCCCCCTCTTGTGCCCCAC	1003
Qy	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260
Db	1004	TGCTGTCCATCCCGGCCCTGGCTTTCGCGAACCTGGGCGCCCTCTCTTCCCGGCTG	1063
Qy	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280
Db	1064	CACAGCTGTGCTGCCCATGCCCCACACCTTCGCCCGGCTCTTCTGGCTGAGCTGTGC	1123
Qy	281	SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu	300
Db	1124	AGCTGGATGCACATCATGACCTTCACGCTGTTTACACGGATTTCGTGGCGAGGGCTG	1183
Qy	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly	320
Db	1184	TACCAGGCGGTGCCACAGCTGAGCGGCGACCGAGGCGCGGAGACACTATGATGAAGGC	1243
Qy	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340
Db	1244	GTTCCGATGGCGAGCTGGGGCTGTTCCTGCAGTGGCGCATCTCCCTGGTCTCTCTCTG	1303
Qy	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla	360
Db	1304	GTCATGACCCGCTGGTGCAGCGATTTCGCACTCGAGCAGCTATTTCGCCAGTGTGGCA	1363
Qy	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla	380
Db	1364	GCTTTCCTGTGTGCTCCGGTGCCACATGCCCTGCCACAGTGTGGCGTGGTGACAGCT	1423
Qy	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400
Db	1424	TCAGCCGCCCTCACCGGGTTCACTTCTCAGCCCTGCAGATCTCTGCCCTACACACTGCC	1483
Qy	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	420
Db	1484	TCCCTCTACCACCGGAGAAGCAGGTGTTCTCTGCCCAATACCGAGGGGACACTGGAGT	1543
Qy	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440
Db	1544	GCTAGCAGTAGGACACGCTGTATGACCACTTCCTTCGACAGCCCTTAAGCCCTGGAGCTCC	1603
Qy	441	PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu	460
Db	1604	TTCCCTAATGGACACGTGGGTGCTGGAGCAGTGGCTGCCACCTCCACCCCGGCTC	1663
Qy	461	CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla	480
Db	1664	TGCGGGGCCCTCTGCCTGTATGCTCCGTACGTGTGGTGGTGGTAGCCCAACGAGGCC	1723
Qy	481	ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500
Db	1724	AGGCTGTCTCCGGGCGGGGCATCTGCCCTGGACCTTCGCCATCTCTGGATGGCTCTCGT	1783
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Db	1784	CTGTCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTTCAGCTCAGCCAGCTCTGTC	1843
Qy	521	ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	540
Db	1844	ACTGCCTATATGTGTCTCCGAGGCGCTGGGTCTGGCTGGCATTTACTTTGCTACACAG	1903

Qy	541	ValValPheAspLysSerAspLeuAlaLysTyrSerAla	553
Db	1904	GTAGTATTTCACAAGACGACTTTGGCCAAATACTCAGCG	1942
RESULT 7			
US-09-759-143-110			
; Sequence 110, Application US/09759143			
; Patent No. US2002022248A1			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Dillon, Davin C.			
; APPLICANT: Mitcham, Jennifer L.			
; APPLICANT: Harlocker, Susan L.			
; APPLICANT: Jiang, Yuqi			
; APPLICANT: Henderson, Robert A.			
; APPLICANT: Kalos, Michael D.			
; APPLICANT: Fanger, Gary R.			
; APPLICANT: Retter, Marc W.			
; APPLICANT: Stolk, John A.			
; APPLICANT: Day, Craig H.			
; APPLICANT: Vedvick, Thomas S.			
; APPLICANT: Carter, Darrick			
; APPLICANT: Li, Samuel			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skeiky, Yasir A.W.			
; APPLICANT: Hepler, William			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR T			
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
; FILE REFERENCE: 210121.427C23			
; CURRENT APPLICATION NUMBER: US/09/759,143			
; CURRENT FILING DATE: 2001-01-12			
; NUMBER OF SEQ ID NOS: 934			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 110			
; LENGTH: 3410			
; TYPE: DNA			
; ORGANISM: Homo sapien			
US-09-759-143-110			
Alignment Scores:			
Pred. No.:	0	Length:	
Score:	553.00	Matches:	
Percent Similarity:	100.00%	Conservative:	
Best Local Similarity:	100.00%	Mismatches:	
Query Match:	100.00%	Indels:	
DB:	10	Gaps:	
US-09-593-793A-113 (1-553) x US-09-759-143-110 (1-3410)			
Qy	1	MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLys	
Db	284	ATGTGTCAGAGGCCTGTGGGTGAGCGCCCTGCTCGCGCACCGGA	
Qy	21	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGl	
Db	344	GTCACCTGCTAACCTTTGCCCTGGAGTGTTGTTGGCGCGCAG	
Qy	41	ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMe	
Db	404	CCTCTGCTGCTGGAGGTGGGGGTAGAGAGAAGTTTCATGACCAT	
Qy	61	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlase	
Db	464	CCAGTGTGTGGGCCCTGGTCTGTGTCCCGCTCCTTAGGCTCAGCCAG	
Qy	81	ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGl	
Db	524	CGCATGTGGCCGCCGCCGCCCTTCATCTGGCACTGCTCTGTCGG	
Qy	101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysPr	
Db	584	TTTCTCATCCCAAGGCCGCGCTGGCTAGCAGGGCTGCTGTGCC	

Db 404 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAAGTTCATGACCATGCTGCTGGGCATTGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAAGTGGCGCTGGTCTGTGCTGCCGCTCTAGGCTCAGCCAGTACCACTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCGCTTTCATCTGGGCACCTGTCTTGGGCATCTCTGCTGAGCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
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QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGSCACTGTCTCATCTTGGCGTGGGCTGCTGGACTTCTGTGGCCAGGTGCTCTTC 703
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Db 704 ACTCCACTGGAGGCGCTGCTCTGTGACTCTTCCGGGACCCGGACCACTGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrIleLeuProAla 180
Db 764 TACTCTGTCTATGCCCTTCATGATCAGTCTTGGGGGCTGCTGGGCTACCTCTGCCCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 824 ATTGACTGGGACACCACTGCTGCTGCGCCCTACCTGGGCACCCAGGAGTGCCTCTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGGCTGCTCACCTCATCTTCTTCACCTGCTGAGCAGCCACACTGCTGTGGTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGCGTGGGCGCCACCGAGCAGCAGAGGGCTGTGGCGCCCTCTTGTCTGCCGCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATGCGCGCGCTGGCTTTCCGGAACCTGGCGCCCTGCTTCCCGCGCTG 1063
QY 261 HisGlnLeuCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGCTGCGCATGCCCGCACCCCTGCGCGGCTCTTCGTGGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCTGTGGCGAGGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCTGCCAGAGCTGAGCGCGGCACCGAGCGCCGAGACACATATGATGAAGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGATGGCAGCCTGGGGCTGTTCCTGCAGTGGCCACTCTCCCTGGTCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrIleLeuAlaSerValAla 360
Db 1304 GTCATGACCGGCTGGTGACCGGATTCGGGCATTCGAGCAGTCTATTTGGCCAGTGGGA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
Db 1364 GCITTTCCCTGGCTGCCGTGCCATGCTGTCCACAGTGTGGCGGTGGTGACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCTCACCGGGTTACCTTCTCAGCCCTGCAGATCTCTGCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCCTCTACACCGGAGAGAGGTGTTCTTCCGCCAAATACCGAGGGGACACTGGAGT 1543

QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGAGACAGCCTGATGACAGCTTCTGCCAGGCCCTAAGCCTGGAGCTCCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCTCTAATGGACACGTGGTGTGGAGCAGTGGCTGCCACGCTCCACCGGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480
Db 1664 TGGCGGGCTCTGCCCTGTGATGCTCTCCGTACGTGTGGTGGTGGTGGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGGTGTTCGGGCGCGGGCATCTGCTGGACCTGCCATCTCGGATAGTGCCTTCTCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCCCATCTCCCTGTTTATGGGTCCATTTGCCAGCTCAGCCAGTCTGC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCCTATATGTGTCTGCCGAGCGCTGGTCTGTGTCGCCATTACTTTGCTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTTGACAAGAGCAGCTTGCCCAATACTACGCG 1942
RESULT 9
US-09-030-606-110
; Sequence 110, Application US/09030606
; Patent No. US20020081580A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; ATTORNEY: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHOD
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,606
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.428C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-606-110
Alignment Scores:

Pred. No.:	0	Length:	3410
Score:	553.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0
US-09-593-793A-113 (1-553) x US-09-030-606-110 (1-3410)			
QY	1	MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu	20
DB	284	ATGGTCCAGAGCTGTGGGTGAGCCCTGCTGGCGCACCCGNAAGCCAGCTCTTGCTG	343
QY	21	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro	40
DB	344	GTCAACCTGCTAACCTTTGGCCGTGGAGGTGTGTTGGCCGCGAGCATACCTATGTGCGG	403
QY	41	ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly	60
DB	404	CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAAAGTTTCATGACCATGGTGTGGGCATTGGT	463
QY	61	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly	80
DB	464	CCAGTCTGGGCTGTGCTGTGCTCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGA	523
QY	81	ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu	100
DB	524	CGTATGCGCGCGCGGCCCTTCATCTGGGCACCTGCTCTGGCATCCTGCTGAGCCCTC	583
QY	101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu	120
DB	584	TTTCTCATCCCAAGGGCGGCTGGCTAGCAGGGCTGCTGTGCCGAGTCCAGGCCCTG	643
QY	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe	140
DB	644	GAGCTGGCACTGCTCATCTTGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGCTTC	703
QY	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160
DB	704	ACTCCACTGGAGGCCCTGCTCTGACCTCTCCGGGACCCGACCACTGTGCGCAGGCC	763
QY	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180
DB	764	TACTCTGTATGCCCTTCATGATCATGCTTGGGGGCTGCTGGGCTACCTCCTGCTGCC	823
QY	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe	200
DB	824	ATTGACTGGGACCACTGGCCCTGGCCCTACCTGGGCACCCAGGAGGTGCTCTTTT	883
QY	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
DB	884	GCCCTGCTCACCTCATCTTCCTACCTGCGTAGCAGCCACACTGCTGTGGCTGAGGAG	943
QY	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
DB	944	CGAGCGCTGGGCCCCCACCAGGACGAGCAAGGGCTGTGCGGCCCTCTCTGTGCGCCCC	1003
QY	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260
DB	1004	TGCTGTCCATGCGGGCCCGCTTGGCTTCCGGAACCTGGGCGCCCTGCTTCCCGGCTG	1063
QY	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280
DB	1064	CACCAGCTGTGTCGCGCATGCCCCGACCCCTGCGCGGCTCTTCGTGGCTGAGCTGTGC	1123
QY	281	SerTrpMetalLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlyLeu	300
DB	1124	AGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTGCTGGCGAGGGCTG	1183
QY	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly	320
DB	1184	TACCAGGGCGTGCCAGAGCTAGCGGGCACCCGAGGGCCCGGAGACACTATGATGAAGC	1243

QY	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340
DB	1244	GTTCGGATGGGAGCGCTGGGCTGTTCCTGCGAGTGGCCATCCTCCGTCTCTCTCTG	1303
QY	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla	360
DB	1304	GTCATGGACCGGCTGGTGCGGACTTCGAGCACTCTATTTGGCCAGTGTGGCA	1363
QY	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla	380
DB	1364	GCTTTCCCTGTGGCTGCCGCTGCCACATGCTTCCACAGTGTGCCGTGTGACAGCT	1423
QY	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400
DB	1424	TCAGCGCCCTCACCGGTTCACTTCTCAGCCCTGCAGATCTGCGCTTACACACTGGCC	1483
QY	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	420
DB	1484	TCCTCTACCCCGGAGAGAGGCTTCTTCCGCCCAATACCGAGGGGACACTGGAGGT	1543
QY	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440
DB	1544	GCTAGCAGTGACGACAGCCTGATGACCACTTCTTCCAGGCCCTAAGCCTGGAGCTCC	1603
QY	441	PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProProAlaLeu	460
DB	1604	TTCCCTAATGGACACGCTGGGTGCTGGAGCAGTGCCCTGCTCCACCTCCACCCGCGTC	1663
QY	461	CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla	480
DB	1664	TCGGGGGCTGCTGCTGTGATCTCCCTGCTGCTGGGTGGGTGGGAGCCACCGAGGCC	1723
QY	481	ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500
DB	1724	AGGGTGGTTCCGGCGCGGGGCACTGCGCTGGACCTGCGCATCTCGATAGTGCCTTCTG	1783
QY	501	LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
DB	1784	CTGTCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTTGCCAGTCCAGCTCAGCTGTC	1843
QY	521	ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	540
DB	1844	ACTGCTATATGTTGTTGCCCGAGCGCTGGGTCTGGTCCCATTTACTTTGCTACACAG	1903
QY	541	ValValPheAspLysSerAspLeuAlaLysTyrSerAla	553
DB	1904	GTAGTATTGACAGAGCGACTTGGCCAAATACTCAGCG	1942
RESULT 10			
US-09-822-827-110			
; Sequence 110, Application US/09822827			
; Patent No. US20020081680A1			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
; FILE REFERENCE: 210121.534C1			
; CURRENT APPLICATION NUMBER: US/09/822,827			
; CURRENT FILING DATE: 2001-03-28			
; NUMBER OF SEQ ID NOS: 982			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 110			
; LENGTH: 3410			
; TYPE: DNA			
; ORGANISM: Homo sapien			
US-09-822-827-110			
Alignment Scores:			
Pred. No.:	0	Length:	3410
Score:	553.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0


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DB: 10 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-822-827-110 (1-3410)
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Db 284 ATGGTCAGAGGCTGGGGTACCGCCCTGCTCGCGCACCGGAAAGCCAGCTCTTGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTrpValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTGGCCGACGATCACCCTATGTGCCG 403
QY 41 ProLeuLeuLeuValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGAAGTGGGGTAGAGGAAGTTTCATGACCATGTGTGCTGGGCATTGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlyIleSerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGGCTGGTGTGTGCCGCTCCTAGGCTCAGCCAGTACCACTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCCCTTCATCTGGCACCTGTCTTGGGCATCTGCTGACGCTC 593
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCAAAGGCGCGCTGGCTAGCAGGCTGTGTGCCCGATCCAGCGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGTCTATCTTGGGCGTGGGCTGTCTGGACTTCTGTGCCAGGTGTCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGAGGCGCTCTCTCTGACCTCTCCGGGACCGGACCACTGTCCGAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTCTATGCCCTTCATGATCAGTCTTGGGGCTGTCTGGGCTACCTCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 824 ATTGATGGGACACCACTAGTGCCTTGGCCCTTACCTGGGACCCAGGAGGAGTGCTCTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGCTGCTCACCTCATCTTCTTCTACCTGCGTAGCAGCCACACTGCTGTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGCGTGGGCCCCACCGAGCCAGCAGAAAGGCTGTCCGCCCTCTCTGTGCCGCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGTGTCCATGCGCGGCGCGCTTGGCTTTCGGAACCTGGCGCCCTGCTTCCCGCGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGCTGCGCATGCCCGCCGACCTGCGCGCGCTCTTCTGTGGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPheValGlyGluGlyLeu 300
Db 1124 AGCTGATGGCACTCATGACCTTCACGCTGTTTTACACGATTTCTGGCGGAGGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTrpAspGluGly 320
Db 1184 TACCAGGGCTGCCAGAGCTGAGCGCGGACCGAGCGCGGAGACACTATGATGAAGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGCAGCCTGGGCTGTCTTCGACGTGCGCCCATCTCCCTGGTCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
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Db 1304 GTCATGACCGGCTGTGTGAGCGATTTCGACACTCGAGCAGTCTATTTCGCCAGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCTGCTGTGCTGCCGTCACATGCTGTCCACAGTGTGCCGCTGGGTGAGAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCCCTCACCGGTTTCACCTTCTCAGCCCTGCAGATCTCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCCTCTACACCGGAGAGCAGGTTCCTGCCAAATACCGAGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGCAGACAGCCTGATGACAGCTTCTCCAGGCCCTAAGCCTGAGGCTCCC 1603
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Db 1604 TTCCCTTAATGGACACGCTGGTGTGGAGGAGTGGCTGCTCCACCTCCACCCGCGCTC 1663
QY 461 CysGlyAlaSerAlaCysaspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TGGGGGCGCTCTGCCCTGTATGTCTCCGTACGTGTGTGGTGGGTGAGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGTGTGTCGGGGCGGGGCGGATCTGCTGGACCTGCCATCTCTGGATAGTGGCTTCCG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCACAGTGGCCCCATCCCTGTTTATGGGCTCCATGTCCAGCTCAGCCAGTCTGT 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCCTATATGTTGTCTGCCGAGGCTGGGTCTGTGTGCCATTTACTTTGTGTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTACGCG 1942

RESULT 11
US-09-115-453-110
; Sequence 110, Application US/09115453B
; Patent No. US20020090372A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; FILE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-115-453-110

Alignment Scores:
Pred. No.: 0 Length: 3410
Score: 553.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-115-453-110 (1-3410)
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Qy	21	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro	40
Db	344	GTCAACTGCTAACCTTTGGCTTGGAGGTGTGTTTGGCCGACAGGCATCACCTATGTGCGG	403
Qy	41	ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly	60
Db	404	CCTCTGCTGTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGTGCTCGGGCATTTGGT	463
Qy	61	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly	80
Db	464	CCAGTGTGGCGCTGTGCTGTGCCCGCTCTAGCGTCAGCCAGTACACCTGCGCGTGA	523
Qy	81	ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu	100
Db	524	CGCTATGGCCCGCCGGCCCTTCATCTGGGCACATGTCTCTTGGGCATCCTGCTGAGCCTC	583
Qy	101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu	120
Db	584	TTTCTCATCCAAAGGCCGCGCTAGCAGGCGTCTGTGCCCGGATCCCAGGCCCTTG	643
Qy	121	GluLeuAlaLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe	140
Db	644	GAGCTGGCACGTCTATCTGGCGGTGGGGCTGTCTGGAGACTCTCTGTGGCCAGGTGTGCTTC	703
Qy	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160
Db	704	ACTCCATGGAGCGCTGCTCTGACCTCTTCCGGGACCCGGACCATGTCTGGCAGGCC	763
Qy	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180
Db	764	TACTCTGCTATGCTTCATGATCAGTCTTGGGGCTGCCCTGGGTACCTCTCCCTGCC	823
Qy	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe	200
Db	824	ATTGACTGGGACACCATGTCGCTGGCCCTTACCTGGGCACCCAGGAGGAGTGCCTCTTT	883
Qy	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
Db	884	GGCTTGCTCACCTCATCTCTCTCACTCGGTAGCAGCACACATGCTGGTGGCTGAGGAG	943
Qy	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
Db	944	GCAGCGTGGGCCCCACCGAGCCAGCAGAAGGCGTGTGGGCCCTCTCTTCGCGCCAC	1003
Qy	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260
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Qy	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280
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Qy	281	SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu	300
Db	1124	AGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCTGTGGGGCAGGGCTG	1183
Qy	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly	320
Db	1184	TACCAGGGCTGCCAGAGCTAGCGGGCACCGAGGCCCGGAGACACTATGATGAAGGC	1243
Qy	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340
Db	1244	GTTTCGGAATGGGACCTGGGGCTGTTCCTGCACTGAGTCGCGCATCTCCCTGGTCTCTCTG	1303
Qy	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla	360
Db	1304	GTCATGAGCCGGCTGTGTGACGATTCGGCACTCAGCAGGTCTATTGGCCAGGTGGCA	1363
Qy	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla	380

Db	1364	GC	TTTCCCTGGCGTGGCGGTGCACATGCTTCCACAGTGTGGCGTGGTGCACAGCT	1423
Qy	381	Ser	AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400
Db	1424	TC	AGCGCGCCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC	1483
Qy	401	Ser	LeuTyrHisArgGluIuysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	420
Db	1484	TCC	CTCTACCAACCGGGAGAGCAGGTGTTCTTCGCCAAATACCGAGGGACACTGGAGGT	1543
Qy	421	Ala	SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440
Db	1544	GCT	AGCAGTGGAGNACGCTGATGACACAGCTTCTTCGCAGAGCCCTTAGCCTGGAGCTCCC	1603
Qy	441	Phe	ProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu	460
Db	1604	TTCC	CTAATGGACACGTGGGTGCTGGAGGCAGTGGCTCTCCACACCTCCACCGCGCTC	1663
Qy	461	Cys	GlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrClnAla	480
Db	1664	TGC	GGGGCCCTCGCCTGTGATGTCCTCCGACGTGTGGTGGTGGGAGCCACCGAGGCC	1723
Qy	481	Arg	ValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500
Db	1724	AGGT	TGTTCCGGGCCGGGCATCTGCCTGGACCTGCCATCCTGGATAGTGCTTCCTG	1783
Qy	501	Leu	SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
Db	1784	CTGT	CCCAGGTGGGCCCATCCCTGTGTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC	1843
Qy	521	Thr	AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	540
Db	1844	ACT	GCTATATGGTGHGCTCGCCGAGGCCCTGGGTGTGGTCCCATTTACTTTGCTACACAG	1903
Qy	541	Val	ValPheAspLysSerAspLeuAlaLysTyrSerAla	553
Db	1904	GTAC	GATTTTCACAGAGCGACTTTGGCCAAATACTCAGCG	1942

RESULT 12

US-10-012-896-704

Sequence 704, Application US/10012896
Publication No. US20020183251A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yudlu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedwick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10

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; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-704

Alignment Scores:
Pred. No.: 1.18e-294 Length: 4034
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x US-10-012-896-704 (1-4034)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 281 ATGGTCCAGAGGCTGTGGGTGAGCGCCCTGCTCGCGCACCAGGAAAGCCAGCTCTTGCTG 340
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrValPro 40
Db 341 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCGCCAGGCATCCTATGTGCGG 400
QY 41 ProLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGly 60
Db 401 CCTCTGCTGCTGAAGTGGGTGAGAGAGAGAGTTGATGACCATGTGCTGGGCATGTGT 460
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 461 CCAGTGTGGCGCTGCTGTCTGCCCTCTTAGGCTCAGGCAGTGACCACTGGCGTGA 520
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 521 CGCTATGGCGCGCGCGCCCTTCATCTGGGCACTGCTCTGGGCATCTGCTGAGCCTC 580
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTCTCATCCCAAGGCGCGGTGGTAGCAGGGCTGCTGTGCCGGATCCCAAGGCCCTG 640
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 641 GAGCTGGCACTGCTATCTGGCGTGGGCTGCTGGACTTCTGTGGCCAGGTGCTCTTC 700
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGGCCCTGCTCTGACCTTTCCGGGACCCCGGACCACTGTGCCAGGCC 760
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 761 TACTCTGTATGCTTCATGATCAGTCTTGGGGGTGCTGGGTACCTCTGCTGCTGCC 820
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 821 ATTGACTGGACACCACTGCTGCCCTTACCTGGGCACCCAGGAGGAGTGCCTCTTT 880
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db 881 GGCTGCTCACCCTCATCTTCCTACCTGCTAGCAGCCACACTGCTGTGCTGAGGAG 940
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 941 GCAGCGCTGGGCCCCACCGAGCCAGCAGAGGGCTGTGCGCCCCCTCTTGTGCGCCAC 1000
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1001 TGCTGTCCATGCGGCGCGCTTGGCTTTCGGAACCTGGCGCCCTGCTTCCCGCGCTG 1060
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1061 CACCAGCTGTGCTGCGCATGCCCGCACCTTCCGCGCGGCTCTTCTGTGCTGAGCTGTGC 1120

QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1121 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGATTTCTGGCGGAGGCGCTG 1180
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTrpAspGluGly 320
Db 1181 TACCAGGGCGTCCCGAGAGCTGAGCGGCGCACCGAGGCCGAGACACTATGATGAAGGT 1240

RESULT 13
US-09-895-793-704
; Sequence 704, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-704

Alignment Scores:
Pred. No.: 1.18e-294 Length: 4034
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-895-793-704 (1-4034)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 281 ATGGTCCAGAGGCTGTGGGTGAGCGCCCTGCTCGCGCACCAGGAAAGCCAGCTCTTGCTG 340
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrValPro 40
Db 341 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCGCCAGGCATCCTATGTGCGG 400
QY 41 ProLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGly 60
Db 401 CCTCTGCTGCTGAAGTGGGTGAGAGAGAGAGTTGATGACCATGTGCTGGGCATGTGT 460
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 461 CCAGTGTGGCGCTGCTGTCTGCCCTCTTAGGCTCAGGCAGTGACCACTGGCGTGA 520
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 521 CGCTATGGCGCGCGCGCCCTTCATCTGGGCACTGCTCTGGGCATCTGCTGAGCCTC 580
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTCTCATCCCAAGGCGCGGTGGTAGCAGGGCTGCTGTGCCGGATCCCAAGGCCCTG 640
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 641 GAGCTGGCACTGCTATCTGGCGTGGGCTGCTGGACTTCTGTGGCCAGGTGCTCTTC 700
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGGCCCTGCTCTGACCTTTCCGGGACCCCGGACCACTGTGCCAGGCC 760
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 761 TACTCTGTATGCTTCATGATCAGTCTTGGGGGTGCTGGGTACCTCTGCTGCTGCC 820
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 821 ATTGACTGGACACCACTGCTGCCCTTACCTGGGCACCCAGGAGGAGTGCCTCTTT 880
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db 881 GGCTGCTCACCCTCATCTTCCTACCTGCTAGCAGCCACACTGCTGTGCTGAGGAG 940
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 941 GCAGCGCTGGGCCCCACCGAGCCAGCAGAGGGCTGTGCGCCCCCTCTTGTGCGCCAC 1000
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1001 TGCTGTCCATGCGGCGCGCTTGGCTTTCGGAACCTGGCGCCCTGCTTCCCGCGCTG 1060
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1061 CACCAGCTGTGCTGCGCATGCCCGCACCTTCCGCGCGGCTCTTCTGTGCTGAGCTGTGC 1120
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Db 461 CCAAGTCTGGCGCTGTGTGTCCTGGCTCTAGGCTCAGCCAGTGACCACCTGGCGCTGGA 520
QY 81 ArqTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 521 CGCTATGGCGCGCGCGCCCTTCATCTGGGCACTGCTCTGGGCACTGCTGTGACCCCTC 580
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTGCCGCGATCCAGGCCCTG 640
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 641 GAGCTGGCACTGCTCATCTGGCGGTGGGGCTGCTGGACTTCTGTGGCCAGGTGCTCTTC 700
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGCCCTGCTCTGTGACCTCTTCCGGGACCCGGACCACTGTGCGCAGGCC 760
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 761 TACTCTGTCTATGCCCTTCATGATCAGTCTTGGGGGCTGCTGGGCTACCTCTCGCTGCC 820
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 821 ATTGACTGGGACACCAAGTGCCTGGCGCCCTACCTGGGCACCCAGGAGGTGCCTCTTT 880
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db 881 GGCTGCTCACCCTCACTCTCTCACCCTGGTAGCAGCCACACTGCTGGTGGCTGAGGAG 940
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 941 GCAGCGCTGGCGCCCAACCGAGCCAGCAGAAAGGCTGTCGGCCCTCTTGTGCGCCAC 1000
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1001 TGTGTGTCATGGCGGCGCTGGCTTTCCGGAACTGGCGCCCTGCTTCCCGGCTG 1060
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1061 CACCAGCTGTGTGCGCGATGCCCGCACCCCTGGCGGCTCTCTGCTGCTGAGCTGTGC 1120
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1121 AGCTGATGGCACTCATGACTTACCTTACCGCTTTTACACGATTTCTGCGCGAGGGGCTG 1180
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1181 TACCAGGGCTGCCAGAGCTGAGCGGGCACCGGAGCCCGAGACACTATGATGAAGGT 1240

RESULT 14

US-09-895-814-704
; Sequence 704, Application US/09895814
; Publication NO. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-704

Alignment Scores:
Pred. No.: 1.18e-294 Length: 4034
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 9 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-895-814-704 (1-4034)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db 281 ATGGTCCAGAGCTGTGGGTGAGCGCCCTGCTGGCGCACCCGAAAGCCAGCTCTTGTG 340
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 341 GTCACCTGCTAACCTTTGGCCTGGAGGTGCTTTGGCGCAGGCATCACCTATGTGCG 400
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 401 CCTCTGCTCTGGAAGTGGGGTAGAGGAGAAGTTCATGACCATGGTGTGGGCATTG 460
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 461 CCAGTGTGGGCTGTGTGTCTCCCGCTCCTAGGCTCAGCCAGTACCCAGTGGCGTGA 520
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 521 CGCTATGGCGCGCGCGCCCTTCATCTGGGCACTGCTCTTGGGCACTCTGCTGAGCCCTC 580
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTGCCGCGATCCAGGCCCTG 640
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 641 GAGCTGGCACTGCTCATCTGGCGGTGGGGCTGCTGGACTTCTGTGGCCAGGTGCTCTTC 700
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGCCCTGCTCTCTGACCTCTTCCGGGACCCGGACCACTGTGCGCAGGCC 760
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 761 TACTCTGTCTATGCCCTTCATGATCAGTCTTGGGGCTGCTGGGCTACCTCTCGCTGCC 820
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 821 ATTGACTGGGACACCAAGTGCCTGGCGCCCTACCTGGGCACCCAGGAGGTGCCTCTTT 880
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db 881 GGCTGCTCACCCTCATCTCTTCTCACCCTGGTAGCAGCCACACTGCTGGTGGCTGAGGAG 940
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
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Db 941 GCAGCGCTGGGCCCCACCAGCAGCAGAGAGGGCTGTGCGCCCCCTCTGTCTGCCCCAC 1000
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1001 TGTGTCCATGCCGGGCCCCCTGGCTTCCGGAACCTGGGCGCCCTGTCTCCCGGCTG 1060
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1061 CACCAGCTGTGCTGCCGCATGCCCGCACCCCTGCGCGGCTCTTCGTGGCTGAGCTGTC 1120
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrThrAspPheValGlyGluGlyLeu 300
Db 1121 AGCTGGATGGCACTCATGACCTTTCACGCTTTTACACGGATTTCGTGGCGAGGGCTG 1180
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1181 TACCAGGGCTGCCAGAGCTGAGCGGGCACCAGAGGCCCGGAGACACTATGATGAAGGT 1240

RESULT 15
US-09-759-143-704
; Sequence 704, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-704

Alignment Scores:
Pred. No.: 1.18e-294 Length: 4034
Score: 320.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.87% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-759-143-704 (1-4034)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
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QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 341 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTTGGCGCAGGCATCACCTATGTGCG 400
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
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Db 401 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATTGTTGTTGGCATTTGGT 460
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
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QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 521 CGCTATGGCGCGCGCGCGCTTCATCTGGGCACTGTCTTGGGCATCTCTGCTGAGCCTC 580
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTTCTCATCCCAAGGCGCGCTGCTGCTAGCAGGGCTGCTGTGCGCGGATCCAGGCGCCCTG 640
QY 121 GluLeuAlaLeuLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 641 GAGCTGGCACTGTCTATCTTGGCGGTGGGCTCTGGACTTCTGTGCCAGGTGTGCTTC 700
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGAGCCACTGTGCGCCAGGCC 760
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 761 TACTCTGTCTATGCTTTCATGATCAGTCTTGGGGGTGCTTGGGCTACCTCTGCGCTGCT 820
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 821 ATTGACTGGGACACCACTGCTGCGGCCCCCTACCTGGGACCCAGGAGGAGTGCCTCTCTT 880
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 881 GGCCTGCTCACCCTCATCTTCTCCTACCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAG 940
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 941 GCAGCGCTGGGCCCCACCAGCAGCAGAGGGGCTGTCGCGCCCCCTCTTGTGCGCCCCAC 1000
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1001 TGTGTCCATGCCGGGCGCGCTGTGGCTTTCGGAACCTGGGCGCCCTGCTTCCCCGGCTG 1060
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1061 CACCAGCTGTGCTGCGCGCATGCCCGCACCCCTGCGCGGCTCTCTGCTGAGCTGAGCTGTC 1120
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrThrAspPheValGlyGluGlyLeu 300
Db 1121 AGCTGGATGGCACTCATGACCTTTCACGCTTTTACACGGATTTCGTGGCGAGGGCTG 1180
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1181 TACCAGGGCTGCCAGAGCTGAGCGGGCACCAGAGGCCCGGAGACACTATGATGAAGGT 1240

RESULT 16
US-09-780-669-704
; Sequence 704, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
```

```
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-704

Alignment Scores:
Pred. No.:      1.18e-294      Length:      4034
Score:          320.00        Matches:      320
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:      57.87%      Indels:       0
DB:              10          Gaps:          0

US-09-593-793A-113 (1-553) x US-09-780-669-704 (1-4034)

Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db 281 ATGGTCCAGAGGCTGTGGGTAGCGCGCTGTGGCGCACCGAAAGCCAGCTCTGTG 340
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 341 GTCAACCTGCTAACCTTTGGCGTGGAGGTGTGTTGGCGCAGGCATCACCTATGTGCG 400
Qy 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 401 CCTATGGCCGCCGCCGCCCTTCATCTGGGCACCTGTCTTGGGCATCTGCTGAGCCCTC 580
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTCTCATCCCAAGGCCGCGCTGTGTACAGGCTGTGTGCCCCGGATCCCGAGGCCCTGT 640
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyValCysPhe 140
Db 641 GAGCTGGCAGCTGCTCATCTTGGCGTGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTC 700
Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGGCCCTGCTCTCTACCTCTTCCGGACCGCCGACCACTGTGCGCAGGCC 760
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 761 TACTCTGTATATGCTTTCATATCATGCTTGGGGGCTGCCCTGGGCTACCTCTGCGCTGCC 820
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 821 ATTGACTGGGACACAGTGGCCCTGCCCTACCTATGGGCACCCAGGAGAGTGCCTCTTT 880
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 881 GGCCTGCTCACCTCTCTCTCATCTGCTGCTAGCAGCCACACTGCTGCTGCTGAGGAG 940
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Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 941 GCAGCGCTGGGCCCCACCGAGCCAGCAGAGGGCTGTGGGCCCTCTCTTGTGCCCCAC 1000
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1001 TGCTGTCCATGCGCGCGCGCTTGGCTTTCGGAAACCTGGGCGCCTGCTTCCCGGGCTG 1060
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1061 CACCAGCTGTGCTGCCGATGCCCGCAGCCCTGCGCGGCTCTGCTGGCTGAGCTGTGC 1120
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlyLeu 300
Db 1121 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACAGGATTTGCTGGCGAGGGCTG 1180
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1181 TACCAGGGCGTGCCAGAGCTGAGCGGGCACCGGAGCGCGGAGACACTATGATGAAGGT 1240

RESULT 17
US-09-822-827-704
; Sequence 704, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-704

Alignment Scores:
Pred. No.:      1.18e-294      Length:      4034
Score:          320.00        Matches:      320
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:      57.87%      Indels:       0
DB:              10          Gaps:          0

US-09-593-793A-113 (1-553) x US-09-822-827-704 (1-4034)
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Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db 281 ATGGTCCAGAGGCTGTGGGTGAGCGCGCTGTGGCGCACCGAAAGCCAGCTCTGTG 340
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 341 GTCAACCTGCTAACCTTTGGCGTGGAGGTGTGTTGGCGCAGGCATCACCTATGTGCG 400
Qy 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 401 CCTCTGCTGTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGCTGCTGGCATTTGG 460
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 461 CCAGTGTGGCGCTGGTGTGTGCTCCGCTCTAGGCTCAGCCAGTACCATGTGGCGTGA 520
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 521 CGCTATGGCCCGCGCGCGCTTTCATCTGGGCACCTGTCTTGGGCATCTCTGCTGAGCCT 580
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTCTCATCCCAAGGCCGCGCTGTGTAGCGGCTGTGCTGCTGCTGCTGCTGCTGCTG 640
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Db 1192 GTGGGCGAG 1200
RESULT 19
US-09-895-793-851
; Sequence 851, Application US/09895793
; Publication NO. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-851
Alignment Scores:
Pred. No.: 6,29e-241 Length: 1203
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservativeness: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 9 Gaps: 0
US-09-593-793a-113 (1-553) x US-09-895-793-851 (1-1203)
QY 36 IleThrTyrValProLeuLeuLeuGluValGlyValGluGlyPheMetThrMet 55
Db 412 ATCACCCTATGTCCCGCTCTGCTGTGGAAGTGGGGTAGAGAGAAGTTTCATGACCATG 471.
QY 56 ValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSer 75
Db 472 GTGCTGGGCGATGGTTCAGTGTGGCCCTGGTCTGTGTCCTCTCTGAGCTCAGCCAGT 531
QY 76 AspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGly 95
Db 532 GACCACTGGCGTGGAGCTATGCGCCCGCCGCTTCATCTGCGCATGTCTTGGCG 591
QY 96 IleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysPro 115
Db 592 ATCCCTGCTGAGCCTCTTTCTCATCCCAAGGCGCGCTGCTAGCAGGGCTGCTGCGCG 651
QY 116 AspProArgProLeuLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCys 135
Db 652 GATCCAGGCCCTGGAGCTGGCATGCTCATCCCTGGGCGTGGGCTGCTGACTTCTGT 711
QY 136 GlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAsp 155
Db 712 GGCCAGGTGTGCTTCACTCCACTGGAGGCGCTGCTCTGACCTCTTCCGGGACCCGAC 771
QY 156 HisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGly 175
Db 772 CACTGTGCCAGGCGCTACTCTGTCTATGCTTCAATCATGCTTTGGGGGCTGCCCTGGGC 831
QY 176 TyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln 195
Db 832 TACCTCTGCTGCCATTGACTGGGACACCATGCGCTGGCCCCCTACCTGGGACCCAG 891
QY 196 GluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu 215
Db 892 GAGGAGTGCTCTTTGGCGCTGCTCACCTCATCTTCTCCTCACCTGCGTAGCAGCCACTG 951
QY 216 LeuValAlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaPro 235
Db 952 CTGGTGGCTGAGGAGGAGCGCTGGGCGCCACCGAGCAGAGGGGCTGCGGCGCC 1011
QY 236 SerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAla 255
Db 1012 TCCTTGTGCCCGCTGCTGCTCCATGCGCGGCGCGCTTGGCTTCCGGAACTGGGCGCC 1071
QY 256 LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe 275
Db 1072 CTGCTTCCCGCGCTGCACCATGCTGTCTGCCGATGCTGCCGACCTGCCGCGGCTTTC 1131
QY 276 ValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPhe 295
Db 1132 GTGGCTGAGCTGTGAGCTGGATGGCATCATGACCTTCACGCTGTGTTTACACGGATTTC 1191
QY 296 ValGlyGlu 298
Db 1192 GTGGGCGAG 1200
... RESULT 20
US-09-895-814-851
; Sequence 851, Application US/09895814
; Publication NO. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-895-814-851

Alignment Scores:

Pred. No.: 6,29e-241 Length: 1203
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-895-814-851 (1-1203)

QY 36 IleThrTyrValProProLeuLeuLeuGluValGlyValGlyValGluLysPheMetThrMet 55
|||||
Db 412 ATCACCTATGTGGCGCTGTGCTGTGGAAGTGGGGTAGAGGAGTTCATGACCATG 471
QY 56 ValLeuGlyIleGlyProValLeuLeuGlyValCysValProLeuLeuGlySerAlaSer 75
|||||
Db 472 GTGCTGGGCATGTGTCAGTGTGGGCTGTGTCGTCCCGCTCCTAGGCTCAGCCAGT 531
QY 76 AsphistTrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGly 95
|||||
Db 532 GACCACTGGCGTGGACGTATGGCGCGCGCGCTTCATCTGGGACGTCTCTGGGC 591
QY 96 IleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysPro 115
|||||
Db 592 ATCCTGTGAGCCTCTTCTCATCCCAAGGGCGGCTGTAGCAGGGCTGTCTGGCCG 651
QY 116 AspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCys 135
|||||
Db 652 GATCCAGGGCCCTGGAGCTGTCTCATCTGGGCGTGGGCTGTCTGGACTTCTGT 711
QY 136 GlyGlnValCysPheTrpProLeuGluAlaLeuLeuSerAlaLeuAspPheProAsp 155
|||||
Db 712 GCGCAGGTGTCTACTCCACCTGGAGCCCTGCTCTCTGACCTCTTCCGGACCCGAC 771
QY 156 HisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGly 175
|||||
Db 772 CACTGTGCGCAGGCCTACTCTGTATGCTTCATGATCATGCTTGGGGCTGCCTGGGC 831
QY 176 TyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln 195
|||||
Db 832 TACCTCTGCGTGCCTACTTACCTGGGACACAGTGGCCCTTCCGGACCCAG 891
QY 196 GluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu 215
|||||
Db 892 GAGGAGTGCTCTTGGCGTGTCACTCATCTTCTCCTGCGTAGCAGCCACCTG 951
QY 216 LeuValAlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaPro 235
|||||
Db 952 CTGGTGGCTGAGGAGCAGCGCTGGGCCCCACCGAGCCAGCAGAGGGCTGTGGGCC 1011
QY 236 SerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAla 255
|||||
Db 1012 TCTTGTGCGCCCTGCTGTCTCATGCGGGCCCGCTTGGCTTTCGGAGACCTTGGCGCC 1071
QY 256 LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe 275
|||||
Db 1072 CTGCTTCCCGGCTGACACAGCTGTGCTGCGCATGCGCCGCGACCTTGGCCCGCTCTTC 1131
QY 276 ValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPhe 295
|||||
Db 1132 GTGGCTGAGCTGTGAGCTGGATGGCACTCATGACCTTACAGCTGTGTTTACACGGATTTC 1191
QY 296 ValGlyGlu 298
|||||
Db 1192 GTGGGCGAG 1200

RESULT 21

US-09-759-143-851

; Sequence 851, Application US/09759143

; Patent No. US2002022248A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-851

Alignment Scores:
Pred. No.: 6,29e-241 Length: 1203
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-759-143-851 (1-1203)

QY 36 IleThrTyrValProProLeuLeuLeuGluValGlyValGlyValGluLysPheMetThrMet 55
|||||
Db 412 ATCACCTATGTGGCGCTGTGCTGTGGAAGTGGGGTAGAGGAGTTCATGACCATG 471
QY 56 ValLeuGlyIleGlyProValLeuLeuGlyValCysValProLeuLeuGlySerAlaSer 75
|||||
Db 472 GTGCTGGGCACTTGGTCCAGTGTGGGCTGGTGTGTGTCCTCCTAGGCTCAGCCAGT 531
QY 76 AsphistTrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGly 95
|||||
Db 532 GACCACTGGCGTGGACGTATGGCGCGCGCGCTTCATCTGGGACGTCTCTTGGGC 591
QY 96 IleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysPro 115
|||||
Db 592 ATCCTGTGAGCCTCTTCTCATCCCAAGGGCGGCTGTAGCAGGGCTGTCTGGCCG 651
QY 116 AspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCys 135
|||||
Db 652 GATCCAGGGCCCTGGAGCTGTGCTCATCTGGGCGTGGGCTGTCTGGACTTCTGT 711
QY 136 GlyGlnValCysPheTrpProLeuGluAlaLeuLeuSerAlaLeuAspPheProAsp 155
|||||
Db 712 GCGCAGGTGTGCTTCACTCCACTGGAGGCGCTGTCTCTGACCTTTCGGGACCCGAC 771
QY 156 HisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGly 175
|||||
Db 772 CACTGTGCGCAGGCCTACTTGTCTATGCTTCATGATCATGCTTGGGGCTGCCTGGGC 831
QY 176 TyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln 195
|||||
Db 832 TACCTCTGCGTGCCTACTTACCTGGGACACAGTGGCCCTTCCGGACCCAG 891
QY 196 GluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu 215

|||||
Db 892 GAGGAGTGCTCTTGGCGCTGCTCACCCATCTTCTCACCTGCGTAGCAGCCACACTG 951
QY 216 LeuValAlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaPro 235
Db 952 GTGGTGGCTGAGAGGACGCGCTGGGCCCCACCGAGCCAGCAGGGGTGTCGGCCCC 1011
QY 236 SerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAla 255
Db 1012 TCCCTGTGCCCCACTGCTGTCATGCGCGGCCGCTTGCGCTTCCGGAACTGGCGCC 1071
QY 256 LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe 275
Db 1072 CTGCTTCCCGGCTGCACCACTGCTGCCGCGTCCCGCCAGCCCGCTGCTCTTC 1131
QY 276 ValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPhe 295
Db 1132 GTGGCTGAGCTGTGAGCTGGATGGACATCATGACCTTCACGCTGTTTTACACGGATTTC 1191
QY 296 ValGlyGlu 298
Db 1192 GTGGCGGAG 1200

RESULT 22
US-09-780-669-851
; Sequence 851, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-851

Alignment Scores:
Pred. No.: 6, 29e-241 Length: 1203
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 10 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-780-669-851 (1-1203)

QY 36 IleThrTyrValProLeuLeuGluValGlyValGluGlyPheMetThrMet 55
|||||

Db 412 ATCACCTATGTGCCGCTCTGCTGCTGGAAGTGGGGTAGAGAGAAGTTTCATGACCATG 471
QY 56 ValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSer 75
Db 472 GTGCTGGGCATTGGTCCAGTGTGGGCCGTGGTGTCTCCCTCCCTAGGCTCAGCCAGT 531
QY 76 AspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGly 95
Db 532 GACCACTGGCGTGGAGCTATATGCCCGCCGCTTCATCTGGGCACACTGCTCTGGGC 591
QY 96 IleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysPro 115
Db 592 ATCCCTGCTGAGCTCTTCTCATCCAGGGCGGTGGCTAGCAGGGGTGTGTGCCG 651
QY 116 AspProArgProLeuGluLeuAlaLeuIleLeuGlyValGlyLeuLeuAspPheCys 135
Db 652 GATCCAGGCCCTGGAGCTGGACTGCTCATCTCCGGCGTGGGCTGGTGGACTTCTGT 711
QY 136 GlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAsp 155
Db 712 GCCAGGTGCTCTCACTCCACTGGAGGCCCTGCTCTGACCTTCCGGGACCCGGAC 771
QY 156 HisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGly 175
Db 772 CACTGTGCGCAGGCGCTACTCTGCTATGCTTTCATCATCAGTCTTGGGGCTGCTGGC 831
QY 176 TyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln 195
Db 832 TACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 891
QY 196 GluGlyCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu 215
Db 892 GAGGAGTGCCTCTTGGCGCTGCTCACCTCATCTTCTCACCTGCTGCTGCTGCTGCT 951
QY 216 LeuValAlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaPro 235
Db 952 CTGGTGGCTGAGAGGACGCGCTGGGCCCCACCGAGCCAGCAGAGGGGTGTGCGGCC 1011
QY 236 SerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAla 255
Db 1012 TCCCTGTGCCCCACTGCTGCTCCATGCGGGCGCGCTTGGCTTCCGGAACTGGCGCC 1071
QY 256 LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe 275
Db 1072 CTGCTTCCCGGCTGCACCACTGCTGCTGCCGCTGCTGCCGCTGCTGCCGCTGCTTTC 1131
QY 276 ValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPhe 295
Db 1132 GTGGCTGAGCTGTGAGCTGGATGGACATCATGACCTTCACGCTGTTTTACACGGATTTC 1191
QY 296 ValGlyGlu 298
Db 1192 GTGGCGGAG 1200

RESULT 23
US-09-822-827-851
; Sequence 851, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.53AC1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-851

Alignment Scores:

Pred. No.: 6,29e-241 Length: 1203
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 10 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-827-851 (1-1203)

QY 36 IleThrTyrValProLeuLeuValGlyValGluGluCysPheMetThrMet 55
Db 412 ATACCTATGTGGCCCTCTGCTGCTGGAAGTGGGGTAGAGAGAAGTTTCATGACCATG 471
QY 56 ValLeuGlyIleGlyProValLeuGlyValCysValProLeuLeuGlySerAlaSer 75
Db 472 GTGCTGGGCATTGGTCAGTGTGGGCTGTCTGTCTCCGCTCCTAGGCTCAGCCAGT 531
QY 76 AspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGly 95
Db 532 GACCACCTGGCGTGGACGCTATGGCCGCGCGCGCTTCATCTGGGCACCTGTCTTGGGC 591
QY 96 IleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysPro 115
Db 592 ATCTGCTGAGCCTCTTCTCATCCCAAGGGCGGCTGGCTAGCAGGGCTGTGTGCCCG 651
QY 116 AspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCys 135
Db 652 GATCCAGGCGCTGGAGCTGGCAGCTGCTCATCTGGCGGTGGGCTGTGGACCTTCTGT 711
QY 136 GlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAsp 155
Db 712 GGCCAGGTGTCTACTCCACTGGAGGCCCTGCTCTCTGACCTCTCCGGGACCCGGAC 771
QY 156 HisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGly 175
Db 772 CACTGTGGCGAGCCCTACTCTGTCTATGGCTTCATGATCAGTCTGGGGGCTGCCTGGGC 831
QY 176 TyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln 195
Db 832 TACTCTGCTGCCATTGACTGGGACACAGTGGCCTGGCCGCCCTACCTGGGCACCCAG 891
QY 196 GluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu 215
Db 892 GAGGAGTGCCTCTTGGCCTGCTCAGCCCTCATCTCTCCTCAGTGTAGCAGCCACACTG 951
QY 216 LeuValAlaGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaPro 235
Db 952 CTGGTGGCTGAGGAGGAGCGCTGGGGCCCGACCGAGCCAGCAAGGGCTGTGGCCCCC 1011
QY 236 SerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAla 255
Db 1012 TCCTTGTGGCCCCACTGTCTCATCGCGGCCGCTTGGCTTCCGGAACTTGGCGGCC 1071
QY 256 LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe 275
Db 1072 CTGCTTCCCGCGGTGCACACAGCTGTCTGCGCATGCCCGCACCTGCGCGGCTCTTC 1131
QY 276 ValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPhe 295
Db 1132 GTGGCTGAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACAGGGATTTC 1191
QY 296 ValGlyGlu 298
Db 1192 GTGGGCGAG 1200

RESULT 24

US-10-012-896-702
; Sequence 702, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 702
; LENGTH: 4894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-702

Alignment Scores:
Pred. No.: 2,39e-240 Length: 4894
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
DB: 9 Gaps: 0

US-09-593-793a-113 (1-553) x US-10-012-896-702 (1-4894)
QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
Db 1311 GCATTGGTCCAGTGTGGCCCTGGTGTGTCTGCCCTCCTAGGCTCAGCCAGTGACCAC 1370
QY 78 TrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
Db 1371 TGGCGTGGACGCTATGGCCGCCGCCCTTCATCTGGGCACCTGTCTTGGGCATCTTG 1430
QY 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
Db 1431 CTGAGCCTCTTCTCATCCAAAGGCGCGCTGGCTAGCAGGGCTGTGTGCCGGATCCC 1490
QY 118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
Db 1491 AGGCCCTCGAGCTGGACTGTCTCATCTCCCTGGGCTGGGCTGTCTGTGGCCAG 1550
QY 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
Db 1551 GTGTGCTTCCACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGACCCGGACCACTGT 1610
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
Db 1611 CGCCAGGCTACTCTGTCTATGCTTTCATGATCAGTCTTGGGGGCTGTGTGGGCTACCTC 1670
QY 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
Db 1671 CTGCTTGCCTTACTGTGGACACCACTGTGGCCCTTACTTGGGCACCCAGGAGGAG 1730


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|||||
Db 2031 GAGGGGCTGTACAGGGCGTGCACAGAGTGAGCGGGACCGAGGCGCGGACACTAT 2090
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QY 318 AspGluGly 320
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Db 2091 GATGAAGGT 2099
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RESULT 29
US-09-822-827-702
; Sequence 702, Application US/09822827
; Patent No. US200020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 702
; LENGTH: 4894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-702
Alignment Scores:
Pred. No.: 2,39e-240 Length: 4894
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 10 Gaps: 0
US-09-593-793a-113 (1-553) x US-09-822-827-702 (1-4894)
QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
|||||
Db 1311 GGCATTGGTCCAGTGTGGCGCTGGTCTGTGTCGCCCTCCTAGGCTCAGCCAGTACCAC 1370
|||||
QY 78 TrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
|||||
Db 1371 TGGCGTGGACGCTATGGCGCGCGCGCTTCATCTGGGCACATGTCCTTGGGCATCCCTG 1430
|||||
QY 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
|||||
Db 1431 CTGAGCCTCTTCTCATCCAGGGCGGCTGGCTAGCAGGCTGTGTGCCGGATCCC 1490
|||||
QY 118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
|||||
Db 1491 AGCCCTGGAGCTGGCACTGCTCATCTCCTGGCGTGGCGTGGCTGTGTGCCAG 1550
|||||
QY 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
|||||
Db 1551 GTGTGCTTCACTCCACTGAGGCGCTGTCTCTGACCTCTTCGGGACCGGACCACTGT 1610
|||||
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
|||||
Db 1611 CGCCAGGCTACTCTCTCTATGCTTCATGATCAGTCTTGGGGGTGCTGGGCTACCTC 1670
|||||
QY 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
|||||
Db 1671 CTGCTTGCCTTACCTGACATGGACACCACTGCTGCTGGCGCTTACCTGGGACCGAGGAG 1730
|||||
QY 198 CysLeuPheGlyLeuLeuThrIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
|||||
Db 1731 TGCCCTTTTGGCTGTCTACCTCCTCATCTTCTCCTACCTGGCTAGCAGCCACACTGTG 1790
|||||
QY 218 AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
|||||
Db 1791 GCTGAGAGGACGCGCTGGGCGCCCGGAGCCAGCAGAGAGGCTGTGCGGCCCTCTCTTG 1850
|||||
QY 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
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Db 1851 TCGCCCACTGTGTCCATGCGGGCGCGCTTGGCTTTCGGGAACCTGGGCGCCCTGCTT 1910
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QY 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277
|||||
Db 1911 CCCCCGCTGACACAGCTGTGCTGCCGATGCCCGCACCTGCGCGCGGCTCTTCTGTGGCT 1970
|||||
QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
|||||
Db 1971 GAGCTGTGAGCTGGATGGCACTCATGACCTTACAGCTGTTTACACGATTTCTGTGGGC 2030
|||||
QY 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
|||||
Db 2031 GAGGGCTGTACAGGGCGTGCACAGAGTGAGCGCGGACCGAGGCGCGGAGACTAT 2090
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QY 318 AspGluGly 320
|||||
Db 2091 GATGAAGGT 2099
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RESULT 30
US-10-012-896-705
; Sequence 705, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meadner, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-705
Alignment Scores:
Pred. No.: 3,35e-240 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 9 Gaps: 0
US-09-593-793a-113 (1-553) x US-10-012-896-705 (1-6976)
QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
|||||
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Db 1202 GGCAATGGTCCAGTGTGCGCCCTGGTCTGTGTCCCGCTCCTAGGCTACCCAGTGACCAC 1261
QY 78 TTPArqGlyArgTyrGlyArgArgProPheIleTTPAlaLeuSerLeuGlyIleLeu 97
|||||
Db 1262 TGGCGTGGACGCTATGCGCGCGCCCTTCATCTGGGCACCTGCTTGGGCATCCTG 1321
QY 98 LeuSerLeuPheLeuIleProArgAlaGlyTTPLeuAlaGlyLeuLeuCysProAspPro 117
|||||
Db 1322 CTGAGCCTCTTCTCATCCCAAGGCGCGCTGGCTAGCAGGCGTGTGTGCCGGATCCC 1381
QY 118 ArgProLeuGluLeuAlaLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
|||||
Db 1382 AGGCCCTGGAGCTGGCACTGTCTATCTCCGGCGTGGGCTGTGGACTTCTGTGGCCAG 1441
QY 138 ValCysPheThrProLeuGluAlaLeuSerAspLeuPheArgAspProAspHisCys 157
|||||
Db 1442 GTGTGCTTCACTCCACTGGAGCGCTGTCTCTGACCTTCTCCGGGACCCGACCACTGT 1501
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
|||||
Db 1502 CGCCAGGCGCTACTCTGTCTATGCTTCATGCTTCATGCTTGGGGCTGTGGCTACCTC 1561
QY 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlnGlu 197
|||||
Db 1562 CTGCCCTGGCATTCAGTGGACACCACTGCTCCCTGGCCCTTACCTGGGCACCCAGGAGAG 1621
QY 198 CysLeuPheGlyLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
|||||
Db 1622 TGGCTCTTGGGCTGTCTACCTTCATCTTCTTCCCTGCTAGCAGCCACACTGCTGGTG 1681
QY 218 AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
|||||
Db 1682 GCTGAGGAGGAGCGCTGGGCGCCACCCAGGAGGAGGCTGTGGCCCTCCTCTTG 1741
QY 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
|||||
Db 1742 TCGCCCCACTGCTGTCCATGCGGGCGCGCTTGGCTTTCGGAACTGGGCGCCCTGCTT 1801
QY 258 ProArgLeuHisGlnLeuCysCysArgMetProArgTTPLeuArgArgLeuPheValAla 277
|||||
Db 1802 CCGCGGCTGCACGAGTGTGTGCGCATGCCCGCACCCCGCGGCTCTTCGTGGCT 1861
QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
|||||
Db 1862 GAGCTGTGCAGTGGATGCACTCATGACCTTCACGCTCTTTTACAGGATTTCTGGGCG 1921
QY 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
|||||
Db 1922 GAGGGGCTGTACAGGGCGTGGCCAGAGCTGAGCGGGGACCCGAGGCGCGGAGACACTAT 1981
QY 318 AspGluGly 320
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Db 1982 GATGAAGGT 1990

RESULT 31

US-09-895-793-705
; Sequence 705, Application US/09895793
; Publication No. US20020192763A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John H.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-705

Alignment Scores:

Pred. No.: 3,35e-240 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 9 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-895-793-705 (1-6976)

QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
|||||
Db 1202 GCATTTGGTCCAGTGTGGGCTGTGTCTGTCTGCCCTCTAGGCTACCCAGTGACCAC 1261
QY 78 TTPArqGlyArgTyrGlyArgArgProPheIleTTPAlaLeuSerLeuGlyIleLeu 97
|||||
Db 1262 TGGCGTGGACGCTATGCGCGCGCCCTTCATCTGGGCACCTGCTTGGGCATCCTG 1321
QY 98 LeuSerLeuPheLeuIleProArgAlaGlyTTPLeuAlaGlyLeuLeuCysProAspPro 117
|||||
Db 1322 CTGAGCCTCTTCTCATCCCAAGGCGCGCTGGCTAGCAGGCGCTGTGTGCCGGATCCC 1381
QY 118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
|||||
Db 1382 AGGCCCTGGAGCTGGCACTGTCTATCTCCGGCGTGGGCTGTGGACTTCTGTGGCCAG 1441
QY 138 ValCysPheThrProLeuGluAlaLeuSerAspLeuPheArgAspProAspHisCys 157
|||||
Db 1442 GTGTGCTTCACTCCACTGGAGCGCTGTCTCTGACCTTCTCCGGGACCCGACCACTGT 1501
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
|||||
Db 1502 CCGCAGGCGCTACTCTGTCTATGCTTCATGATGATGCTTGGGGGCTGCTGGGCTACCTC 1561
QY 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGlu 197
|||||
Db 1562 CTGCCCTGGCATTCAGTGGACACCACTGCTCCCTGGCCCTTACCTGGGCACCCAGGAGAG 1621
QY 198 CysLeuPheGlyLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
|||||
Db 1622 TGGCTCTTGGGCTGTCTACCTTCATCTTCTTCCCTGCTAGCAGCCACACTGCTGGTG 1681
QY 218 AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
|||||
Db 1682 GCTGAGGAGGAGCGCTGGGCGCCACCCAGGAGGAGGCTGTGGCCCTCCTCTTG 1741
QY 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
|||||
Db 1742 TCGCCCCACTGCTGTCCATGCGGGCGCGCTTGGCTTTCGGAACTGGGCGCCCTGCTT 1801
QY 258 ProArgLeuHisGlnLeuCysCysArgMetProArgTTPLeuArgArgLeuPheValAla 277
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Db 1802 CCCGGCTGCACCGCTGTCTCCGCATGCCCGCCACCCCTGCGCGGCTCTTCGTGGCT 1861
QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
Db 1862 GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTTCGTGGGC 1921
QY 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
Db 1922 GAGGGCTGTACAGGGCGTGGCCAGAGCTGAGCCGGGACCGGAGCCGGAGACACTAT 1981
QY 318 AspGluGly 320
Db 1982 GATGAAGGT 1990
RESULT 32
US-09-895-814-705
; Sequence 705, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-705
Alignment Scores:
Pred. No.: 3,35e-240 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 9 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-895-814-705 (1-6976)
QY 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
Db 1202 GCATTGGTCCAGTGTGGCGCTGGGTCTGTGTCGCCGCTCCTAGGCTACGCCAGTACCAC 1261
QY 78 TrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
Db 1262 TGCGTGGAGCGTATGCGCGCGCGCCCTTCATCTGGCACTGTCTTGGCATCTCG 1321
QY 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
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Db 1322 CTGAGGCTCTTTCTCATCCAAAGGGCCGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCC 1381
QY 118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
Db 1382 AGGCCCTCGAGCTGGCACTGCTCATCTTGGCGTGGGCTGCTGGACTTCTGTGGCCAG 1441
QY 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
Db 1442 GTGTGCTTCACTCCACTCGGAGGCCCTGTCTCTGTACCTTTCGGGACCCGGACCACTGT 1501
QY 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
Db 1502 CGCCAGGCTTACTCTGTCTATGCTTCATGATCAGTCTTGGGGGCTGCCCTGGGCTACCTC 1561
QY 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
Db 1562 CTGCCCTGCCATTGACTGGGACACCACTGCGCTGGCCCCCTACTGGGACACCCAGGAGGAG 1621
QY 198 CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
Db 1622 TGCTCTTTGGCTGCTCACCTCATCTTCCACCTGCTAGCAGCCACACTGCTGGTG 1681
QY 218 AlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
Db 1682 GCTGAGGAGGCGCGCTGGGCCCCACCGAGCCAGCAAGAGGCTGTGCGCCCCCTCCTTG 1741
QY 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
Db 1742 TCGCCCCCACTGCTGTCCATGCGCGGCCCTTGGCTTCCGGAACCTGGCGGCCCTGCTT 1801
QY 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277
Db 1802 CCGCGGCTGCACAGCTGTGCTGCGCATGCCCGCACCTGCGCGGCTCTTCGTGGCT 1861
QY 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
Db 1862 GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTTTTACACGGATTTCTGTGGC 1921
QY 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
Db 1922 GAGGGCTGTACAGGGCGTGGCCAGAGCTGAGCCGGGACCGGAGCCCGGAGACACTAT 1981
QY 318 AspGluGly 320
Db 1982 GATGAAGGT 1990
RESULT 33
US-09-759-143-705
; Sequence 705, Application US/09759143
; Patent No. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
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; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-705

Alignment Scores:
Pred. No.: 3,35e-240 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-759-143-705 (1-6976)
Qy 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
Db 1202 GGCATTGGTCCAGTCTGGGCGCTGCTGTGTCCGGCTCCTAGGCTCAGCCAGTGACCAC 1261
Qy 78 TrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
Db 1262 TGGCGTGGACGCTATGGCGCGCGCGCCCTTCATCTGGGCACCTGCTCTGGGCATCCTG 1321
Qy 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
Db 1322 CTGAGCCCTTTTCTCATCCCAAGGCGCGCTGGCTAGCAGGCGTCTGTGCCCGGATCCC 1381
Qy 118 ArgProLeuGluLeuAlaLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
Db 1382 AGGCCCTTGGAGCTGGGACTGCTCATCTGGGCGTGGGCGCTGCTGGGCGTCTGTGGCCAG 1441
Qy 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
Db 1442 GTGTGCTTCATCCACCTGGAGCCCTGCTCTCTGACCTCTTCCGGACCCGACCATCTG 1501
Qy 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyCysLeuGlyTyrLeu 177
Db 1502 CGCCAGGCGCTACTGCTGTATGCCTTCATGATCATGCTTGGGGGCTGCTGGGCTACCTC 1561
Qy 178 LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
Db 1562 CTGCCTGCCATTGACTGGGACACCACTGCTGCTGGCCCTTACCTGGGACCCAGGAGAG 1621
Qy 198 CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
Db 1622 TGCCCTTTTGGCCCTGCTCACCTCATCTCTCCTCACCTGCGTAGCACACACACTGCTGTG 1681
Qy 218 AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
Db 1682 GCTGAGGAGGAGCGCTGGGCGCCACCGAGCCAGCAGAGGCGTGTCCGGACCCCTCCCTTG 1741
Qy 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
Db 1742 TCGCCCACTGCTGTCCATGCGGGCGCGCTGGCTTTCCGGACCTGGGGCGCCCTGCTGT 1801
Qy 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277
Db 1802 CCCCAGCTGCACACAGCTGCTGCGGCATGCCCCGACCCCTGCGCGCGCTCTTCTGTGCT 1861
Qy 278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
Db 1862 GAGCTGTGAGCTGGATGGCACTCATGACCTTCAGCTGCTTTTACACGATTTTCTGTGGGC 1921
Qy 298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
Db 1922 GAGGGGCTGTACCAAGGGGCTGCCACAGACTGAGCGGGGCACCGAGGGCCCGGAGACAT 1981
Qy 318 AspGluGly 320
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Db 1982 GATGAAGCT 1990
RESULT 34
US-09-780-669-705
; Sequence 705, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/097780.669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-705

Alignment Scores:
Pred. No.: 3,35e-240 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-780-669-705 (1-6976)
Qy 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77
Db 1202 GGCATTGGTCCAGTCTGGGCGCTGCTGTGTCCGGCTCCTAGGCTCAGCCAGTGACCAC 1261
Qy 78 TrpArgGlyArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97
Db 1262 TGGCGTGGACGCTATGGCGCGCGCGCCCTTCATCTGGGCACCTGCTCTGGGCATCCTG 1321
Qy 98 LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
Db 1322 CTGAGCCCTTTTCTCATCCCAAGGCGCGCTGGCTAGCAGGCGTCTGTGCCCGGATCCC 1381
Qy 118 ArgProLeuGluLeuAlaLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
Db 1382 AGGCCCTTGGAGCTGGGACTGCTCATCTGGGCGTGGGCGCTGCTGGGCGTCTGTGGCCAG 1441
Qy 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
Db 1442 GTGTGCTTCATCCACCTGGAGCCCTGCTCTCTGACCTCTTCCGGACCCGACCATCTG 1501
Qy 158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyCysLeuGlyTyrLeu 177
Db 1502 CGCCAGGCGCTACTGCTGTATGCCTTCATGATCATGCTTGGGGGCTGCTGGGCTACCTC 1561
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Qy	178	LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGlu	197
Db	1562	CTGCCTGCCATTGACTGGGACACAGTGCCTGGCCCTACCTGGGCACCCAGAGGAG	1621
Qy	198	CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal	217
Db	1622	TGCCTCTTTTGGCTGCTCACCCCTCATCTTCCCTACCTGCGTAGCAGCCACACTGCTGGTG	1681
Qy	218	AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu	237
Db	1682	GCTGAGGAGGACGGCTGGGCCCCACCCAGACCCAGAAAGGGCTGTCGGCCCCCTCCTCTG	1741
Qy	238	SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu	257
Db	1742	TCGCCCCACACTGCTGCATGCCGGGGCCGCTTGGCTTTCCGGAAGCTGGCGGCCCTGCTT	1801
Qy	258	ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAla	277
Db	1802	CCCCGGCTGCACACAGCTGCTGCCGCATGCCCGGACCCCTGCGCGGCTCTTCGTGGCT	1861
Qy	278	GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly	297
Db	1862	GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGAATTCGTGGGC	1921
Qy	298	GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaAArgHisTyr	317
Db	1922	GAGGGGCTGTACCAAGGCGCTGCCAGAGCTGAGCGGGCACCCGAGGCCCGGAGACACTAT	1981
Qy	318	AspGluGly 320	
Db	1982	GATGAAGGT 1990	
RESULT 35			
US-09-822-827-705			
; Sequence 705, Application US/09822827			
; Patent No. US20020081680A1			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
; FILE REFERENCE: 210121-534C1			
; CURRENT APPLICATION NUMBER: US/09/822,827			
; CURRENT FILING DATE: 2001-03-28			
; NUMBER OF SEQ ID NOS: 982			
; SOFTWARE: FastSEQ for Windows Version 3.0			
; SEQ ID NO 705			
; LENGTH: 6976			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-822-827-705			
Alignment Scores:			
Pred. No.: 3,35e-240 Length: 6976			
Score: 263.00 Matches: 263			
Percent Similarity: 100.00% Conservative: 0			
Best Local Similarity: 100.00% Mismatches: 0			
Query Match: 47.56% Indels: 0			
DB: 10 Gaps: 0			
US-09-593-793A-113 (1-553) x US-09-822-827-705 (1-6976)			
Qy	58	GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis	77
Db	1202	GGCATTGGTCCCATGCTGGGCGCTGGTCTGTGCCGCTCCCTAGCGCTCAGCCAGTGACCAC	1261
Qy	78	TrpArgGlyArgTyrGlyArgArgPropheIleTrpAlaLeuSerLeuGlyIleLeu	97
Db	1262	TGGCGTGAGCGCTATGGCCGCCCGCCGCCCTTCATCTGGGCACATGCTCTGGGCATCTCTG	1321
Qy	98	LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro	117
Db	1322	CTGAGCCTCTTTCTCATCCAAAGGCGGCTGGCTAGCAGGGCTGCTGTGCCGGATCCC	1381

Qy	118	ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuAspPheCysGlyGln	137
Db	1382	AGGCCCTGGAGCTGGCACTGCATCCTGGGCGTGGGCTGCTGCAGCTTCTGTGGCCAG	1441
Qy	138	ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys	157
Db	1442	GTGTGCTTCACCTCCACCTGGAGGCCCTGCTCTGACACTCTCCCGGACCCGAGCACCTGT	1501
Qy	158	ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu	177
Db	1502	CGCCAGGCCTACTCTGCTATGCTTCATGATCAGTCTTGGGGGCTGCTGGGTACCTC	1561
Qy	178	LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu	197
Db	1562	CTGCCTGCCATTGACTGGGACACAGTGGCCCTGGCCCTTACCTGGGCACCCAGAGGAG	1621
Qy	198	CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal	217
Db	1622	TGCTCTTTTGGCTGGCTACCCCTCATCTTCCCTACCTGGGTAGCACCACACTGCTGGTG	1681
Qy	218	AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu	237
Db	1682	GCTGAGGAGGCGCTGGGCCCCACCGAGCAGCAGAGGCGTCTCGGCCCTCCTTG	1741
Qy	238	SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu	257
Db	1742	TCGCCCACTGCTGCTCCATGCCGGGCCGCTGGCTTTCCGGAACCTGGGGCGCTGCTT	1801
Qy	258	ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAla	277
Db	1802	CCCCGGCTGCACCACTGCTGCTCCCGCATGCCCGCACCTCGCCGGGCTCTCTGTGGCT	1861
Qy	278	GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly	297
Db	1862	GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACCGTGTTTACACGATTTCTGTGGC	1921
Qy	298	GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr	317
Db	1922	GAGGGCTGTACCAAGGCGTGGCCAGAGCTGAGCGGGCACCGAGGCCCGGAGACACTAT	1981
Qy	318	AspGluGly 320	
Db	1982	GATGAAGGT 1990	
RESULT 36			
US-10-012-896-703			
; Sequence 703, Application US/10012896			
; Publication No. US20020183251A1			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Dillon, Davin C.			
; APPLICANT: Mitcham, Jennifer L.			
; APPLICANT: Harlocker, Susan L.			
; APPLICANT: Jiang, Yuqiu			
; APPLICANT: Kalos, Michael D.			
; APPLICANT: Retter, Marc W.			
; APPLICANT: Stolk, John A.			
; APPLICANT: Day, Craig H.			
; APPLICANT: Vedvick, Thomas S.			
; APPLICANT: Carter, Darrick			
; APPLICANT: Li, Samuel X.			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skeiky, Yasir A.W.			
; APPLICANT: Hepler, William T.			
; APPLICANT: Henderson, Robert A.			
; APPLICANT: Hural, John			
; APPLICANT: McNeill, Patricia D.			
; APPLICANT: Houghton, Raymond L.			
; APPLICANT: Vinals de Bassols, Carlota			
; APPLICANT: Foy, Teresa			
; APPLICANT: Fanger, Gary R.			
; APPLICANT: Wantanabe, Yoshihiro			

```
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012.896
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-703

Alignment Scores:
Pred. No.: 6.32e-214 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x US-10-012-896-703 (1-2904)
Qy 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 810 GAGGCGTTCGGATGGGCGAGCTGGGGCTGTTCTCGCAGTCGCCATCTCCCTGCTTC 869
Qy 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 870 TCTCTGGTCATGGACCGGCTGGTCAGCGATTTCGGCACTCGAGCAGTCTATTGGCCAGT 929
Qy 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal 378
Db 930 GTGGCAGCTTTCCCTGTGGCTGCCGCTGCACATGCTCCACAGTGTGGCGTGGTG 989
Qy 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 990 ACAGCTTCAGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCTCCCTACACA 1049
Qy 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 1050 CTGGCTCCCTCTACACCGGAGAGCAGGTGTTCTTCGCCCAATAACCGAGGGACACT 1109
Qy 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 1110 GGAGTGCTACAGTGAGGACAGCTGTATGACCAAGCTTCTCTGCCAGGCCCTAAGCCTGGA 1169
Qy 439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProPro 458
Db 1170 GCTCCCTTCCCTAATGGACAGTGGGTGCTGGAGGACGTGGCTTCCACCTCCACCC 1229
Qy 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
Db 1230 GCGCTCTCGGGGGCTCTGCTGTGATGTCCTCCGTACGTGTGGTGGTGAGGCCACC 1289
Qy 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 1290 GAGGCCAGGGGTGTTCGGGGCGGGGCATCTGCCGTGGACCTCGCCATCTCGATAGTGCC 1349
Qy 499 PheLeuLeuSerGlnValAlaProSerSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 1350 TTCCTGTGTCAGGTGGCCCATCCTGTTATATGGGCTCCATGTGCCAGCTCAGCCAG 1409
Qy 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 1410 TCTGTCACTGCCTATATGGTGTCTCGCGCAGGCCCTGGGTCTGGTCGCCATTTACTTGTCT 1469
Qy 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1470 ACACAGGTAGTATTGTGACAAGAGGACTTGGCCAAATACTCAGCG 1514

RESULT 37
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US-09-895-793-703
; Sequence 703, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895.793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-703

Alignment Scores:
Pred. No.: 6.32e-214 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-895-793-703 (1-2904)
Qy 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 810 GAGGCGTTCGGATGGGCGAGCTGGGGCTGTTCTTCGACGTGCGCATCTCCCTGCTTC 869
Qy 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 870 TCTCTGGTCATGGACCGGCTGGTCAGCGATTTCGGCACTCGAGCAGTCTATTGGCCAGT 929
Qy 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal 378
Db 930 GTGGCAGCTTTCCCTGTGGCTGCCGCTGCACATGCTCCACAGTGTGGCGTGGTG 989
Qy 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 990 ACAGCTTCAGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCTCCCTACACA 1049
Qy 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 1050 CTGGCTCCCTCTACACCGGAGAGCAGGTGTTCTTCGCCCAATAACCGAGGGACACT 1109
Qy 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 1110 GGAGTGCTACAGTGAGGACAGCTGTATGACCAAGCTTCTCTGCCAGGCCCTAAGCCTGGA 1169
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QY 439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProPro 458
DB 1170 GCTCCCTTCCCTTAATGGACACGTGGTGTGGAGGAGTGGCTGCTCCACCTCCACCC 1229
QY 459 AlaLeuGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
DB 1230 GCGCTCTCGGGGGCTCTCCCTGTGATGTCTCCGTACGTGTGGTGGGTGAGCCAC 1289
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
DB 1290 GAGGCCAGGTGTTCCGGCGGGGCGGCATCTCCCTGGACCTCGCCATCTGGATAGTGC 1349
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
DB 1350 TTCTGCTGTCCAGGTGGCCCATCTCTGTTATGGGTCCATTTGTCAGCTCAGCCAG 1409
QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
DB 1410 TCTGTACGTGCTATATGTTGTCTCCGAGGCTGGGTCTGGTCCCATTTACTTTGCT 1469
QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 1470 ACACAGGTAGTATTGACAAGAGCGACTTGGCCAAATACTACAGCG 1514

RESULT 38

US-09-895-814-703
; Sequence 703, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895.814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-895-814-703

Alignment Scores:
Pred. No.: 6,328-214 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
DB: 9 Gaps: 0

US-09-593-793a-113 (1-553) x US-09-895-814-703 (1-2904)

QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
DB 810 GAGGCGTTCGATGGCAGCGCTGGGCTGTTCCTGCAGTGGCCATCTCCCTGGTCTTC 869
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
DB 870 TCTCTGGTCTATGACCGCGCTGGTGGAGCATTCGGCAGCTCGAGCGACTTATTTGGCAGT 929
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
DB 930 GTGGCAGCTTTCCTGTGGCTGCCGTGCCACATGCCTGTCCACAGTGTGGCCGTGGTG 989
QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
DB 990 ACAGCTTCAGCGCGCTCACCGGGTTCACCTTCTCAGCGCTGCAGATCTCGCTTACACA 1049
QY 399 LeuAlaSerLeuTyrHisArgGlnValPheLeuProLysTyrArgGlyAspThr 418
DB 1050 CTGGGCTCCCTTACACCGGGAGAGCAGGTGTTCTGCCCAATACCGAGGGGACACT 1109
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
DB 1110 GGAGTGTCTAGCAGTGAGACAGCTGTGATGCTCCTGCCAGGCCCTAAGCCTGGA 1169
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
DB 1170 GCTCCCTTCCCTAATGGACACGTGGTGTGGAGGAGTGGCTGCTCCACCTCCACCC 1229
QY 459 AlaLeuGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
DB 1230 GCGCTCTCGGGGGCTCTCCCTGTGATGTTCTCCGTACGTGTGGTGGGTGAGCCAC 1289
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
DB 1290 GAGGCCAGGTGGTTCGGGGCGGGGCATCTGCTGGACCTGCCATCTGGATAGTGC 1349
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
DB 1350 TTCTGCTGTCCAGGTGGCCCATCTCTGTTATGGGTCCATTTGTCAGCTCAGCCAG 1409
QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
DB 1410 TCTGTACTGCTATATGTTGTCTCCGAGGCTGGGTCTGGTCCCATTTACTTTGCT 1469
QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 1470 ACACAGGTAGTATTGACAAGAGCGACTTGGCCAAATACTACAGCG 1514

RESULT 39

US-09-759-143-703
; Sequence 703, Application US/09759143
; Patent No. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; DIAGNOSIS OF PROSTATE CANCER

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; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-703

Alignment Scores:
Pred. No.: 6,32e-214 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-759-143-703 (1-2904)

QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
DB 810 GAGGCGGTTCGGATGGGAGCGCTGGGGCTGTTCCTGCAGTGGCCATCTCCCTGGTCTTC 869

QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
DB 870 TCTCTGGTCATGGACCGGCTGGTGCGGATTCGGCAGCTCGAGCAGTCTATTGGCCAGT 929

QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal 378
DB 930 GTGGCAGCTTCCCTGTGGCTGGCGGTGCCACATGCCGTGCCACAGTGTGCCCGTGGTG 989

QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
DB 990 ACAGCTTCAGCGCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCTGCCCTTACACA 1049

QY 399 LeuAlaSerLeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGlyAspThr 418
DB 1110 GGAGTGTCTAGCAGTGAGGACAGCGCTGATGACACAGCTTCTCCGACGCGCTTAAGCCTGGA 1169

QY 439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProPro 458
DB 1170 GCTCCCTTCCCTTAATGGACACGTGGGTGTCCGACGTGGTGGGTGAGGCCACCC 1229

QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
DB 1230 GCGCTCTCGGGGGCTCTGCGGTGTGTCTCCGTACGTGGTGGGTGAGGCCACCC 1289

QY 479 GluAlaArgValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
DB 1290 GAGGCCAGGGTGTTCGGGGCGGGGATCTGCGTGGACCTCGCCATCCTGGATAGTGC 1349

QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
DB 1350 TTCCTGCTGTCCAGTGGCGCCCATCCCTGTTTATGGGCTCCATTTGTCAGCTCAGCCAG 1409

QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
DB 1410 TCTGTCACTGCCATATATGGTGTCTCCCGAGGCCCTGGGTGTGGTGGCCATTACTTTGCT 1469

QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 1470 ACACAGGTAGTATTGACAAGCGGACTTGGCCAAATACTACGCG 1514

RESULT 40
US-09-780-669-703
; Sequence 703, Application US/09780669
; Patent No. US20020051977A1
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; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-703

Alignment Scores:
Pred. No.: 6,32e-214 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-780-669-703 (1-2904)

QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
DB 810 GAGGCGGTTCGGATGGGAGCGCTGGGGCTGTTCCTGCAGTGGCCATCTCCCTGGTCTTC 869

QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
DB 870 TCTCTGGTCATGGACCGGCTGGTGCGGATTCGGCAGCTCGAGCAGTCTATTGGCCAGT 929

QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal 378
DB 930 GTGGCAGCTTCCCTGTGGCTGGCGGTGCCACATGCCGTGCCACAGTGTGCCCGTGGTG 989

QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
DB 990 ACAGCTTCAGCGCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCTGCCCTTACACA 1049

QY 399 LeuAlaSerLeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgGlyAspThr 418
DB 1050 CTGGGCTCCCTCTACACCGGGAGAGGAGGTGTTCCTGCCAATACCGAGGGGACACT 1109

QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
DB 1110 GGAGTGTCTAGCAGTGAGGACAGCGCTGATGACACAGCTTCTCCGACGCGCTTAAGCCTGGA 1169

QY 439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProPro 458
DB 1170 GCTCCCTTCCCTTAATGGACACGTGGGTGTCCGACGTGGTGGGTGAGGCCACCC 1229

QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
```

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Db 1230 GCGCTCGGGGCCCTCCCTCGTGTGATGCTCCGTACGTGTGGTGGGTGAGCCACC 1289
QY 479 GluAlaArgValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 1290 GAGCCAGGGTGTCCGGCGGGGCGGCATCTCGCTGGAGCTCGCCCATCTCGATAGTGCC 1349
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 1350 TTCTCTGCTGCCAGGTGCCCATCCCTGTTTATGGGTCCATTGTCCAGCTCAGCCAG 1409
QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 1410 TCTGTCACTGCCTATATGTTCTGCCGAGGCGCTGGTCTGGTCCCATTTACTTTGCT 1469
QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1470 ACACAGGTAGTATTGACAAGAGCGACTTGGCCAAATACTCAGCG 1514

RESULT 41
US-09-822-827-703
; Sequence 703, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-703

Alignment Scores:
Pred. No.: 6,32e-214 Length: 2904
Score: 235.00 Matches: 235
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.50% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-822-827-703 (1-2904)
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 810 GAGGGCGTTTCGGATGGCGAGCGCTGGGCTGTTCTCGAGTGGCCATCTCCCTGGTCTTC 869
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 870 TCTCTGGTATGACCGCGGTGGTGGCAGGATTCGGCACATCGAGCAGTCTATTGGCCAGT 929
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 930 GTGGCAGCTTTCCTCTGGCTGCCGTGCCACATGCTGTCCACAGTGTGGCGGTGGT 989
QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 990 ACAGCTTCAGCGCCCTCACCGGGGTTTCACCTTCTCAGCCCTGCAGATCTCGCCCTACACA 1049
QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 1050 CTGGCCCTCCCTTACACCGCGGAGAGCGGTGTTCTCTCCCAAAATACCGAGGGGACACT 1109
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 1110 GGAGGTGCTAGCAGTGGAGACAGCCTGATGACAGCTTCTCTCCAGGCGCTTAGCGCTGGA 1169
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProPro 458
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Db 1170 GTCTCCCTTCCCTAAATGGACACGTGGGTGCTGGAGGCGAGTGGCTTCCCACTCCACCC 1229
QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
Db 1230 GCGCTCTCGCGGGCGCTCTCCCTGTGATGCTCTCGTACGTGTGGTGGGTGAGCCACC 1289
QY 479 GluAlaArgValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 1290 GAGCCAGGGTGTTCGGCGGGGCGGCATCTGCTGGAGCTCGCCCATCTCGATAGTGCC 1349
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 1350 TTCTCTGCTGCCAGGTGCCCATCCCTGTTTATGGGTCCATTGTCCAGCTCAGCCAG 1409
QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 1410 TCTGTCACTGCCTATATGTTCTGCCGAGGCGCTGGTCTGGTCCCATTTACTTTGCT 1469
QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1470 ACACAGGTAGTATTGACAAGAGCGACTTGGCCAAATACTCAGCG 1514

RESULT 42
US-10-012-896-1010
; Sequence 1010, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1010
; LENGTH: 1065
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-1010

Alignment Scores:
Pred. No.: 1.13e-168 Length: 1065
Score: 187.00 Matches: 187
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 33.82% Indels: 0
DB: 9 Gaps: 0
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US-09-593-793a-113 (1-553) x US-10-012-896-1010 (1-1065)

QY 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
DB 478 ATGGACCGCTGGTGCAGCGATTTCGCACTCGAGCAGTCTATTGGCCAGTGGCAGCT 537
QY 362 PheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSer 381
DB 538 TTCCCTGTGGCTGCCGGTCCCATGCCGTGTCCACAGTGTGCCCGTGGTGCAGAGTTCA 597
QY 382 AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401
DB 598 GCCGCCCTCACCAGGTTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCC 657
QY 402 LeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAla 421
DB 658 CTCTACCAACCGGAGAGAGGTTTCTTCCGCCCAATACCGAGGGGACACTGGAGTGTCT 717
QY 422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
DB 718 AGCAGTGGAGCAGACCTGATGACCACTTCTTCCAGGCGCTTAAGCCTGGAGCTCCCTTC 777
QY 442 ProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeuCys 461
DB 778 CCTAATGGACAGTGGGTGCTGGAGCAGTGGCTGCTCCCACTCCACCCGCGCTCTGC 837
QY 462 GlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAlaArg 481
DB 838 GGGGCTCTGCCCTGTGATGCTCTCCGTACGTGTGGTGGTGGTGGTGGTGGTGGTGGTGG 897
QY 482 ValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501
DB 898 GTGGTTCGGGCGGGGCACTGCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTG 957
QY 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521
DB 958 TCCAGGTGGCGCCCATCCCTGTTATGGGCTCCATTGTCAGCTCAGCCAGCTGTGCTACT 1017

QY 522 AlaTyrMetValSerAlaAla 528
DB 1018 GCCTATATGCTGCTCGCGCC 1038

RESULT 43
US-09-232-880-10
; Sequence 10, Application US/09232880
; Publication No. US20020182596A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
; FILE REFERENCE: 210121.428C6
; CURRENT APPLICATION NUMBER: US/09/232,880
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-880-10

Alignment Scores:
Pred. No.: 5,84e-107 Length: 789
Score: 122.00 Matches: 122
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.06% Indels: 0

DB: 9 Gaps: 0
US-09-593-793a-113 (1-553) x US-09-232-880-10 (1-789)
QY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376
DB 12 GCAGTGTGGCAGCTTTCCTGTGGCTGGCGTGGCCATGCTGTGCCACAGTGTGGCC 71
QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396
DB 72 GTGGTGACAGCTTACCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCTGCC 131
QY 397 TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly 416
DB 132 TACACACTGGCTCCCTCTTACCACCGGGAGAGCAGGTCTTCTGCCCAATACCGAGG 191
QY 417 AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
DB 192 GACACTGGAGGTGCTAGCAGTAGGACAGCCTGATGACCACTTCTTCCAGGCCCTAAG 251
QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro 456
DB 252 CCTGGAGCTCCCTTCCCTAATGGACACGCTGGGTGCTGGAGGAGCTGGCTGCCACCT 311
QY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476
DB 312 CCACCCGGCTCTCGGGGSCCTTGCCTGTGATGCTCCGTACGTGCTGGTGGTGGTGAG 371
QY 477 ProThr 478
DB 372 CCCACC 377

RESULT 44
US-10-012-896-10
; Sequence 10, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: 9, 380, 451, 565, 582, 716, 718, 758, 762, 765, 768, 771,
; LOCATION: 779, 783
; OTHER INFORMATION: n = A,T,C or G
US-10-012-896-10

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Alignment Scores:	5.84e-107	Length:	789
Pred. No.:	122.00	Matches:	122
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	22.06%	Gaps:	0
DB:	9		

US-09-593-793A-113 (1-553) x US-10-012-896-10 (1-789)

357	QY	AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla	376
12	Db	GCCAGTGTGCACGTTTCCCTGTGGCTGCCGGTGCCACATGCTGTCCACAGTGTGGCC	71
377	QY	ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro	396
72	Db	GTGGTGACAGCTTCAGCGCGCCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCTCGCC	131
397	QY	TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly	416
132	Db	TACACACTGGCCTCCCTCTACACACCGGGAGACAGGTGTTCTGCCCAAAATACCGAGGG	191
417	QY	AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys	436
192	Db	GACACTGGAGGTGCTAGCAGTAGGACACGCTGTATCACCAGCTTCTCGCCAGGCGCTAAG	251
437	QY	ProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProPro	456
252	Db	CCTTGGAGCTCCCTTCCCTAATGTGACACAGTGGGTGCTGTGGAGGAGTGGCTGTCTCCACCT	311
457	QY	ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGlu	476
312	Db	CCACCGCGGTCTTCGGGGCGCTCTGCCTGTGTATGTCTCCGTACGTGTGGTGGGTGAG	371
477	QY	ProThr	478
372	Db	CCCAACC	377

RESULT 45

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US-09-895-793-10
; Sequence 10, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Cardick, Thomas S.
; APPLICANT: Vedvick, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlos
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND
; TITLE OF INVENTION: DIAGNOSIS OF P

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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 04:50:30 ; Search time 2882 Seconds
(without alignments)
5584.265 Million cell updates/sec

Title: US-09-593-793A-113
Perfect score: 553
Sequence: 1 MVQRLWVSRLLHRKQAQLL.....AIYFATQVVFVFKSLAKYSA 553

Scoring table:
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Word size 3 amino acids = 9 nucleotides

Total number of hits satisfying search parameters: 3872064 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US09593793/runat_13022003_161426_21820/app_query.fasta.1.711
-DB=GenEmbl -QFMT=fastap -SUFFIX=olig.rge -MINMATCH=0.1 -DOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=100
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40: em_hgtgo_mus.*
41: em_hgtgo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

length of match

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	3320	6	AX327336 Sequence
2	553	100.0	3410	6	AX106329 Sequence
3	553	100.0	3410	6	AX140620 Sequence
4	553	100.0	3410	6	AX200480 Sequence
5	553	100.0	3410	6	AX267136 Sequence
6	553	100.0	3410	6	AX429961 Sequence
7	553	100.0	3410	9	AY033593 Homo sapi
8	501	90.6	2133	6	AX343857 Sequence
9	320	57.9	1593	6	AX343860 Sequence
10	320	57.9	4034	6	AX200095 Sequence
11	320	57.9	4034	6	AX267730 Sequence
12	263	47.6	1203	6	AX201078 Sequence
13	263	47.6	1203	6	AX267877 Sequence
14	263	47.6	4894	6	AX200093 Sequence
15	263	47.6	4894	6	AX267728 Sequence
16	263	47.6	6976	6	AX200096 Sequence
17	263	47.6	6976	6	AX267731 Sequence
18	263	47.6	157988	2	AC096533 Homo sapi
19	255	46.1	2152	6	AR112295 Sequence
20	252	45.6	2143	6	AR112294 Sequence
21	235	42.5	2477	9	AL832933 Homo sapi
22	235	42.5	2904	6	AX200094 Sequence
23	235	42.5	2904	6	AX267729 Sequence
24	158	28.6	3514	9	AB060851 Macaca fa
25	131	23.7	2917	9	AB062977 Macaca fa
26	122	22.1	789	6	AX106229 Sequence
27	122	22.1	789	6	AX140520 Sequence
28	122	22.1	789	6	AX200380 Sequence
29	122	22.1	789	6	AX267036 Sequence
30	85	15.4	258	6	AR112280 Sequence
31	82	14.8	247	6	AR112283 Sequence
32	71	12.8	217	6	AR112281 Sequence
33	71	12.8	255	6	AR112282 Sequence
34	69	12.5	406	11	HSPE54C06
35	63	11.4	198037	2	AC126523
36	59	10.7	2611	10	BC034084 Mus muscu
37	59	10.7	3354	10	BC031381 Mus muscu
38	59	10.7	178567	2	AC107837 Mus muscu
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42	20	3.6	60	6	AX201081 Sequence
43	20	3.6	60	6	AX267880 Sequence
44	12	2.2	57	6	AX201091 Sequence
45	12	2.2	57	6	AX267890 Sequence
46	11	2.0	149430	2	AC119299 Rattus no
47	11	2.0	162209	9	CNS01R1H Human chr
48	11	2.0	184361	2	AC098929 Rattus no
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51	10	1.8	1980	9	AF511533	Homo sapi
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55	10	1.8	68577	2	AC128149	Rattus no
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57	10	1.8	127456	2	AC119380	Rattus no
58	10	1.8	130935	2	AF0004192	Oryza sat
59	10	1.8	143702	2	AC128427	Rattus no
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62	10	1.8	160154	2	AL391066	Homo sapi
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67	10	1.8	179779	2	AP005315	Oryza sat
68	10	1.8	185152	2	AL732371	Homo sapi
69	10	1.8	191601	2	AC105598	Rattus no
70	10	1.8	197632	10	AL672039	Mouse DNA
71	10	1.8	327927	3	AE003439	Drosophil
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92	9	1.6	903	6	AX210614	Sequence
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95	9	1.6	1020	14	AF511734	Hepatitis
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100	9	1.6	2806	9	AK027163	Homo sapi

ALIGNMENTS

RESULT 1	AX327336	3320 bp	DNA	linear	PAT 07-JAN-2002
LOCUS	AX327336	Sequence 1 from Patent WO0181577.			
DEFINITION	AX327336				
ACCESSION	AX327336				
VERSION	AX327336.1	GI:18097882			
KEYWORDS	human.				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1				
AUTHORS	Lau, T., Lin, R.J., Parkes, D., Parry, G., Schneider, D.W., Steinbrecher, R., van Heut, P.T. and Wu, J.				
TITLE	Dna encoding the prost 03 polypeptide				
JOURNAL	Patent: WO 0181577-A 01-NOV-2001;				
FEATURES	SCHERING AKTIENSELLSCHAFT (DE)				
source	Location/Qualifiers				
	1..3320				

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Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
DB:	6	Gaps:	0		
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Qy 21	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAAGlylleThrTyrValPro 40				
Db 342	GTCAACCTGCTAACTTTGGCTGGAGGTGTGTTGGCGCAGGAGCATCACCTATGTCGG 401				
Qy 41	ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlylleGly 60				
Db 402	CTCTGCTGCTGAAGTGGGGTAGAGAGAGATTCTAGCATGCTGTGGGCATTGT 461				
Qy 61	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgly 80				
Db 462	CCAGTGTGGGCTGTGTGTCTCCCTCTAGGCTCAGCCAGTGACCATGGCGTGA 521				
Qy 81	ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlylleLeuLeuSerLeu 100				
Db 522	CGCTATGCCCGCGCGCCCTTCATCTGGGCACGTCTTGGGCATCTGCTGAGCCCTC 581				
Qy 101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuCysProAspProArgProLeu 120				
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Qy 121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140				
Db 642	GAGCTGGCAGCTCTCATCTGGCGTGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTC 701				
Qy 141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160				
Db 702	ACTCCACTGGAGGCGCTCTCTGACCTCTCCGGGACCCCGGACCATGTGTCAGCCGC 761				
Qy 161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180				
Db 762	TACTCTGTCTATGCCCTTCATGATCACTTGTGGGGCTGCTGGGGTACTCTCTGCTGCC 821				
Qy 181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200				
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Qy 201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220				
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AELCSWALMTFTLFTYDFVGGELYQGVPRAEPTGEARRHDEGVGRMSGLFLQCAI
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QY	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
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QY	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260
Db	1004	TGCTGTCCATGCGCGGCCCGCTTGGCTTTCCGGAACCTGGCGCCCTGCTTCCCGCGCTG	1063
QY	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280
Db	1064	CACCAGCTGTGTCGCGCATGCCCGCAGCCCTGCGCGGCTCTTCTGGCTGAGCTGTGC	1123
QY	281	SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu	300
Db	1124	AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCTGGCGAGGGCGTG	1183
QY	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly	320
Db	1184	TACCAGGGCTGCCAGAGCTGAGCCGGGCACCGAGGCGCGGAGACACTATGATGAAGC	1243
QY	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340
Db	1244	GTTCCGATGGCAGCTGGGGCTGTCTCCAGTGGCCATCTCCCTGGTCTCTCTCTG	1303
QY	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla	360
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QY	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla	380
Db	1364	GCCTTCCCTGTGCTGCCGTGCCATGCCTGCCACAGTGTGGCGGTGACAGCT	1423
QY	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400
Db	1424	TCAGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCTGCCCTACACACTGGCC	1483
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QY	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440
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QY	441	PheProAsnGlyHisValGlyAlaGlyLysSerGlyLeuLeuProProProAlaLeu	460
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QY	461	CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla	480
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QY	481	ArgValValProGlyArgGlyLecysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500
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QY	501	LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
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QY	521	ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	540
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Db	1904	GTAGTATTTGACAAGAGCAGCTTGGCCAAATATCTCAGCG	1942
RESULT 3			
AX140620			
LOCUS			
DEFINITION Sequence 110 from Patent WO0134802.			
3410 bp DNA linear PAT 31-MAY-2001			

ACCESSION	AX140620		
VERSION	AX140620.1	GI:14280737	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3410)		
AUTHORS	Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Reed, S.G., Kalos, M.D., Retter, M.W., Stolk, J.A., Day, C.H., Skeiky, Y.A. and Wang, A.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer		
JOURNAL	Patent: WO 0134802-A 110 17-MAY-2001;		
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US-09-593-793A-113 (1-553) x AX140620 (1-3410)			
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Db	344	GTCACCTGCTAACCTTTGGCGCTGGAGGTGTGTTGGCGCAGGCATCACCTATGTGCG	403
QY	41	ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly	60
Db	404	CTCTGCTGCTGGAAGTGGGGTAGAGGAGATTTCATGACCATGGTGTGGGCATTGCT	463
QY	61	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTyrArgGly	80
Db	464	CCAGTGTGTGGGCTGGTGTGTCTCCGCTCCTAGGCTCAGCCAGTGCACCTGGCGTGA	523
QY	81	ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu	100
Db	524	CGCTATGGCGCGCGCGCTTCATCTGGGCACGTCTCTGGGCATCTCTGTGAGCCCTC	583
QY	101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu	120
Db	584	TTTCTCATCTCCAAGCGCGGCTGGCTAGCAGGGCTGCTGTGCCGATCCAGGCCCTTG	643
QY	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe	140
Db	644	GAGCTGGCACTGCTCATCTCTGGCGGTGGGCGTGTGGACTTCTGTGGCCAGGTGTGCTTC	703
QY	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160
Db	704	ACTCCACTGGAGGCGCTGCTCTGACCTCTTCGSGGACCCGCGACACCTGTGCCAGGCC	763
QY	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180
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QY	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe	200
Db	824	ATTGACTGGACACACAGTGCCTTGGCCCTTACCTACCTGGGCGACCCGAGGAGGTGCTCTTT	883
QY	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220

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Qy	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280	ORGANISM	Homo sapiens				
Db	1064	CACCAGCTGTGTCGCATGCCCCGCCACCTGCGCGGCTCTGCTGCTGAGCTGTGC	1123	REFERENCE	1 (bases 1 to 3410)				
Qy	281	SerTyrMetAlaLeuMetThrPheThrLeuPheThrLeuAspPheValGlyGluGlyLeu	300	AUTHORS	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,				
Db	1124	AGCTGATGGCACTCATGACCTTCAGCTGTGTTTACACGATTTCTGGGCGAGGGCTG	1183	REED,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,					
Qy	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly	320	STOLK,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.					
Db	1184	TACCAGGGCGTGCCAGAGCTGAGCGGGCACCAGGCCCCGAGACACTATGATGAAGC	1243	TITLE	Compositions and methods for the therapy and diagnosis of prostate				
Qy	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340	JOURNAL	Patent: WO 0151633-A 110 19-JUL-2001;				
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Qy	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla	380	ORIGIN					
Db	1364	GCTTTCCCTGTGCTGCGGTGCCACATGCTTCCACAGTGTGGCGTGTGACAGCT	1423	Alignment Scores:					
Qy	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400	Pred. No.:	0	Length:	3410		
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Qy	401	SerLeuTyrHisArgGluGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	420	Percent Similarity:	100.00%	Conservative:	0		
Db	1484	TCCCTCTACACCGGAGAGAGGTGTCTTCCGCCAAATACCGAGGGGACACTGGAGGT	1543	Best Local Similarity:	100.00%	Mismatches:	0		
Qy	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440	Query Match:	100.00%	Indels:	0		
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REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
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JOURNAL Patent: WO 0173032-A 110 04-OCT-2001;
CORIXA CORPORATION (US)
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ACCESSION AX429961
VERSION AX429961.1 GI:21541123
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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AUTHORS Reed,S.G., Xu,J., Dillon,D.C., Retter,M.W. and Harlocker,S.L.
TITLE Compositions and methods for the therapy and diagnosis of breast
cancer
JOURNAL Patent: WO 0198339-A 100 27-DEC-2001;
CORIXA CORPORATION (US)
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AUTHORS	Xu, J., Kalos, M., Stolk, J.A., Zasloff, E.J., Zhang, X., Houghton, R.L., Filho, A.M., Nolasco, M., Badaro, R. and Reed, S.G.		
TITLE	Identification and characterization of protein, a novel prostate-specific protein		
JOURNAL	Cancer Res. 61 (4), 1563-1568 (2001)		
MEDLINE	21139094		
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REFERENCE	2 (bases 1 to 3410)		
AUTHORS	Xu, J., Kalos, M., Stolk, J.A., Zasloff, E.J., Zhang, X., Houghton, R.L., Filho, A.M., Nolasco, M., Badaro, R. and Reed, S.G.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-APR-2001) Antigen Discovery, Corixa Corporation, 1124 Columbia Street, Seattle, WA 98104, USA		
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QY	41	ProLeuLeuGluGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly	60
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LOCUS Sequence 3 from Patent WO0200892.
ACCESSION AX343857
VERSION AX343857.1 GI:18491926
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REFERENCE
AUTHORS
TITLE
JOURNAL
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Db 844 GACTTCTGTGGCAGGTGTGCTTACATCCACTGGAGGCCCTGCTCTGTGACCTCTTCCCG 903
QY 153 AspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGly 172
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QY 513 IleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeu 532
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QY 553 Ala 553
Db 2104 GCG 2106

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LOCUS AX343860 1593 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 6 from Patent WO0200892.
ACCESSION AX343860
VERSION AX343860.1 GI:18491927
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS cabazon Silva,T.E. and Delisse,A.M.
TITLE Triple fusion proteins comprising ubiquitin fused between
thioredoxin and a polypeptide of interest
JOURNAL Patent: WO 0200892-A 6 03-JAN-2002;
SmithKline Beecham Biologics SA (BE)
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Db 724 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAGATTTCATGACCATGGTGTGGGCATGGT 783
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QY	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe	140
DB	964	GAGCTGGCACTGCTCATCTGGCGCTGGGCTGCTGGACTTCTGTGGCCAGGTGCTTC	1023
QY	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160
DB	1024	ACTCCACTGGAGGCCCTGCTCTGACCTTCCCGGACCCGACACACTGTCGCCAGGCC	1083
QY	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180
DB	1084	TACTCTGTATGCCCTTCATGATCAGCTTGGGGCTGCTGGCTACCTCCTGCTGCC	1143
QY	181	IleAspTyrPAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe	200
DB	1144	ATTGACTGGGACACCACTGCTGGCCCTTACCTGGGCACCCAGGAGGTGCTCTTT	1203
QY	201	GlyLeuLeuThrIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
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QY	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280
DB	1384	CACCAGCTGTGCTGGCGATCCCGCACCCCTGGCGCGGCTTCTGGTGGCTGAGCTGTGC	1443
QY	281	SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu	300
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LOCUS	Sequence 625 from Patent WO0151633.		
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ACCESSION	AX200995		
VERSION	AX200995.1 GI:15390822		
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REFERENCE	1 (bases 1 to 4034)		
AUTHORS	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Red,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer		
JOURNAL	Patent: WO 0151633-A 625 19-JUL-2001;		
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DB	401	CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAAGTTTCATGACCATGCTGCTGGCATTTG	460
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DB	521	CGCTATGGCGCGCGCGGCTTTCATCTGGGCATCTCCTTGGGCATCCTGTGAGCCTC	580
QY	101	PheLeuIleProArgAlaGlyTirProLeuAlaGlyLeuLeuCysProAspProArgProLeu	120
DB	581	TTTCTCATCCCAAGGCGGCTGGCTAGCAGGGCTGCTGTGCCGATCCAGGCCCTG	640
QY	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe	140
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QY	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160
DB	701	ACTCCACTGGAGGCTGCTCTGACCTTCTCCGGGACCCGACCTGTGCCAGGCC	760
QY	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180
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LOCUS AX267730 4034 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 704 from Patent WO0173032.
ACCESSION AX267730
VERSION AX267730.1 GI:16516402
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedwick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 704 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES
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Score: 320.00 Matches: 320
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DB 461 CCAGTGTGGGCTGGTGTGTGTCGCGCTCCTAGGCTCAGCCAGTCAACCACTGGCGTGA 520
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QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
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QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
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LOCUS AX201078
DEFINITION Sequence 708 from Patent WO0151633.
ACCESSION AX201078
VERSION AX201078.1 GI:15390883
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1203)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 708 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
1 .1203
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 175 a 415 c 368 g 245 t
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Pred. No.: 1.82e-271 Length: 1203
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
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Db	592	ATCCTGTGTAGCCTCTTTCTCATCCAAAGGCGCGCTGGCTAGCAGGCTGCTGTGCCCG	651
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Db	652	GATCCAGGCGCCCTGGAGCTGGCACTGTCTCATCTCTGGCGTGGGCTGCTGGACTTCTGT	711
Qy	136	GlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAsp	155
Db	712	GGCCAGGTGTGCTTCACTCCACTGGAGCCCTGCTCTGTGACCTTCCCGGAGCCCGGAC	771
Qy	156	HisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGly	175
Db	772	CACGTGCGCCAGGCTACTCTGTCTATGCTTCATGATCAGTCTTGGGGGCTGCCTGGGC	831
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DEFINITION	Sequence 851 from Patent WO0173032.		
ACCESSION	AX267877		
VERSION	AX267877.1	GI:16516515	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedick,R.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T. and Henderson,R.A.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer.		
JOURNAL	Patent: WO 0173032-A 851 04-OCT-2001;		
FEATURES	CORIXA CORPORATION (US)		
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SOURCE human.
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4894)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W.,
Stolk, J.A., Skeiky, Y.A., Wang, A., and Meagher, M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 623 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 928 a 1448 c 1354 g 1163 t 1 others
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Alignment Scores:
Pred. No.: 6,55e-271 Length: 4894
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 6 Gaps: 0
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QY 318 AspGluGly 320
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RESULT 15
AX267728
LOCUS AX267728 4894 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 702 from Patent WO0173032.
ACCESSION AX267728
VERSION AX267728.1 GI:16516400
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T.
and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 702 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
1..4894
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 928 a 1448 c 1354 g 1163 t 1 others
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Pred. No.: 6,55e-271 Length: 4894
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
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AX200996 Sequence 626 from Patent WO0151633. linear PAT 29-AUG-2001
LOCUS AX200996
DEFINITION AX200996
ACCESSION AX200996
VERSION AX200996.1 GI:15390823
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 6976)
Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W.,
Stolk, J.A., Skeiky, Y.A., Wang, A. and Weagher, M.J.
Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 626 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source Location/Qualifiers
BASE COUNT 1312 a 1996 c 1961 g 1706 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 9,05e-271 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 47.56% Indels: 0
DB: 6 Gaps: 0

US-09-593-793A-113 (1-553) x AX200996 (1-6976)
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RESULT 17
AX267731
LOCUS AX267731
DEFINITION Sequence 705 from Patent WO0173032. linear PAT 26-OCT-2001
ACCESSION AX267731
VERSION AX267731.1 GI:16516403
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T.
and Henderson, R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer.
JOURNAL Patent: WO 0173032-A 705 04-OCT-2001;
CORIXA CORPORATION (US)
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source Location/Qualifiers
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Pred. No.: 9,05e-271 Length: 6976
Score: 263.00 Matches: 263
Percent Similarity: 100.00% Conservativeness: 0
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DB 1922 GAGGGGCTGTACAGGGCTGCCAGAGCTGAGCGGGGACCCAGGCGCCGGAGACTAT 1981
QY 318 AspGluGly 320
DB 1982 GATGAGGT 1990
RESULT 18
AC096533

LOCUS AC096533 157988 bp DNA linear HTG 18-SEP-2001
DEFINITION Homo sapiens chromosome 1 clone RP11-6B6, WORKING DRAFT SEQUENCE, 7
unordered pieces.
ACCESSION AC096533 AL365261
VERSION AC096533.1 GI:15638681
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 157988)
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 157988)
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
COMMENT On Sep 18, 2001 this sequence version replaced gi:9931838.

Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwghtgs@u.washington.edu
Drafting Center: SC

Project Information
Center project name: chr-1
Center clone name: RP11-6B6 (sc0601)

Summary Statistics
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET; 57% of reads
Chemistry: Dye-terminator Big Dye; 43% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 154688 bases at least Q40
Consensus quality: 156347 bases at least Q30
Consensus quality: 157058 bases at least Q20
Insert size: 157388; sum-of-contigs
Quality coverage: 7.3x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 6264: contig of 6264 bp in length
* 6265 6364: gap of unknown length
* 6365 15785: contig of 9421 bp in length
* 15786 15885: gap of unknown length
* 15886 27947: contig of 12062 bp in length
* 27948 28047: gap of unknown length
* 28048 51992: contig of 23945 bp in length
* 51993 52092: gap of unknown length
* 52093 81154: contig of 29062 bp in length
* 81155 81254: gap of unknown length
* 81253 118813: contig of 37559 bp in length
* 118814 118913: gap of unknown length
* 118914 157988: contig of 39075 bp in length.
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Qy MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
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Qy PheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAlaSer 381
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RESULT 21
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DEFINITION AL832933
ACCESSION AL832933.1 GI:21733520
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2477)
AUTHORS Ansong, W., Winkler, U., Mewes, H.W., Weil, B. and Wiemann, S.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKF2p666D0110) is available at the R2PD in Berlin.
Please contact the R2PD: Ressourcenzentrum, Heubnerweg 6, 14059
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Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
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DEFINITION Sequence 624 from Patent WO0151633.
ACCESSION AX200994
VERSION AX200994.1 GI:15390821
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 2904)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 624 19-JUL-2001;
CORIXA CORPORATION (US)
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BASE COUNT 542 a 875 c 773 g 714 t
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Query Match: 42.50% Indels: 0
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AX267729 2904 bp DNA linear PAT 26-OCT-2001
LOCUS AX267729
DEFINITION Sequence 703 from Patent WO0173032.
ACCESSION AX267729
VERSION AX267729.1 GI:16516401
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 703 04-OCT-2001;
CORIXA CORPORATION (US)
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Pred. No.: 4.17e-241 Length: 2904
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Db 1470 ACACAGGTAGTATTGACAAGAGCGACTTGGCCAAATACTCAGCG 1514
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ACCESSION			
VERSION AB060851.1 GI:13874496			
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;			
Cercopithecinae; Macaca.			
REFERENCE			
AUTHORS Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M.,			
Terao K., Suzuki Y., Sugano,S. and Hashimoto,K.			
TITLE Isolation of full-length cDNA clones from macaque brain cDNA			
libraries			
JOURNAL Unpublished			
REFERENCE 2 (bases 1 to 3514)			
AUTHORS Hashimoto.K., Osada.N., Hida.M., Kusuda,J. and Sugano,S.			
TITLE Direct Submission			
JOURNAL Submitted (27-Apr-2001) Katsuyuki Hashimoto, National Institute of			
Infectious Diseases, Division of Genetic Resources; 23-1, Toyama			
1-chome, Shinjuku-ku, Tokyo 162-8640, Japan			
(E-mail:khashien@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/,			
Tel:-81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)			
COMMENT			
Lab host: TOP10			
Vector: pME18S-FL3 (Acc.No. AB009864)			
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R. Site2: DraIII (CACCATGTG)			
Description: 1st strand cDNA was primed with an oligo(dT) primer			
[ATGTGGCTTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized			
using specific 5' and 3' primers and amplified by PCR. The PCR			
product was digested with SfiI and size selection was performed to			
exclude fragments <1.5kb. The SfiI-digested PCR product was cloned			
into distinct DraIII sites of pME18S-FL3. XhoI sites just outside			
the DraIII sites can be used to isolate the cDNA insert. Libraries			
were constructed by oligo-capping method			
(Sugano et al., , Institute of Medical Science, University of			
Tokyo).			
Custom primer used for sequencing			
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3' end primer [CGACCTGCAGCTCGACACA] }.			
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QY	260	euHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuC	280
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QY	280	ysSerTrpMetAlaLeuMetThrPheThrLeuPheThrThrAspPheValGlyGluGlyL	300
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QY	300	euTyrGlnGlyValProArgAlaGluPro-GlyThrGluAlaArgArgHisTrpAspGlu	319
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QY	320	GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSer	339
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QY	340	LeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValIleLeuAlaSerVal	359
Db	1471	CTGCTCATGACCGGCTGTGTGACGATTCGGCACTCGAGCACTATCTGGCCAGTGTG	1530
QY	360	AlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThr	379
Db	1531	GCAGCTTTCCTGTGGCTGGCGGTGGCAGTGCCTGTCCACAGTGTGGTGTGGAGC	1590
QY	380	AlaSerAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeu	399
Db	1591	GCCTCACCGCCCTCACTGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACATG	1650
QY	400	AlaSerLeuTyrHisArgGluLys-GlnValPheLeuProTyrTyrArgGlyAspThr-G	419
Db	1651	GCCTCCCTCTACCAACCGGGAGAG-GCAGGTGTCTCTGCCCAATACCGAGGGAGCGC-TG	1708
QY	419	lyGlyAla-SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly	438
Db	1709	GAGGCAC-TAGCAGTGGAGCAGCCGTGATGCTCTCCGAGGCGCTTAAAGCTTGA	1767
QY	439	AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProPro	458
Db	1768	GCTCCCTTCCCTAATGCACAGCTGGGTGTGGAGGAGTGGCTCTCCACCTCCACCC	1827
QY	459	AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr	478
Db	1828	CGCTCTGCGGGGCTCTGCTCGCATGTCTCTGATGCTGTGTGTGTGTGTGTGTGTGT	1887
QY	479	GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla	498
Db	1888	GAGGCCAGGTGTGTCCGGCGCGGCGCATCTCCCTGGACCTCGCCATCTCGGATGTCC	1947
QY	499	PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln	518
Db	1948	TTCTGCTGTCCAGGTGGCGGCTGCTGTTCATGGGCTTCCATGCTCAGCTCAGCCAG	2007
QY	519	SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla	538
Db	2008	TCGTCTCACTACCTATATGTGTCTGTCGAGCGCTGGGTGTGTGTGTGTGTGTGTGTGT	2067
QY	539	ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSer	552
Db	2068	ACACAGGTAGTATTGACAGAGCGCACTTGGCCAAATACG	2109
RESULT	25		
LOCUS	AB062977	2917 bp	linear
DEFINITION	Macaca fascicularis brain cDNA clone:QmoA-10594, full insert		

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US-09-593-793A-113 (1-553) x AB062977 (1-2917)			
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Db	69	GTCCCACTCTAGGCTACGCCAGTACCACTGGCGGGACCGTATGGCCGGCGGGCC	128
Qy	88	PheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGly	107
Db	129	TTCACTGGGCGCTGCTTGGGCACTCTGCTGAGCCTCTTTCTCATCCCAAGGCGTGC	188
Qy	108	TrpLeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeuIleLeu	127
Db	189	TGGCTGGCAGGCGTGTGTGGCCGATCCAGGCCCTGGAGCTGGCACTGCTCATCTG	248
Qy	128	GlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeu	147
Db	249	GGCGTGGGCTGCTGGACTTCTGTGGCCAGGTGTCTTCACTCCACTGGAGGCCCTGCTC	308
Qy	148	SerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyrAla-PheMe	167
Db	309	TCTGACCTGTTCCGGGACCCGACCACTGTCCGAGGCCACTCCGTCTATAC-CTTCAT	367
Qy	167	tileSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAl	187
Db	368	GATCACTCTTGGGGCTGCTGGGCTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTG	427
Qy	187	aleuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePh	207
Db	428	CCTGGCCCCCTACCTGGGACCCAGGAGGTGCTCTTTGGCCCTGCTCACCTCATCTT	487
Qy	207	eLeuThrCysValAlaAlaThrLeuLeuValAlaGluAlaAlaLeuGly-ProThrG	227
Db	488	CCTCACTCGGTAGCAGCCACACTGCTGGTGCCGAGGAGGAGCACTGGGCCCCGCC-G	546
Qy	227	luProAlaGlyLeuSerAlaProSerLeuSerPro--HisCysCysProCysArg-A	246
Db	547	AGCCAGCGGAAGGGTGTGTGCCCCCTCCCTGCC-GT-CCCACCTGCTGCTGCTG-GG	603
Qy	246	laArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysA	266
Db	604	CCCGCTGGCTTTCGGGAACCTTGGCGGCCCTGCTTCCCGGCTGACCAGCTGTGCTGCC	663
Qy	266	rgMetProArgThrLeuArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuM	286
Db	664	GCATGCCCGCCACCTGCGCCGGCTCTCGTGCGTGAGCTGTGAGTGGGCACTCA	723
Qy	286	etThrPheThrLeuPheTyrThrAspPheValGlyGlyLeuTyrGlnGlyValProA	306
Db	724	TGACCTTCACGCTGTTTACACGGATTCGTGGCGAGGGGCTATACCAGGCGGTGCCA	783
Qy	306	rgAlaGluPro-GlyThrGluAlaArgArgHisTyrAspGluGlyValArgMetGlySer	325
Db	784	GAGCTGAGCT-GGGACCGAGCGCCGGAGACACTATGATGAAGGCGTTCGGATGGCAGT	842
Qy	326	LeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMet-AspArgLe	345
Db	843	CTGGGGCTGTCTCTGAGTGCCCATCTCCCTGGGTCTTCTCTCTGCTGT-GGACCGGCT	901
Qy	345	uValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAl	365
Db	902	GGTGACCGATTCGGCACTCGAGCACTATCTGCGCAGTGTGGCAGCTTTCCTGTGGC	961
Qy	365	alaGlyAlaThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuTh	385
Db	962	TGCCGGTCCAGTGCCTGCCAGTGTGGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG	1021
Qy	385	rcGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisAr	405
Db	1022	TGGGTTCACCTTCTCAGCCCTCAGATCTGCCCCCTACACACTGGGCTCCCTCTACACCG	1081
Qy	405	gGluIys-GlnValPheLeuProLysTyrArgGlyAspThr-GlyGlyAla-SerSerG	424

Db	1082	GGAGAG - GCAGGTGTCTCTGCCCAATACCGAGGGACGC - TGGAGGCAC - TAGCAGTGA	1138
Qy	424	uASerSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnG	444
Db	1139	GGACAGCTGATGACAGCTTCTCTGCCAGGCCCTTAAAGCTGGAGCTCCCTTCCCTAATGG	1198
Qy	444	yHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlase	464
Db	1199	ACAGTGGGTGCTGGAGGACGTGGCTTGCTTCCGCTCCACCCGCGCTCTCGGGGCGTC	1258
Qy	464	rAlaCysaspValSerValArgValValValGlyGluProThrGluAlaArgValValPr	484
Db	1259	TGCCTGCGATGTCTGTACGTGTGGTGGTGAGCCACCGAGGCGAGGTGGTTCC	1318
Qy	484	oGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnVa	504
Db	1319	GGCGCGGGGCACTGCTGCGGACCTCGCCATCTGGATAGTGCCTTCTGCTGCCAGGT	1378
Qy	504	lAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMe	524
Db	1379	GGCCCGTCCCTGTTTCATGGGCTCCATCGTCCAGCTCAGCCAGTCTGTCTACGTATAT	1438
Qy	524	tValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAs	544
Db	1439	GGTGTCTGCTCGAGGCTGGGTCTGGTTGCCATTTACTTTGCTACACAGGTAGTATTGA	1498
Qy	544	pLysSerAspLeuAlaLysTyrSer	552
Db	1499	CAAGAGCGACTTGGCCAAATACTCG	1523
RESULT 26			
LOCUS	AX106229	789 bp	DNA linear PAT 30-APR-2001
DEFINITION	Sequence 10 from Patent WO0125272.		
ACCESSION	AX106229		
VERSION	AX106229.1 GI:13921915		
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Xu, J., Skeiky, Y.A., Reed, S.G. and Cheever, M.A.		
TITLE	Compositions and methods for therapy and diagnosis of prostate cancer		
JOURNAL	Patent: WO 0125272-A 10 12-APR-2001;		
FEATURES	CORIXA CORPORATION (US)		
source	1. 789		
misc_feature	/organism="Homo sapiens" /db_xref="taxon:9606"		
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ORIGIN	14 others		
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Score:	122.00		
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US-09-593-793A-113 (1-553) x AX106229 (1-789)			
Qy	357	AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla	376
Db	12	GCAGTGGGAGCTTTCCCTGTGGCTGGGTGGAGTCCATGCTCTCCACAGTGTGCC	71
Qy	377	ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro	396

Db 72 GTGGTACAGCTTCACGCCGCCCTCACCGGGTTACACCTTCTCAGCCCTGCAGATCTCGCCC 131
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QY 417 AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
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Db 192 GACACTGGAGGTCTAGCAGTGAAGACAGCTCATCACCAGCTTCTCGCAGGCCCTAAG 251
QY 437 ProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPro 456
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Db 252 CTTGGAGCTCCCTTCCCTAATGACACCGTGGGTGGAGGAGTGGCTGTCTCCACCT 311
QY 457 ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGlu 476
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Db 312 CCACCCGCGCTCGCGGGCCCTCTGCCTGTGTATGTCTCCGTAGCTGTGGTGGGTGAG 371
QY 477 ProThr 478
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Db 372 CCCACC 377
RESULT 27
AX140520
LOCUS AX140520 789 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 10 from Patent WO0134802.
ACCESSION AX140520
VERSION AX140520.1 GI:14280638
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 789)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Skeiky,Y.A., and Wang,A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0134802-A 10 17-MAY-2001;
CORIXA CORPORATION (US)
FEATURES
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Percent Similarity: 100.00% Conservative: 0
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QY 397 TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly 416
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QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396
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Db 372 CCCACC 377
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AX200380
LOCUS AX200380 789 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 10 from Patent WO0151633.
ACCESSION AX200380
VERSION AX200380.1 GI:15390176
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 789)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 10 19-JUL-2001;
CORIXA CORPORATION (US)
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QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396
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ACCESSION ARL12280					
VERSION ARL12280.1 GI:14092180					
KEYWORDS					
SOURCE Unknown.					
ORGANISM Unknown.					
REFERENCE 1 (bases 1 to 258)					
AUTHORS Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Roberts-Rapp,L., Russell,J.C., Stroupe,S.D. and Yu,H.					
TITLE Reagents and methods useful for detecting diseases of the prostate					
JOURNAL Patent: US 6130043-A 10-OCT-2000;					
FEATURES Location/Qualifiers					
source 1..258					
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ACCESSION ARL12283					
VERSION ARL12283.1 GI:14092183					
KEYWORDS					
SOURCE Unknown.					
ORGANISM Unknown.					
REFERENCE 1 (bases 1 to 247)					
AUTHORS Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Roberts-Rapp,L., Russell,J.C., Stroupe,S.D. and Yu,H.					
TITLE Reagents and methods useful for detecting diseases of the prostate					
JOURNAL Patent: US 6130043-A 10-OCT-2000;					
FEATURES Location/Qualifiers					
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/dev_stage="adult"
BASE COUNT      97 a 128 c 115 g 66 t
ORIGIN

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QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
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RESULT 35
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LOCUS      Rattus norvegicus clone CH230-65F14, *** SEQUENCING IN PROGRESS
DEFINITION      Rattus norvegicus clone CH230-65F14, *** SEQUENCING IN PROGRESS
ACCESSION      AC126523
VERSION        AC126523.1 GI:21700488
KEYWORDS       HTG; HTGS_PHASE1.
SOURCE         Norway rat.
ORGANISM       Rattus norvegicus
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               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
               Rattus.
REFERENCE      1 (bases 1 to 198037)
AUTHORS       Munzy,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
               Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayale,M., Banks,T.,
               Barbara,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
               Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
               Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
               Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
               Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
               Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
               Davila,M.C., Davis,C., Davy-Carroll,L., Dederich,D.A.,
               Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
               Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
               Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
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               Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
               Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
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               Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
               Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
               Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,

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TITLE
JOURNAL
REFERENCE      2 (bases 1 to 198037)
AUTHORS       Worley,K.C.
TITLE         Direct Submission
JOURNAL       Submitted (06-JUL-2002) Human Genome Sequencing Center, Department
               of Molecular and Human Genetics, Baylor College of Medicine, One
               Baylor Plaza, Houston, TX 77030, USA
REFERENCE      3 (bases 1 to 198037)
AUTHORS       Worley,K.C.
TITLE         Direct Submission
JOURNAL       Submitted (14-JUL-2002) Human Genome Sequencing Center, Department
               of Molecular and Human Genetics, Baylor College of Medicine, One
               Baylor Plaza, Houston, TX 77030, USA
COMMENT       ----- Genome Center
               Center: Baylor College of Medicine
               Center code: BCM
               Web site: http://www.hgsc.bcm.tmc.edu/
               Contact: hgsc-help@bcm.tmc.edu
               ----- Project Information
               Center project name: GRBQ
               Center clone name: CH230-65F14
               ----- Summary Statistics
               Sequencing vector: Plasmid;
               Chemistry: Dye-terminator Big Dye; 100% of reads
               Assembly program: Phrap; version 0.990329
               Consensus quality: 149884 bases at least Q40
               Consensus quality: 159599 bases at least Q30
               Consensus quality: 166549 bases at least Q20
               -----
               * NOTE: Estimated insert size may differ from sequence length
               * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
               * NOTE: This is a 'working draft' sequence. It currently
               * consists of 65 contigs. The true order of the pieces
               * is not known and their order in this sequence record is
               * arbitrary. Gaps between the contigs are represented as
               * runs of N, but the exact sizes of the gaps are unknown.
               * This record will be updated with the finished sequence
               * as soon as it is available and the accession number will
               * be preserved.
               *
               * 1063: contig of 1063 bp in length
               * 1163: gap of unknown length
               * 1164
               * 2326: contig of 1162 bp in length
               * 2426
               * 3556: gap of unknown length
               * 3557
               * 3656: gap of unknown length
               * 3657
               * 4752: contig of 1096 bp in length
               * 4753
               * 4852: gap of unknown length
               * 4853
               * 5972: contig of 1120 bp in length
               * 5973
               * 6072: gap of unknown length
               * 7818: contig of 1746 bp in length
               * 7819
               * 7918: gap of unknown length
               * 7919
               * 9266: contig of 1348 bp in length

```

```
* 9267 9366: gap of unknown length
* 9367 10614: contig of 1248 bp in length
* 10615 10714: gap of unknown length
* 10715 11914: contig of 1200 bp in length
* 11915 12014: gap of unknown length
* 12015 14075: contig of 2061 bp in length
* 14076 14175: gap of unknown length
* 14176 15601: contig of 1426 bp in length
* 15602 15701: gap of unknown length
* 15702 17277: contig of 1576 bp in length
* 17278 17377: gap of unknown length
* 17378 18557: contig of 1280 bp in length
* 18558 18757: gap of unknown length
* 18758 20392: contig of 1635 bp in length
* 20393 20492: gap of unknown length
* 20493 21641: contig of 1149 bp in length
* 21642 21741: gap of unknown length
* 21742 23412: contig of 1671 bp in length
* 23413 23512: gap of unknown length
* 23513 25087: contig of 1575 bp in length
* 25088 25187: gap of unknown length
* 25188 26859: contig of 1672 bp in length
* 26860 26959: gap of unknown length
* 26960 28698: contig of 1739 bp in length
* 28699 28798: gap of unknown length
* 28799 30716: contig of 1918 bp in length
* 30717 30816: gap of unknown length
* 30817 32509: contig of 1693 bp in length
* 32510 32609: gap of unknown length
* 32610 34220: contig of 1611 bp in length
* 34221 34320: gap of unknown length
* 34321 35560: contig of 1240 bp in length
* 35561 35660: gap of unknown length
* 35661 37768: contig of 2108 bp in length
* 37769 37868: gap of unknown length
* 37869 39562: contig of 1694 bp in length
* 39563 39662: gap of unknown length
* 39663 41676: contig of 2014 bp in length
* 41677 41776: gap of unknown length
* 41777 43658: contig of 1882 bp in length
* 43659 43758: gap of unknown length
* 43759 45824: contig of 1866 bp in length
* 45825 45724: gap of unknown length
* 45725 48100: contig of 2376 bp in length
* 48101 48200: gap of unknown length
* 48201 50489: contig of 2289 bp in length
* 50490 50589: gap of unknown length
* 50590 52329: contig of 1740 bp in length
* 52330 52429: gap of unknown length
* 52430 54544: contig of 2115 bp in length
* 54545 54644: gap of unknown length
* 54645 56752: contig of 2108 bp in length
* 56753 56852: gap of unknown length
* 56853 58639: contig of 1787 bp in length
* 58640 58739: gap of unknown length
* 58740 60931: contig of 2192 bp in length
* 60932 61031: gap of unknown length
* 61032 63481: contig of 2450 bp in length
* 63482 63581: gap of unknown length
* 63582 66000: contig of 2419 bp in length
* 66001 66100: gap of unknown length
* 66101 68760: contig of 2660 bp in length
* 68761 68860: gap of unknown length
* 68861 71024: contig of 2164 bp in length
* 71025 71124: gap of unknown length
* 71125 73169: contig of 2045 bp in length
* 73170 73269: gap of unknown length
* 73270 76108: contig of 2839 bp in length
* 76109 76208: gap of unknown length
* 76209 79687: contig of 3479 bp in length
* 79688 79787: gap of unknown length
* 79788 82504: contig of 2717 bp in length
* 82505 82604: gap of unknown length

* 82605 86873: contig of 4269 bp in length
* 86874 86973: gap of unknown length
* 86974 91613: contig of 4640 bp in length
* 91614 91713: gap of unknown length
* 91714 94992: contig of 3279 bp in length
* 94993 95092: gap of unknown length
* 95093 97134: contig of 2042 bp in length
* 97135 97234: gap of unknown length
* 97235 100423: contig of 3189 bp in length
* 100424 100523: gap of unknown length
* 100524 104682: contig of 4159 bp in length
* 104683 104782: gap of unknown length
* 104783 108313: contig of 3531 bp in length
* 108314 108413: gap of unknown length
* 108414 113868: contig of 5455 bp in length
* 113869 113968: gap of unknown length
* 113969 117889: contig of 3821 bp in length
* 117790 117889: gap of unknown length
* 117890 120979: contig of 3090 bp in length
* 120980 121079: gap of unknown length
* 121080 123743: contig of 2664 bp in length
* 123744 123843: gap of unknown length

Alignment Scores:
Pred. No.: 4,36e-55 Length: 198037
Score: 63.00 Matches: 90
Percent Similarity: 97.83% Conservative: 0
Best Local Similarity: 97.83% Mismatches: 1
Query Match: 11.39% Indels: 2
DB: 2 Gaps: 0
US-09-593-793a-113 (1-553) x AC126523 (1-198037)

Qy 118 ArgProLeuGluLeuAlaLeuLeuLeuLeuValGlyLeuLeuAspPheCysGlyGln 137
Db 161757 AGGCCCTCGAGTTGGCTGCTCATCTTGGAGTGGGCTCTGGACTTTTGGCGCCAG 161816
Qy 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
Db 161817 GTGTCTTTTACTCCACTGGAGGCCTTACTCTCGACCTTCCGGGACCCAGACCACTGC 161876
Qy 158 ArgGlnAlaTyr-SerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrIle 177
Db 161877 CCCCAGGCTT-CTCTGTCTATGCTTTCATGATCATGACCTCGGGGGCTGCTGGGTACCT 161935
Qy 177 uLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluG1 197
Db 161936 CTTACTGCAATGACTGGGACCAACCGCCCTTGGCCCCCTTACCTAGGCACCTCAGGAAGA 161995
Qy 197 uCysLeuPheGlyLeuLeuThrLeuIlePheLeu 208
Db 161996 ATGCCCTCTTCGGCCCTCCCTCACCCCTCATTTTCTC 162029

RESULT 36
BC034084
LOCUS BC034084 2611 bp mRNA linear ROD 07-AUG-2002
DEFINITION Mus musculus, clone IMAGE:4457452, mRNA, partial cds.
ACCESSION BC034084
VERSION BC034084.1 GI:21707615
KEYWORDS
SOURCE
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Strausberg, R.
Direct Submission
Submitted (02-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
REMARK
COMMENT
Contact: MGC help desk
```

Email: cgapbs-re@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 43 Row: p Column: 14
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES

Location/Qualifiers

1..2611

/organism="Mus musculus"

/db_xref="taxon:10090"

/map="FVB/N"

/clone="IMAGE:4457452"

/tissue_type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy."

/clone_lib="NCI_CGAP_Mam1"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

<1..1353

/codon_start=1

/product="Unknown (protein for IMAGE:4457452)"

/protein_id="AAH34084.1"

/db_xref="GI:21707616"

/db_xref="LocusID:212980"

/translation="PRAGWLAGLIPDRPLELALLLGVGLDFGCGVCTPPEALL
 SDFRDPHCQATSVAFMISLGCGLGLLPALDWDTSVLAPYLGTEECFLGLTL
 IFLCMAATLVETAVLGPPEAGLLVSASVSRCCPCVHGLAFNLGTLFRLQQL
 CCRMPTRLRFLVAFELCSWMALMTFTLYTDFVGEGLYQGVPAEPGTEARRHYDEGI
 RMGSLGLFLOCAISLVFLSMDRLVOKFTRSVYASVMTFPVAAATCLSHSVVVT
 ASAAITGTFESALOTLPYTLASLYHREKQVLPKYRGDAGSGGSDSTTFLPGPKP
 GALPENGHVSGSGILAPPALCGASCNDVSMRVVVGPEPEARVWTGRCICLDLAIL
 DSATLLSVAFLFMGSLVQSHSVTAYMWSAAGLGLVLIYFATQVVFVDKNDLAKYSV
 "

CDS

BASE COUNT 519 a 728 c 691 g 673 t

Alignment Scores:

Pred. No.: 1.63e-52 Length: 2611
 Score: 59.00 Matches: 59
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 10.67% Indels: 0
 DB: 10 Gaps: 0

US-09-593-793a-113 (1-553) x BC034084 (1-2611)

QY 262 GlnLeuCyssArgMetProArgThrLeuArgArgLeuPheValAlaGlnLeuCyssSer 281

Db 475 CAGCTGTGTCGGCGGACCTCGACCCCTACCCGACCTCTTGTGGTGAGCTGTGCAGC 534

QY 282 TrpMetAlaLeuMetPheThrLeuPheThrAspPheValGlyGlyLeuTyr 301

Db 535 TGGATGGCACTTATGACTTTCACACTGTTCTACACGGACTTCGTGGGAGGGGCTGTAC 594

QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320

Db 595 CAGGTGTACCCAGAGCGGACCGAGCCAGCGGCGGACGACACATGATGAGGC 651

RESULT 37

LOCUS

BC031381 3354 bp mRNA linear ROD 07-AUG-2002
 DEFINITION Mus musculus, clone MGC:32471 IMAGE:5050610, mRNA, complete cds.
 ACCESSION BC031381

BC031381.1 GI:21594808

KEYWORDS

SOURCE mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 3354)
 AUTHORS Strausberg,R.
 TITLE Direct Submission

JOURNAL

Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT

Contact: MGC help desk

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,

Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,

Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 45 Row: 1 Column: 2
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES

Location/Qualifiers

1..3354

/organism="Mus musculus"

/db_xref="taxon:10090"

/map="FVB/N"

/clone="MGC:32471 IMAGE:5050610"

/tissue_type="Liver, normal. 5 month old male mouse."

/clone_lib="NCI_CGAP_L19"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

443..2104

/codon_start=1

/product="Unknown (protein for MGC:32471)"

/protein_id="AAH31381.1"

/db_xref="GI:21594809"

/db_xref="LocusID:212980"

/translation="MIQRLNASRLRHRKQALLLVLLTFTCLEVLAAGITYVPPLLL
 EVGVEKFTMWIGIGPVGLVSVPLGCSADQWRGRRPPIWALSGLVLSLFL
 IPRAGWLAGLIPDRPLELALLLGVGLDFGCGVCTPPEALLSDFRDPHCQQA
 FSVYAFMISLGCGLGLLPALDWDTSVLAPYLGTEECFLGLTLFRLQQL
 EAVLGPPEAGLLVSASVSRCCPCVHGLAFNLGTLFRLQQLCCRMPTRLRFLV
 AELCSWMALMTFTLYTDFVGEGLYQGVPAEPGTEARRHYDEGIRMGSLGLFLOCAI
 SLVFLSMDRLVOKFTRSVYASVMTFPVAAATCLSHSVVVTASAATLGTTFFSAL
 QILPYTLASLYHREKQVLPKYRGDAGSGGSDSTTFLPGPKGALFPNGHVSGS
 SGILAPPALCGASCDVSMRVVVGPEPEARVWTGRCICLDLAILSDATLLSVAFLS
 FMGSLVQSHSVTAYMWSAAGLGLVLIYFATQVVFVDKNDLAKYSV"

BASE COUNT 662 a 922 c 934 g 836 t

ORIGIN

Alignment Scores:
 Pred. No.: 2.05e-52 Length: 3354
 Score: 59.00 Matches: 59
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 10.67% Indels: 0
 DB: 10 Gaps: 0

US-09-593-793a-113 (1-553) x BC031381 (1-3354)

OY 8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeuValAsnLeuLeuThrPheGly 27
|||||
Db 464 AGCGCTGCTAGCGACCGAAAGCTCAGCTCTGCTGGTCAACCTGCTTCACCTTTGGC 523
OY 28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProProLeuLeuLeuGluValGly 47
|||||
Db 524 CTGAGGTGCTGCTGCTGCGCGATTACCTATGTGCCACCCCTCTGCTGGGAAGTCGGG 593
OY 48 ValClnGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66
|||||
Db 584 GTGAGGAGAAATTCATGACCATGTGGTGGGATGGCCCATGCTAGCCCTGGTT 640

RESULT 38
AC107837/c
LOCUS
DEFINITION Mus musculus clone RP23-272H13, WORKING DRAFT SEQUENCE, 13 ordered
pieces
AC107837
VERSION AC107837.2 GI:20148020
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 178567)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,A., Allen,N.,
TITLE Mammals: A Genome
JOURNAL Science
REFERENCE 2 (bases 1 to 178567)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,A., Allen,N.,
TITLE Mammals: A Genome
JOURNAL Science

TITLE
JOURNAL
AUTHORS

TITLE
JOURNAL
AUTHORS

Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (14-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 14, 2002 this sequence version replaced gi:18308540.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L20597
Center clone name: 272_H13
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 175041 bases at least Q40
Consensus quality: 176485 bases at least Q30
Consensus quality: 177028 bases at least Q20
Insert size: 182000; agarose-fp
Insert size: 177367; sum-of-contigs
Quality coverage: 7.7 in Q20 bases; agarose-fp
Quality coverage: 7.9 in Q20 bases; sum-of-contigs

----- This is a 'working draft' sequence. It currently
* consists of 13 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 58509: contig of 58509 bp in length
* 58510 58609: gap of 100 bp
* 58610 59459: contig of 850 bp in length
* 59460 59559: gap of 100 bp
* 59560 60623: contig of 1064 bp in length
* 60624 60723: gap of 100 bp
* 60724 62950: contig of 2227 bp in length
* 62951 63050: gap of 100 bp
* 63051 65309: contig of 2259 bp in length
* 65310 65409: gap of 100 bp
* 65410 67839: contig of 2430 bp in length
* 67840 67939: gap of 100 bp
* 67940 69956: contig of 2017 bp in length
* 69957 70056: gap of 100 bp
* 70057 73550: contig of 3494 bp in length
* 73551 73650: gap of 100 bp
* 73651 81298: contig of 7648 bp in length
* 81299 81398: gap of 100 bp
* 81399 91238: contig of 9840 bp in length
* 91239 91338: gap of 100 bp
* 91339 127752: contig of 36414 bp in length
* 127753 127852: gap of 100 bp
* 127853 177486: contig of 49634 bp in length
* 177487 177586: gap of 100 bp
* 177587 178567: contig of 981 bp in length.

Location/Qualifiers
1..178567
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-272H13"
/clone_lib="RPCI-23 Female Mouse BAC"
misc_feature 1..58509
/note="assembly_fragment"

clone_end:SP6
vector_side:left"
misc_feature 58610..59459
/note="assembly_fragment"
misc_feature 59560..60623
/note="assembly_fragment"
misc_feature 60724..62950
/note="assembly_fragment"
misc_feature 63051..65309
/note="assembly_fragment"
misc_feature 65410..67839
/note="assembly_fragment"
misc_feature 67940..69956
/note="assembly_fragment"
misc_feature 70057..73550
/note="assembly_fragment"
misc_feature 73651..81298
/note="assembly_fragment"
misc_feature 81399..91238
/note="assembly_fragment"
misc_feature 91339..127752
/note="assembly_fragment"
misc_feature 127853..177486
/note="assembly_fragment"
misc_feature 177587..178567
/note="assembly_fragment"
clone_end:T7
vector_side:right"
BASE COUNT 47757 a 40927 c 41360 g 47318 t 1205 others
ORIGIN

Alignment Scores:
Pred. No.: 7.69e-51 Length: 178567
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.67% Indels: 0
DB: 2 Gaps: 0

US-09-593-793A-113 (1-553) x AC107837 (1-178567)

Qy 262 GlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAlaGluLeuCysSer 281
|||||
Db 170571 CAGCTGTGCTGCCGATCGCTCGCACCTCTTTGTGGCTGAGCTGTGCAGC 170512
Qy 282 TrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluClyLeuTyr 301
|||||
Db 170511 TGGATGGCACTATGACTTTACACTGTCTACACGGACTTGTGGGGAGAGGGGGCTGTAC 170452
Qy 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
|||||
Db 170451 CAGGGTGTACCCAGAGCGAGCCAGCAGCCAGGCGCCGAGACACTATGATGAAGGT 170395

RESULT 39
AR112284
LOCUS AR112284 231 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 5 from patent US 6130043.
ACCESSION AR112284
VERSION AR112284.1 GI:14092184
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 231)
AUTHORS Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N.,
Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D.,
Roberts-Rapp,L., Russell,J.C., Stroupe,S.D. and Yu,H.
TITLE Reagents and methods useful for detecting diseases of the prostate
JOURNAL Patent: US 6130043-A 5 10-OCR-2000;
FEATURES Location/Qualifiers
1..231
/organism="unknown"
BASE COUNT 41 a 68 c 61 g 61 t

ORIGIN
Alignment Scores:
Pred. No.: 1.11e-26 Length: 231
Score: 34.00 Matches: 57
Percent Similarity: 98.28% Conservative: 0
Best Local Similarity: 98.28% Mismatches: 1
Query Match: 6.15% Indels: 1
DB: 6 Gaps: 0
US-09-593-793A-113 (1-553) x AR112284 (1-231)
Qy 496 AspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGln 515
|||||
Db 3 GATAGTGCTTCTGCTGTCCAGGTGCGCCATCCCTGTTTATGGGTCCCATTTGCCAG 62
Qy 516 LeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIle 535
|||||
Db 63 CTCAGCCAGTCTGTCACCTGCTATATGTTGTCGCCGAGG-CTGGGTCTGGTCCCAT 121
Qy 536 TyrPheAlaThrGlnValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||
Db 122 TACTTTGTACACAGGTAGTATTGACAGAGCGGACTTGGCCAAATACTCAGCG 175
RESULT 40
BC024519
LOCUS BC024519 1593 bp mRNA linear ROD 07-AUG-2002
DEFINITION Mus musculus, clone IMAGE:4984191, mRNA, partial cds.
ACCESSION BC024519
VERSION BC024519.1 GI:19353990
KEYWORDS house mouse.
SOURCE
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 1593)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www.shgc.stanford.edu>
Contact: (Dickson, Mark) mcdpaxil@stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 59 Row: p Column: 15
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.
FEATURES Location/Qualifiers
1..1593
/organism="Mus musculus"
/db_xref="taxon:10090"
/map="FVB/N"
/clone="IMAGE:4984191"
/tissue_type="Colon, normal.. 5 month old male mouse."
/clone_lib="NCI_CGAP_C024"
/lab_host="DH10B"
/note="vector: pCMV-SPORT6"
<1..340
/codon_start=2
CDS

/product="Unknown (protein for IMAGE:4984191)"
/protein_id="AAH24519.1"
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/translation="PNGHVGGSSGILAPPALCGASACDYSMRVVVGPPEARVVVTG
RGICLDLIDSAFLLSQVAPSLFGSIVQLSHVATYVNSAGLGLVATVFATVVF
DNKDLAKYSV"

BASE COUNT 358 a 401 c 398 g 436 t

ORIGIN

Alignment Scores:

Pred. No.: 7,64e-25 Length: 1593
Score: 33.00 Matches: 60
Percent Similarity: 96.77% Conservative: 0
Best Local Similarity: 96.77% Mismatches: 1
Query Match: 5.97% Indels: 2
DB: 10 Gaps: 0

US-09-593-793a-113 (1-553) x BC024519 (1-1593)

QY 485 GlyArgGlyLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnVal 504
|||||
Db 131 GGACGGGCATTGCTGGACCTGCGCATCTGGACAGTGCCTTCTGCTGCCAGGTG 190
QY 505 AlaProSerLeuPheMetGlySerIleValGlnLeuSerGln-SerValThrAlaTyrMe 524
|||||
Db 191 GCTCCGCTCCCTGTTGATGGCTCCATTGTCTCCAGCTGAGCCA-CTCTGTCACTGCCTATAT 249
QY 524 tValSerAlaAlaGlyLeuGlyLeuValAlaIleIleTyrPheAlaThrGlnValValPheAs 544
|||||
Db 250 GTATCAGCTGCAGGCTTGCTGGTCTGCTGCCATTACTTTGCTACACAGAGTAGTGTTCGA 309

QY 544 phys 545

|||||

Db 310 CAAG 313

RESULT 41

AC126523/c

LOCUS

AC126523 198037 bp DNA linear HTG 14-JUL-2002
Rattus norvegicus clone CH230-65F14, *** SEQUENCING IN PROGRESS
***, 65 unordered pieces.

ACCESSION AC126523

VERSION AC126523.1

KEYWORDS HTG: HTGS_PHASE1.

SOURCE Norway rat.

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 198037)

REFERENCE

AUTHORS

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaila,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouch,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
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Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
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Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,

* 11915 12014: gap of unknown length
* 12015 14075: contig of 2061 bp in length
* 14076 14175: gap of unknown length
* 14176 15601: contig of 1426 bp in length
* 15602 15701: gap of unknown length
* 15702 17277: contig of 1576 bp in length
* 17278 17377: gap of unknown length
* 17378 18657: contig of 1280 bp in length
* 18658 18757: gap of unknown length
* 18758 20392: contig of 1635 bp in length
* 20393 20492: gap of unknown length
* 20493 21641: contig of 1149 bp in length
* 21642 21741: gap of unknown length
* 21742 23412: contig of 1671 bp in length
* 23413 23512: gap of unknown length
* 23513 25087: contig of 1575 bp in length
* 25088 25187: gap of unknown length
* 25188 26859: contig of 1672 bp in length
* 26860 26959: gap of unknown length
* 26960 28698: contig of 1739 bp in length
* 28699 30716: gap of unknown length
* 30717 30816: gap of unknown length
* 30817 32509: contig of 1693 bp in length
* 32510 32609: gap of unknown length
* 32610 34220: contig of 1611 bp in length
* 34221 34320: gap of unknown length
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* 35661 37768: contig of 2108 bp in length
* 37769 37868: gap of unknown length
* 37869 39562: contig of 1694 bp in length
* 39563 39662: gap of unknown length
* 39663 41676: contig of 2014 bp in length
* 41677 41776: gap of unknown length
* 41777 43658: contig of 1882 bp in length
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* 43759 45624: contig of 1866 bp in length
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* 45725 48100: contig of 2376 bp in length
* 48101 48200: gap of unknown length
* 48201 50489: contig of 2289 bp in length
* 50490 50589: gap of unknown length
* 50590 52329: contig of 1740 bp in length
* 52330 52429: gap of unknown length
* 52430 54544: contig of 2115 bp in length
* 54545 54644: gap of unknown length
* 54645 56752: contig of 2108 bp in length
* 56753 56852: gap of unknown length
* 56853 58639: contig of 1787 bp in length
* 58640 58739: gap of unknown length
* 58740 60931: contig of 2192 bp in length
* 60932 61031: gap of unknown length
* 61032 63481: contig of 2450 bp in length
* 63482 63581: gap of unknown length
* 63582 66000: contig of 2419 bp in length
* 66001 66100: gap of unknown length
* 66101 68760: contig of 2660 bp in length
* 68761 68860: gap of unknown length
* 68861 71024: contig of 2164 bp in length
* 71025 71124: gap of unknown length
* 71125 73169: contig of 2045 bp in length
* 73170 73269: gap of unknown length
* 73270 76108: contig of 2839 bp in length
* 76109 76208: gap of unknown length
* 76209 79687: contig of 3479 bp in length
* 79688 79787: gap of unknown length
* 79788 82504: contig of 2717 bp in length
* 82505 82604: gap of unknown length
* 82605 86873: contig of 4269 bp in length
* 86874 86973: gap of unknown length
* 86974 91613: contig of 4640 bp in length
* 91614 91713: gap of unknown length

* 91714 94992: contig of 3279 bp in length
* 94993 95092: gap of unknown length
* 95093 97134: contig of 2042 bp in length
* 97135 97234: gap of unknown length
* 97235 100423: contig of 3189 bp in length
* 100424 100523: gap of unknown length
* 100524 104682: contig of 4159 bp in length
* 104683 104782: gap of unknown length
* 104783 108313: contig of 3531 bp in length
* 108314 108413: gap of unknown length
* 108414 113868: contig of 5455 bp in length
* 113869 113968: gap of unknown length
* 113969 117789: contig of 3821 bp in length
* 117790 117889: gap of unknown length
* 117890 120979: contig of 3090 bp in length
* 120980 121079: gap of unknown length
* 121080 123743: contig of 2664 bp in length
* 123744 123843: gap of unknown length

Alignment Scores:
Pred. No.: 6, 21e-23 Length: 198037
Score: 33.00 Matches: 60
Percent Similarity: 96.77% Conservative: 0
Best Local Similarity: 96.77% Mismatches: 1
Query Match: 5.97% Indels: 2
DB: 2 Gaps: 0

US-09-593-793A-113 (1-553) x AC126523 (1-198037)

QY 485 GlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnVal 504
|||||
Db 59276 GGACGGGGCATTTGCTGGACCTTGCATCTCCGACAGTGTCTTCTGCTGCCAGGTG 59217

QY 505 AlaProSerLeuPheMetClySerIleValGlnLeuSerGln-SerValThrAlaTyrMe 524
|||||
Db 59216 GGTCCGTCCCTTTCATGGGCTCCATTGTCAGCTGAGGCCA-CTGTGTACCTGCCTATAT 59158

QY 524 TvalSerAlaAlaGlyLeuGlyLeuValAlaIleIleYrPheAlaThrGlnValValPheAs 544
|||||
Db 59157 GGTATCAGCTGCAGGCTGGGTCTGGTCCCATTTACTTTGTGTACACAGTAGTGTTC 59098

QY 544 pLys 545
|||||
Db 59097 CAAG 59094

RESULT 42
AX201081

LOCUS AX201081 60 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 711 from Patent WO0151633.
ACCESSION AX201081
VERSION AX201081.1 GI:15390884
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
COMPOSITIONS and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 711 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source
Location/Qualifiers
1..60
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 4 a 25 c 16 g 15 t
ORIGIN

Alignment Scores:
Pred. No.: 3.29e-12 Length: 60

Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.62% Indels: 0
DB: 6 Gaps: 0

US-09-593-793A-113 (1-553) x AX201081 (1-60)

Qy 453 LeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgVal 472

Db 1 CTGCTCCACCTCCACCCGCGCTCTGCGGGCGCTCTGCGCTGTGATCTCCGTACGTGTG 60

RESULT 43

AX267880

LOCUS AX267880 60 bp DNA linear PAT 26-OCT-2001

DEFINITION Sequence 854 from Patent WO0173032.

ACCESSION AX267880

VERSION AX267880.1 GI:16516516

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.

and Henderson,R.A.

TITLE Compositions and methods for the therapy and diagnosis of prostate

cancer

JOURNAL Patent: WO 0173032-A 854 04-OCT-2001;

CORIXA CORPORATION (US)

FEATURES Location/Qualifiers

source

1..60

/organism="Homo sapiens"

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BASE COUNT 4 a 25 c 16 g 15 t

ORIGIN

Alignment Scores:

Pred. No.: 3.29e-12 Length: 60

Score: 20.00 Matches: 20

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.62% Indels: 0

DB: 6 Gaps: 0

US-09-593-793A-113 (1-553) x AX267880 (1-60)

Qy 453 LeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgVal 472

Db 1 CTGCTCCACCTCCACCCGCGCTCTGCGGGCGCTCTGCGCTGTGATCTCCGTACGTGTG 60

RESULT 44

AX201091

LOCUS AX201091 57 bp DNA linear PAT 29-AUG-2001

DEFINITION Sequence 721 from Patent WO0151633.

ACCESSION AX201091

VERSION AX201091.1 GI:15390888

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,

Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.

Compositions and methods for the therapy and diagnosis of prostate

cancer

JOURNAL Patent: WO 0151633-A 721 19-JUL-2001;

CORIXA CORPORATION (US)

FEATURES Location/Qualifiers

source

1..57

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BASE COUNT 8 a 5 c 11 g 12 t 21 others

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Score: 12.00 Matches: 12

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.17% Indels: 0

DB: 6 Gaps: 0

US-09-593-793A-113 (1-553) x AX201091 (1-57)

Qy 45 GluValGlyValGluGluLysPheMetThrMetVal 56

Db 19 GARGTNGGNGTGARGAARATTYATGACNATGGTN 54

RESULT 45

AX267890

LOCUS AX267890 57 bp DNA linear PAT 26-OCT-2001

DEFINITION Sequence 864 from Patent WO0173032.

ACCESSION AX267890

VERSION AX267890.1 GI:16516520

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.

and Henderson,R.A.

TITLE Compositions and methods for the therapy and diagnosis of prostate

cancer

JOURNAL Patent: WO 0173032-A 864 04-OCT-2001;

CORIXA CORPORATION (US)

FEATURES Location/Qualifiers

source

1..57

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BASE COUNT 8 a 5 c 11 g 12 t 21 others

ORIGIN

Alignment Scores:

Pred. No.: 0.00118 Length: 57

Score: 12.00 Matches: 12

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.17% Indels: 0

DB: 6 Gaps: 0

US-09-593-793A-113 (1-553) x AX267890 (1-57)

Qy 45 GluValGlyValGluGluLysPheMetThrMetVal 56

Db 19 GARGTNGGNGTGARGAARATTYATGACNATGGTN 54

Search completed: February 19, 2003, 06:11:58

Job time : 3202 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 01:33:08 ; Search time 2887 Seconds
(without alignments)
5574.594 Million cell updates/sec

Title: US-09-593-793a-113
Perfect score: 2861
Sequence: 1 MVQRLWVSRLLRHRKAQLL.....AIYFATQVDFKSLAKYSA 553

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Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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14: gb_vi:*
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38: em_sy:*
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40: em_hgtgo_mus:*
41: em_hgtgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2861	100.0	3320	6	AX327336 Sequence
2	2861	100.0	3410	6	AX106329 Sequence
3	2861	100.0	3410	6	AX140620 Sequence
4	2861	100.0	3410	6	AX200480 Sequence
5	2861	100.0	3410	6	AX267136 Sequence
6	2861	100.0	3410	6	AX429961 Sequence
7	2861	100.0	3410	9	AY033593 Homo sapi
8	2798	97.8	3514	9	AB060851 Macaca fa
9	2716.5	94.9	4034	6	AX200995 Sequence
10	2716.5	94.9	4034	6	AX267730 Sequence
11	2602	90.9	3354	10	BC031381 Mus muscu
12	2601	90.9	2133	6	AX343857 Sequence
13	2566	89.7	2917	9	AB062977 Macaca fa
14	2538.5	88.7	4894	6	AX200993 Sequence
15	2538.5	88.7	4894	6	AX267728 Sequence
16	2144	74.9	6976	6	AX200996 Sequence
17	2144	74.9	6976	6	AX267731 Sequence
18	2144	74.9	157988	2	AC096533 Homo sapi
19	2099	73.4	2611	10	BC034084 Mus muscu
20	2051	71.7	178567	2	AC107837 Mus muscu
c 21	1920.5	67.1	2904	6	AX200994 Sequence
22	1920.5	67.1	2904	6	AX267729 Sequence
23	1742	60.9	198037	2	AC126523 Rattus no
24	1696	59.3	1593	6	AX343860 Sequence
25	1403.5	49.1	1203	6	AX201078 Sequence
26	1403.5	49.1	1203	6	AX267877 Sequence
27	1287	45.0	2152	6	AR112295 Sequence
28	1270	44.4	2143	6	AR112294 Sequence
29	1179.5	41.2	2477	9	HSM804244 Homo sapi
30	919	32.1	789	6	AX108229 Sequence
31	919	32.1	789	6	AX140520 Sequence
32	919	32.1	789	6	AX200380 Sequence
33	919	32.1	789	6	AX267036 Sequence
c 34	673	23.5	198037	2	AC126523 Rattus no
35	512	17.9	1593	10	BC024519 Mus muscu
36	489.5	17.1	1986	10	AF360357 Mus muscu
37	489.5	17.1	1998	10	AF034377 Mus muscu
38	488.5	17.1	1650	9	AF172849 Homo sapi
39	458.5	16.0	18567	2	AC018319 Drosophil
c 40	458.5	16.0	165852	3	AC010022 Drosophil
c 41	458.5	16.0	176929	3	AC091203 Drosophil
c 42	458.5	16.0	286784	3	AE003552 Drosophil
43	456	15.9	1980	5	AF332510 Oryzias l
44	446	15.6	2256	10	AB075229 Rattus no
45	440	15.4	255	6	AR112282 Sequence
c 46	428	15.0	406	11	HSPE54C06 AL033941 H. sapiens
47	423	14.8	258	6	AR112280 Sequence
48	418	14.6	247	6	AR112283 Sequence
49	357	12.5	217	6	AR112281 Sequence
50	347.5	12.1	1858	8	Y16768 Daucus caro

51	346.5	12.1	1661	8	AF021808	Vitis vin
52	346.5	12.1	1796	8	AB036758	Daucus ca
53	346.5	12.1	2135	6	AX306541	Sequence
54	346	12.1	2130	8	AF021809	Vitis vin
c	340	11.9	123280	2	AC117076	Dictyoste
56	338	11.8	1872	8	AF167416	Apium gra
57	338	11.8	1907	8	AF167415	Apium gra
58	337.5	11.8	2004	8	VF293774	V.faba mRNa
59	336.5	11.8	1654	8	AF182445	Vitis vin
60	333	11.6	1954	8	AF063400	Apium gra
61	332.5	11.6	1782	8	AY065840	Brassica
62	330	11.5	1548	6	AX259895	Sequence
63	330	11.5	1773	6	AX36575	Sequence 2
64	330	11.5	1773	6	AR084457	Sequence 3
65	330	11.5	1773	6	I36755	Sequence 3
66	330	11.5	1988	8	STSUCTR	S. tuberosum
67	329.5	11.5	2034	8	AF109922	Pisum sat
68	328.5	11.5	1785	6	AX259876	Sequence
69	328.5	11.5	1785	8	AJ289165	Arabidops
70	327.5	11.4	1713	8	AB071809	Oryza sat
71	325.5	11.4	2137	8	AF166498	Lycopersi
72	324.5	11.3	1695	8	AF191025	Alonsoa m
73	324.5	11.3	1798	8	AY091774	Arabidops
74	324.5	11.3	1969	6	AX36574	Sequence 1
75	324.5	11.3	1969	6	AR084456	Sequence 1
76	324.5	11.3	1969	6	I36754	Sequence 1
77	324.5	11.3	1969	8	SOS21	S. oleraceae
78	323.5	11.3	1570	8	AY113946	Arabidops
79	323.5	11.3	1787	8	AT5UC25	A.thaliana
80	323.5	11.3	1800	8	AY048256	Arabidops
81	323.5	11.3	1803	8	AY088566	Arabidops
82	323.5	11.3	1857	8	AY050986	Arabidops
83	323	11.3	9319	8	DCA303199	Daucus ca
84	318.5	11.1	1985	8	AF242307	Euphorbia
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96	306	10.7	2044	8	HVU272309	Hordeum v
97	305.5	10.7	1861	8	DCSUT1B	Daucus caro
98	305.5	10.7	2132	8	DCSUT1A	Daucus caro
99	304	10.6	2106	8	AF408844	Triticum
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ALIGNMENTS

RESULT 1	AX327336	3320 bp	DNA	linear	PAT 07-JAN-2002
LOCUS	Sequence 1 from Patent WO0181577.				
DEFINITION	AX327336				
ACCESSION	AX327336				
VERSION	AX327336.1	GI:18097882			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	Lin, R.J., Parkes, D., Parry, G., Schneider, D.W.,				
JOURNAL	Steinbrecher, R., van Heuit, P.T., and Wu, J.				
FEATURES	Dna encoding the prost 03 polypeptide				
source	Patent: WO 0181577-A 1 01-NOV-2001;				
	SCHERING AKTIENGESSELLSCHAFT (DE)				
	Location/Qualifiers				
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Qy	21	ValAsnLeuLeuThrpheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
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Qy	41	ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db	402	CCTCTGCTCTGAGAGTGGGGTAGAGGAAGTTCATACCATGCTGGCATGTGT 461
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Qy	81	ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db	522	CGCTATGGCGCGCGCGCTTCATCTGGGCACCTGCTCTGGGCATCTCTGTGAGCCTC 581
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Db	642	GAGCTGGCACTGCTCATCTGGCGCTGGGGCTGCTGGACTTCTGTGGCCAGGTGCTTC 701
Qy	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
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Qy	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
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BEALGPTPEAGLSAPSCPCRLARLRLNIGALLPRLHQLCCMRPTLRLFLV
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Qy	261	His	Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	Val	Ala	Glu	Leu	Cys	280
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Db	1122	AG	CT	GG	AT	GC	AC	TC	AT	GC	CT	TC	AG	CT	GT	TT	T	AC	AG	GA	TT	TC
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Db	1182	TAC	CAG	GG	CG	TG	CC	AG	CT	GAG	CC	GG	CG	CA	CC	AG	CG	CG	GAG	ACA	CT	AT
Qy	321	Val	Arg	Met	Gly	Ser	Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	Leu	340
Db	1242	GTT	CG	AT	GG	CAG	CG	CT	TG	GG	CG	TT	TC	CT	GC	AG	TG	CG	CA	TC	CT	CT
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Db	1302	GTC	AT	GG	AC	CG	CT	GT	GC	AG	CA	TTC	GG	CAC	TG	CT	AT	T	TT	GG	CC	AG
Qy	361	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu	Ser	His	Ser	Val	Ala	Val	Ile	Thr	Ala	380

ACCESSION	AX106329
VERSION	AX106329.1
KEYWORDS	GI:13922014
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3410)
AUTHORS	Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
TITLE	Compositions and methods for therapy and diagnosis of prostate cancer
JOURNAL	Patent: WO 0125272-A 110 12-APR-2001;
FEATURES	CORIXA CORPORATION (US) Location/Qualifiers 1..3410 /organism="Homo sapiens" /db_xref="taxon:9606"
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Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
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Qy 21	VallAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrYrValPro 40
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Db 404	CCTCTGCTGCTGGAAGTGGGGGTACAGAGAGAAGTTCATGACCATTGGTGTGGCCATTGGT 463
Qy 61	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
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Qy 81	ArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
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Qy 101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
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Qy 141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704	ACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCGGGACCCGGACCACTGTGCCAGGCC 763
Qy 161	TyrSerValTyrAlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764	TACTCTGTCTATGCTTTCATGATCAGTCTTGGGGGCTGCTGGGCTACCTTCCTGCCTGCC 823
Qy 181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
Db 824	ATTGACTGGGACACCATGTCCTGGCCCCCTACTCTGGGCACCCAGGAGGAGTGCCTCTTT 883
Qy 201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaIleThrLeuLeuValAlaGlu 220
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Qy	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240	AX140620	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Db	944	GCAGCGTGGGCCCCACCGAGCAGCAGAGAGGCTCGCGCCCTCTCTGTCGCCCCAC	1003	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Qy	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuProArgLeu	260	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Db	1004	TGCTGTCCATGCCGGGCCCTTGGCTTTCCGGAACCTGGGGCCCTGCTCCCGGGTG	1063	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Qy	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Db	1064	CACCAGCTGTCTGCCGATCGCCCGACCCCTCGCGCGCTCTTCTGGCTGAGCTGTC	1123	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Qy	281	SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu	300	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Db	1124	AGCTGGATGGCAGCTCATGAGCTTCACGCTCTTTTACACGATTTCTGGGGCAGGGCTG	1183	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Qy	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly	320	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Db	1184	TACCAGGGCGTGGCCAGAGCTGAGCGGCGACCGAGCGCCGAGACATATATGAAGGC	1243	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Qy	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Db	1244	GTTCGGATGGCAGCCCTGGGCTTCTCTGCAGTGGCCCATCTCCCTGGTCTCTCTG	1303	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Qy	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla	360	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Db	1304	GTCATGACCGCGTGTGTCAGCGATTCGGCAGCTCGAGCAGTCTATTGGCCAGTGGCA	1363	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Qy	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla	380	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Db	1364	GCTTTTCCCTGGCGTGGCGTGCACATGCTCTCCACAGTGTGGCGTGTGACAGCT	1423	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Qy	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Db	1424	TCAGCGCCCTCACCGGGTTTCACTTCTCAGCCCTGCAGATCTGCGCTTACACATGGCC	1483	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Qy	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	420	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Db	1484	TCCCTCTACCAACCGGAGAACAGGTGTTCTCCCAAAATACCGAGGGACACTGGAGGT	1543	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Qy	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Db	1544	GCTAGCAGTAGGACAGCCCTGATGACACAGCTTCTCCAGGCGCTTAAGCCTGGAGCTCC	1603	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Qy	441	PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu	460	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Db	1604	TTCCCTAATGGACACGTGGGTGTGGAGCAGTGGGCTGCTCCACCTCCACCCCGCTC	1663	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Qy	461	CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla	480	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Db	1664	TGCGGGGCTCTGCTGTATGCTCCGTACGTGTGGTGGTGAGCCACCGAGGCC	1723	AX140620.1	GI:14280737	human	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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	PAT 31-MAY-2001
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LOCUS	AX140620 3410 bp DNA linear
DEFINITION	Sequence 110 from Patent WO0134802.

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QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
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QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
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QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyThrAspPheValGlyGluGlyLeu 300
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Db 1544 GCTAGCAGTGAGACAGCCTGATGACCACTTCTGCCAGGCCCTAAGCCTGGAGCTCCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
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Db 1664 TGGGGGGCTCTGCTGTGATGTCTCCGACGFTGGTGGGTGAGGCCACCGAGGCC 1723
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QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
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AX200480
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ACCESSION AX200480
VERSION AX200480.1 GI:15390293
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3410)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 110 19-JUL-2001;
CORIXA CORPORATION (US)
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Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T.
and Henderson, R.A.
Compositions and methods for the therapy and diagnosis of prostate
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JOURNAL
Patent: WO 0173032-A 110 04-OCT-2001;
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AUTHORS Reed,S.G., Xu,J., Dillon,D.C., Rettler,M.W. and Harlocker,S.L.
TITLE Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL Patent: WO 0198339-A 100 27-DEC-2001;
CORIXA CORPORATION (US)
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REFERENCE 1 (bases 1 to 3410)
AUTHORS Xu, J., Kalos, M., Stolk, J. A., Zasloff, E. J., Zhang, X., Houghton, R. L.,
Filho, A. M., Nolasco, M., Badaro, R. and Reed, S. G.
TITLE Identification and characterization of prostein, a novel
prostate-specific protein
JOURNAL Cancer Res. 61 (4), 1563-1568 (2001)
MEDLINE 21139094
PUBMED 11245466
REFERENCE 2 (bases 1 to 3410)
AUTHORS Xu, J., Kalos, M., Stolk, J. A., Zasloff, E. J., Zhang, X., Houghton, R. L.,
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TITLE Direct Submission
JOURNAL Submitted (27-Apr-2001) Antigen Discovery, Corixa Corporation, 1124
Columbia Street, Seattle, WA 98104, USA
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ACCESSION AB060851
VERSION AB060851.1 GI:13874496
KEYWORDS oligo capping; fis (full insert sequence).
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clone.lib:macaque brain cDNA library Qtra clone:Qtra-11310.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
REFERENCE 1 (sites)
AUTHORS Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M.,
Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
TITLE Isolation of full-length cDNA clones from macaque brain cDNA
libraries
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3514)
AUTHORS Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
TITLE Direct Submission
JOURNAL Submitted (27-APR-2001) Katsuyuki Hashimoto, National Institute of
Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
(E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/,
Tel: 81-3-5285-1111(ex.2120), Fax: 81-3-5285-1181)
Lab host: TOPLO
COMMENT Vector: pME18S-FL3 (Acc.No. AB009864)
R. Site1: DraIII (CACTGTGTG)
R. Site2: DraIII (CACCAGTGT)
Description: 1st strand cDNA was primed with an oligo(dT) primer
[ATGTCGCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized
using specific 5' and 3' primers and amplified by PCR. The PCR
product was digested with SfiI and size selection was performed to
exclude fragments <1.5Kb. The SfiI-digested PCR product was cloned
into distinct DraIII sites of pME18S-FL3. XhoI sites just outside
the DraIII sites can be used to isolate the cDNA insert. Libraries
were constructed by oligo-capping method
(Sugano et al., , Institute of Medical Science, University of
Tokyo).
Custom primer used for sequencing
( 5' end primer [CTTCTGCTCTAAAGCTGG] ;
3' end primer [CGACCTGCAGCTCGAGCACA] ).
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FEATURES

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Alignment Scores:

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US-09-593-793A-113 (1-553) x AB060851 (1-3514)

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VERSION AX200995.1 GI:15390822
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 4034)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Haylock, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W.,
Stolk, J.A., Skelky, J.A., Wang, A. and Meagher, M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 625 19-JUL-2001;
CORIXA CORPORATION (US)
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LOCUS AX267730 4034 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 704 from Patent WO0173032.
ACCESSION AX267730
VERSION AX267730.1 GI:16516402
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 704 04-OCT-2001;
CORIXA CORPORATION (US)

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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Pred. No.: 1.89e-168 Length: 4034
Score: 2716.50 Matches: 553
Percent Similarity: 70.09% Conservative: 0
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US-09-593-793A-113 (1-553) x AX267730 (1-4034)
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LOCUS Sequence 3 from Patent WO0200892.
DEFINITION AX343857
ACCESSION AX343857
VERSION AX343857.1 GI:18491926
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequences.
1
REFERENCE
AUTHORS cabazon Silva,T.E. and Delisse,A.M.
TITLE Triple fusion proteins comprising ubiquitin fused between
thioredoxin and a polypeptide of interest
JOURNAL Patent: WO 0200892-A 3 03-JAN-2002;
SmlChKline Beecham Biologics SA (BE)
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DEFINITION sequence.
ACCESSION AB062977
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AB062977.1 GI:14388390
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 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 Cercopithecinae; Macaca.
 REFERENCE
 1 (sites)
 Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M.,
 Terso,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
 Isolation of full-length cDNA clones from macaque brain cDNA
 libraries
 Unpublished
 2 (bases 1 to 2917)
 Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
 Direct Submission
 Submitted (11-JUN-2001) Katsuyuki Hashimoto, National Institute of
 Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
 (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/,
 Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
 COMMENT
 Lab host: TOP10
 Vector: pME18S-FL3 (Acc.No. AB009864)
 R. Site1: DraIII (CACATGCTG)
 R. Site2: DraIII (CACATGCTG)
 Description: 1st strand cDNA was primed with an oligo(dT) primer
 [ATGCGGCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized
 using specific 5' and 3' primers and amplified by PCR. The PCR
 product was digested with SfiI and size selection was performed to
 exclude fragments <1.5kb. The SfiI-digested PCR product was cloned
 into distinct DraIII sites of pME18S-FL3. XhoI sites just outside
 the DraIII sites can be used to isolate the cDNA insert. Libraries
 were constructed by oligo-capping method
 (Sugano et al., Institute of Medical Science, University of
 Tokyo).
 Custom primer used for sequencing
 3' end primer [CTTCTGCTGCTAAAAGCTCCG];
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DEFINITION Sequence 623 from Patent WO0151633.
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VERSION AX200993.1 GI:15390820
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SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 (bases 1 to 4894)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W.,
Stolk, J.A., Skeiky, Y.A., Wang, A. and Meagher, M.J.
Compositions and methods for the therapy and diagnosis of prostate
cancer
TITLE Patent: WO 0151633-A 623 19-JUL-2001;
CORIAX CORPORATION (US)
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Best Local Similarity: 51.11% Mismatches: 2
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LOCUS

DEFINITION

AX267728

ACCESSION

VERSION

KEYWORDS

AX267728 4894 bp DNA linear PAT 26-OCT-2001
Sequence 702 from Patent WO0173032.

AX267728.1 GI:16516400

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y.,
Kalos, M. D., Fanger, G. R., Retter, M. W., Stolk, J. A., Day, C. H.,
Vedvick, T. S., Carter, D., Li, S. X., Wang, A., Skelky, Y. A., Hepler, W. T.
and Henderson, R. A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 702 04-OCT-2001;
CORIXA CORPORATION (US)
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VERSION AX200996.1 GI:15390823
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6976)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 626 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
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/db_xref="taxon:9606"
BASE COUNT 1312 a 1996 c 1961 g 1706 t 1 others
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DEFINITION Sequence 705 from Patent WO0173032.
ACCESSION AX267731
VERSION AX267731.1 GI:16516403
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1
REFERENCE
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0173032-A 705 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
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BASE COUNT 1312 a 1996 c 1961 g 1706 t
ORIGIN
Alignment Scores:
Pred. No.: 8.88e-131 Length: 6976
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Best Local Similarity: 30.48% Mismatches: 2
Query Match: 74.94% Indels: 1257
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US-09-593-793A-113 (1-553) x AX267731 (1-6976)
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BC034084	BC034084	2611 bp	mRNA	linear	ROD 07-AUG-2002
LOCUS	Mus musculus, clone IMAGE:4457452, mRNA, partial cds.				
DEFINITION	BC034084				
ACCESSION	BC034084.1	GI:21707615			
VERSION					
KEYWORDS	house mouse.				
SOURCE	Mus musculus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Strausberg,R.				
REFERENCE	1 (bases 1 to 2611)				
AUTHORS	Direct Submission				
TITLE	Submitted (02-JUL-2002) National Institutes of Health, Mammalian				
JOURNAL	Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk Email: cgabbs@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcdpaxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.				
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 43 Row: p Column: 14 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.				
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CDS					
BASE COUNT	519 a	728 c	691 g	673 t	
ORIGIN					
Alignment Scores:					
Pred. No.:	2,74e-128	Length:	2611		
Score:	2099.00	Matches:	404		
Percent Similarity:	92.65%	Conservative:	12		
Best Local Similarity:	89.98%	Mismatches:	33		
Query Match:	73.37%	Indels:	0		
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US-09-593-793A-113 (1-553) x BC034084 (1-2611)	
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QY 144 GluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerVal 163	
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FEATURES

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ORIGIN

Alignment Scores:

Pred. No.: 3,29e-123 Length: 178567

Score: 2051.00 Matches: 502

Percent Similarity: 32.37% Conservative: 14

Best Local Similarity: 31.49% Mismatches: 36

Query Match: 71.69% Indels: 1042

DB: 2 Gaps: 3

US-09-593-793a-113 (1-553) x AC107837 (1-178567)

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Qy 57 ----- 57

Db 171474 CTTTCATCTTCTTCTTCCAGCTCTGGTGCCTGGGCTGGGTTGTAGGCAGCATTCCTCT 171415

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Qy 57 ----- 57

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LOCUS
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VERSION        AX267729.1 GI:16516401
KEYWORDS
SOURCE
ORGANISM        human.
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                Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS        Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
                Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
                Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T.
                and Henderson, R.A.
TITLE          Compositions and methods for the therapy and diagnosis of prostate
                cancer
JOURNAL        Patent: WO 0173032-A 703 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES        Location/Qualifiers
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                /organism="Homo sapiens"
                /db_xref="taxon:9606"
BASE COUNT      542 a 875 c 773 g 714 t
ORIGIN
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Alignment Scores:
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Score:          1920.50           Matches:     390
Percent Similarity: 77.23%        Conservative: 0
Best Local Similarity: 77.23%      Mismatches:  1
Query Match:     67.13%           Indels:      115
DB:              6                Gaps:         1
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US-09-593-793A-113 (1-553) x AX267729 (1-2904)

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Qy 183 TrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeu 202
Db 61 TGGGACACAGTGGCTGGCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTG 120
Qy 203 LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluAlaAla 222
Db 121 CTCACCTCTCATCTTCCCTCACCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAGCAGC 180
Qy 223 LeuGlyProThrGluProAlaGluCysLeuSerAlaProSerLeuSerProHisCysCys 242
Db 181 CTGGGCCCCACCGAGCCAGCAGAGGGCTGTGCGGCCCTCCTCTGTCGCCCCACTGCTGT 240
Qy 243 ProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGln 262
Db 241 CCATCGCGGGCGCGCTTGGCTTTCGGGAACCTGGGCGGCCCTGCTTCCCGCGCTGCACCG 300
Qy 263 LeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrp 282
Db 301 CTGTGCTGCGCCATGCGCCCGCACCTGCGCGGCTCTTCTGCTGGCTGAGCTGTGAGCTGG 360
Qy 283 MetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGln 302
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Qy	529	GlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValPheAspLysSerAspLeu	548
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LOCUS	AC126523		
DEFINITION	Rattus norvegicus clone CH230-65f14, *** SEQUENCING IN PROGRESS		
ACCESSION	AC126523		

VERSION
KEYWORDS
SOURCE
ORGANISM

AC126523.1 GI:21700488
HTG; HTGS_PHASE1.
Norway rat.

REFERENCE
AUTHORS

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 198037)

REFERENCE
AUTHORS

1 (bases 1 to 198037)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbaria, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,
Bouch, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
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Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Correll, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Haviak, P., Hawes, A., Hernandez, J.,
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Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
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Karlssoon, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulsegue, H.,
Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
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Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G.,
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Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G.,
Scherer, S., Scott, G., Shen, H., Shoshitari, N., Sisson, I.,
Sodergren, E., Sonalike, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
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Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

TITLE
JOURNAL

Direct Submission
Unpublished
2 (bases 1 to 198037)
Worley, K.C.

REFERENCE
AUTHORS

Direct Submission
Submitted (06-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 198037)
Worley, K.C.

REFERENCE
AUTHORS

Direct Submission
Submitted (14-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center

COMMENT

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information

Center project name: GKBO
Center clone name: CH230-65f14
----- Summary Statistics

Sequencing vector: Plasmid;
Chemistry: Dye-terminator; Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329
Consensus quality: 149884 bases at least Q40
Consensus quality: 159599 bases at least Q30
Consensus quality: 166549 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 65 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 108314 108413: gap of unknown length
* 108414 113868: contig of 5455 bp in length
* 113869 113968: gap of unknown length
* 113969 117789: contig of 3821 bp in length
* 117790 117889: gap of unknown length
* 117890 120975: contig of 3090 bp in length
* 120980 121079: gap of unknown length
* 121080 123744: contig of 2664 bp in length
* 123745 123843: gap of unknown length

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US-09-593-793A-113 (1-553) x AC126523 (1-198037)

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QY 57 ----- 57
Db 161424 CCATTCCCTCTCTGAAACAAGCTGTTTATATACCCACACTGAGAGGAGAGAGCCCC 161483
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QY 127 LeuGlyValIleGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeu 146
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QY 147 LeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPhe 166
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QY 167 MetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSer 186
Db 161904 ATGATCAGCCTCGGGGGCTGCTGGCTACCTCTTACCTGCGCATTTGACTGGGACACCA 161963
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Db 162084 GAGCAGCAGAAAGGTGTGTGCTCTCCCGTGTCAAGCCGGTGTCTCATGCTCATGCT 162143
QY 247 ArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArg 266
Db 162144 GCGCTGGCTTTCCGGAATCTGGTACCCTGTTCGCCGGTGCACACAGCTGTGCTGCCGA 162203
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Db 162204 ATGCCCTCGACCCCTCGCGGCTCTTGTGGCCGAGCTGTGCAGCTGTGACACTTATG 162263
QY 287 ThrPheThrLeuPheThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArg 306
Db 162264 ACTTTCACACTCTTCTACAGGACTTCGTGGGAGAGGGCTGTACAGGGTGTCCCCAGA 162323
QY 307 AlaGluProGlyThrGluAlaArgArgHisTyrAspGlu 319
Db 162324 GCAGAGCCAGGTACCGAGCCGCGAGACACTATGATGAAGGTGAGTCTTTGGCACCAGTG 162383
QY 319 ----- 319
Db 162384 GGAACCGCTGTTGGCCACTGTCTGTAGAGGACAGGCCAGGGTTGGGAGATGCTCACAGC 162443
QY 319 ----- 319
Db 162444 CTGGACCATGGCTGATGACTACTCTCTGGGCCCCAGCCCTCTCAGTAAAGGGAAGG 162503
QY 319 ----- 319
Db 162504 ATCTATGTGCGGTGTTCATGAGCACAGCTGCCCTCTTTGTTGTCTCTATTAGGGCTACTA 162563
QY 319 ----- 319
Db 162564 GGTCGTGTGACTCCAATTCCATGGGCTTGTCTCTTCTGCGTCTTCTCTCACCATGC 162623
QY 319 ----- 319
Db 162624 CTTCAGTTTCGGCATTTCCACAGAACTGTCTTAGAGCCAGTGTGGGGGCCATTTTGTGATC 162683
QY 319 ----- 319
Db 162684 CTCACCCCTCTCTCCCTTACACACCTGGCACTCTGCTTCAACAGCCCCGGGCCACATT 162743
QY 319 ----- 319
Db 162744 CGCTAATTGCAATCTAGATGCGGTCTTGCAGCAGGTGGGAGGACTGGGGAGTGGATG 162803
QY 319 ----- 319
Db 162804 CCCCTGGATACTAGTGTCTAGTCTCCCTAGATTGTGTAGGGTCTTACCCCACTTCTTCC 162863
QY 320 ----- GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAl 333
Db 162864 CTCCTCTCCCCCCCCCAGGCAATTCGAATGGCAGCTTGGGGCTCTCTCTCAGTGTGC 162923
QY 333 aIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAl 353
Db 162924 CATCTCCCTGTTCTCTCCCTGTCATGGACAGGTGTGTACAGAAGTTGCGGCACACGGTC 162983
QY 353 aValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHi 373
Db 162984 ACTTACCTGGCCAGTGTGATGACCTTTCCCGTGGCTGCCGCTGCAGCTGCTGTCCCA 163043
QY 373 sSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuG1 393
Db 163044 CAGCGTGGTTGTAGTGACAGCCTCAGTGCCTCACCAGGTTTCACTTCTCAGCCTTGA 163103
QY 393 nIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProly 413

Db 163104 GATCTGCTTACACGCTGCTCCTCTACCATCGAGAACGAGGTA---CTCCCAATT 163160
Qy 413 sTyrArg-----GlyAspThrClyGly 420
Db 163161 GGCTAGATTGGGGGGTGGGGTAGGGTGGGGGGC 163194
RESULT 24
AX343860 AX343860 1593 bp DNA linear PAT 01-FEB-2002
LOCUS AX343860 Sequence 6 from Patent WO0200892.
DEFINITION AX343860
VERSION AX343860.1 GI:18491927
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequences.
REFERENCE
1 cabazon Silva,T.E. and Delisse,A.M.
triple fusion proteins comprising ubiquitin fused between
thioredoxin and a polypeptide of interest
TITLE Patent: WO 0200892-A 6 03-JAN-2002;
JOURNAL SmithKline Beecham Biologics SA (BE)
FEATURES
source location/Qualifiers
1..1593
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Chimaeric (E. coli - human)";
BASE COUNT 308 a 472 c 461 g 352 t
ORIGIN
Alignment Scores:
Pred. No.: 3.57e-102 Length: 1593
Score: 1696.00 Matches: 320
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 59.28% Indels: 0
Gaps: 6
US-09-593-793A-113 (1-553) x AX343860 (1-1593)
Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db 604 ATGGTCCAGAGCTGTGGGTGAGCCGCTGTGCGGCACCGAAGCCAGCTCTGTCTG 663
Qy 21 ValAsnLeuLeuThrPheGlyLeuValCysLeuAlaGlyIleThrTyrValPro 40
Db 664 GTCAACCTGCTAACCTTTGGCTGTGAGGTGTGTTGGCCGAGGATCACCTATGTGCG 723
Qy 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 724 CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAGTTTCATGACCATGTGCTGGGCATTGGT 783
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 784 CCAGTGTGGGCTGTGTGTCTCCGCTGTAGGCTCAGCCAGTGCACCTATGGCGTGA 843
Qy 81 ArgTrpGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 844 CGTATGGCCGCGCGCCCTTCATCTGGGCACATGCTTCTGGGCATCTCTGTAGCCCTC 903
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 904 TTTCTCATCCCAAGGCGCGTGGCTAGCAGGCTGTGTCGCCGATCCAGGCCCTCTG 963
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 964 GAGCTGGCAGCTCATCTCTGGGCTGGGGCTGTGGACTTCTGTGGCAGTGTGCTTC 1023
Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 1024 ACTCCACTGGAGGCGCTCTCTGACCTCTTCGGGACCGGACCTGTGCGCAGGCC 1083
Qy 161 TyrSerValTrpAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180

Db 1084 TACTCTGTCTATGCTTCATGATCAGTCTGGGGCTTCCTGGGCTACCTCTGCTGCTGCC 1143
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 1144 ATTGACTGGACACCAAGTGGCTTGGCCCTACCTTGGCAGCCAGGAGAGTGCCTCTTT 1203
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 1204 GGCCTGCTCACCTCATCTCTACCTACCTGCTGAGCAGCACACTGCTGGTGGCTGAGGAG 1263
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 1264 GCAGCGCTGGGCCACCGAGCAGCAGAGGGCTGTGGCCCTCTCTTTCGCCCCAC 1323
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1324 TGCTGTCCATCGCGGCGCGCTTGGCTTTCGCGAACCCTGGGCGCTCTCTCCCGGCTG 1383
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgAlaGlyLeuPheValAlaGluCys 280
Db 1384 CACCAGCTGTGCTGCCGATGCCCGCCACCTGCGCCGCGCTCTTCTGGCTGAGCTGTGC 1443
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlyLeu 300
Db 1444 AGCTGGATGGCACTCATGACCTTTCACGCTGTTTACACGGATTTCTGGGCGAGGGCTG 1503
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1504 TACCAGGGCTGCCAGAGCTGAGCGGGCACCGAGGCGCGAGACACTATGATGAAGGC 1563
RESULT 25
AX201078 AX201078 1203 bp DNA linear PAT 29-AUG-2001
LOCUS AX201078 Sequence 708 from Patent WO0151633.
DEFINITION AX201078
ACCESSION AX201078
VERSION AX201078.1 GI:15390883
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 1203)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,F.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 708 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source location/Qualifiers
1..1203
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 175 a 415 c 368 g 245 t
ORIGIN
Alignment Scores:
Pred. No.: 3.49e-83 Length: 1203
Score: 1403.50 Matches: 267
Percent Similarity: 97.45% Conservativeness: 0
Best Local Similarity: 97.45% Mismatches: 2
Query Match: 49.06% Indels: 5
Gaps: 1
US-09-593-793A-113 (1-553) x AX201078 (1-1203)
Qy 30 ValCysLeuAlaAlaGly-----IleThrTyrValProLeuLeuLeu 44
Db 379 GTGACATTGGCGCGAGGAGACCCCGGCCGAATTCATCAGCTATGTGCCCTCTGCTGCTG 438
Qy 45 GluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGly 64

Db 439 GAAGTGGGGGTAGAGAGAGTTTCATGACCATGGTCTGGGCATTTGGTCCAGCTGCTGGGC 498
QY 65 LeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGlyArg 84
Db 499 CTGGTCTGTCTCCGCTCTCCTAGGCTCAGGCAGTGCAGCTGGCGTATGGCCGC 558
QY 85 ArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIlePro 104
Db 559 CGCCGGCCCTTTCATCGGCAGTGTCTTGGGCATCTCTGAGCCCTTTCATATCCCA 618
QY 105 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeu 124
Db 619 AGGGCCGGCTGGCTAGCAGGGCTGTCTGGGCATCTCTGAGCCCTTTCATATCCCA 678
QY 125 LeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheTrpProLeuGlu 144
Db 679 CTCATCTCTGGCGTGGGCTGTGGCTACCTCTGCTGCCATTCACCTCCACTGGAG 738
QY 145 AlaLeuLeuSerAspLeuPheArgProAspHisCysArgGlnAlaTyrSerValTyr 164
Db 739 GCCTCTCTCTGACCTCTTCCGGGACCCGGACCACTGTGCGCAGGCTTACTGTCTAT 798
QY 165 AlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAsp 184
Db 799 GCCTCTCTCTGACCTCTTCCGGGACCCGGACCACTGTGCGCAGGCTTACTGTCTAT 798
QY 185 ThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeuLeuThr 204
Db 859 ACCAGTGCCTTGGCGCTGGGCTGTGGCTACCTCTGCTGCCATTCACCTCCACTGGAG 918
QY 205 LeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluLeuAlaLeuGly 224
Db 919 CTCATCTCTCTGACCTCTTCCGGGACCCGGACCACTGTGCGCAGGCTTACTGTCTAT 978
QY 225 ProThrGluProAlaGlyLeuSerAlaProSerLeuSerProHisCysProCys 244
Db 979 CGGGCCGGCTGGCTTTCGGGAACCTTGGGCGCCCTCTCTTGGCGCTTCTTGGCTGTC 1038
QY 245 ArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCys 264
Db 1039 CGGGCCGGCTGGCTTTCGGGAACCTTGGGCGCCCTCTCTTGGCGCTTCTTGGCTGTC 1098
QY 265 CysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAla 284
Db 1099 TGCCGATGCCCGCCGACCCCTGCGCGGCTCTTCTGCTGGCTGAGCTGTGACGTGGATG 1158
QY 285 LeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlu 298
Db 1159 CTCATGACCTTCACGCTGTTTACACGGATTTCTGGGGCGAG 1200

RESULT 26
AX267877
LOCUS AX267877 1203 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 851 from Patent WO0173032.
ACCESSION AX267877
VERSION AX267877.1 GI:16516515
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
XU,J., DILLON,D.C., MITCHAM,J.L., HARLOCKER,S.L., JIANG,Y.,
KALOS,M.D., FANGER,G.R., RETTER,M.W., STOLK,J.A., DAY,C.H.,
VEDVICK,T.S., CARTER,D., LI,S.X., WANG,A., SKEIKY,Y.A., HEPLER,W.T.
and HENDERSON,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 851 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..1203
/organism="Homo sapiens"

BASE COUNT 175 a 415 c 368 g 245 t
ORIGIN
Alignment Scores:
Pred. No.: 3 49e-83 Length: 1203
Score: 1403.50 Matches: 267
Percent Similarity: 97.45% Conservatives: 0
Best Local Similarity: 97.45% Mismatches: 2
Query Match: 49.06% Indels: 5
DB: 6 Gaps: 1
US-09-593-793a-113 (1-553) x AX267877 (1-1203)
QY 30 ValCysLeuAlaAlaGly-----IleThrTyrValProProLeuLeuLeu 44
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QY 45 GluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGly 64
Db 439 GAAGTGGGGTAGAGAGAGATTTCATGACCATGGTCTGGGCATTTGGTCCAGTGTGGGC 498
QY 65 LeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGlyArg 84
Db 499 CTGGTCTGTGTCGCCGTCTTAGGCTCAGCCAGTGCAGCTGGCGTGGAGCGCTATGGCCGC 558
QY 85 ArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIlePro 104
Db 559 CGCCGGCCCTTTCATCTGGGCAGTGTCTTGGGCATCTCTGCTGAGCCCTTCTTCTCATCCCA 618
QY 105 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeu 124
Db 619 AGGGCCGGCTGGCTAGCAGGGCTGTGTGCCGGATTCGCCAGGCCCTTGGAGCTGGCAGCTG 678
QY 125 LeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheTrpProLeuGlu 144
Db 679 CTCATCTCTGGCGTGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAG 738
QY 145 AlaLeuLeuSerAspLeuPheArgProAspHisCysArgGlnAlaTyrSerValTyr 164
Db 739 GCCTCTCTCTGACCTCTTCCGGGACCCGGACCACTGTGCGCAGGCTTACTGTCTAT 798
QY 165 AlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAsp 184
Db 799 GCCTCTCTCTGACCTTCTGGGGCTGCTTGGGCTACCTCTGCTGCCATTCAGTGGGAC 858
QY 185 ThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeuLeuThr 204
Db 859 ACCAGTGCCTTGGCGCTGGGCTGTGGCTACCTTGGGACCCAGGAGGTGCTCTTGGCGCTGCTCAC 918
QY 205 LeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluLeuAlaLeuGly 224
Db 919 CTCATCTCTCTGACCTTTCGGGAACCTTGGGCGCCCTCTCTTGGCGCTTCTTGGCTGTC 978
QY 225 ProThrGluProAlaGlyLeuSerAlaProSerLeuSerProHisCysProCys 244
Db 979 CCCACCGAGCAGCAGAGGGCTGTGGCGCCCTCTCTTGGCGCCCACTGCTGCTCATGC 1038
QY 245 ArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCys 264
Db 1039 CGGGCCGGCTGGCTTTCGGGAACCTTGGGCGCCCTCTCTTGGCGCTTCTTGGCTGTC 1098
QY 265 CysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAla 284
Db 1099 TGCCGATGCCCGCCGACCCCTGCGCGGCTCTTCTGCTGGCTGAGCTGTGACGTGGATG 1158
QY 285 LeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlu 298
Db 1159 CTCATGACCTTCACGCTGTTTACACGGATTTCTGGGGCGAG 1200
RESULT 27
AR112295
LOCUS AR112295 2152 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 16 from patent US 6130043.
ACCESSION AR112295
VERSION AR112295.1 GI:14092195
KEYWORDS Unknown.
SOURCE Unknown.

ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2152)

AUTHORS Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N.,
Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D.,
Roberts-Rapp,L., Russell,J.C., Strope,S.D. and Yu,H.
TITLE Reagents and methods useful for detecting diseases of the prostate
JOURNAL Patent: US 6130043-A 16 10-OCT-2000;
FEATURES Location/Qualifiers

1. 2152
SOURCE
BASE COUNT 419 a 622 c 569 g 542 t
ORIGIN /organism="unknown"

Alignment Scores:

Pred. No.: 2,66e-75 Length: 2152
Score: 1287.00 Matches: 255
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.98% Indels: 0
DB: 6 Gaps: 0

US-09-593-793A-113 (1-553) x AR112295 (1-2152)

Qy 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAsp 318
Db 2 GGGCTGTACACAGGGCGTCCAGAGCTGAGCGGGACCGGAGCGGAGACATATGAT 61
Qy 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGCGGTTCGGATGGGCGCTGGGCTGTCTCGAGTGGCCATCTCCTCGTCTTC 121
Qy 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGTGTCATGACCGCGTGTGCAGGATTCGGCATCTCGACAGTCTATTGGCCAGT 181
Qy 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal 378
Db 182 GTGGCAGCTTTCCCTGTGGCTGCGGGTGCCACATGCTGTCCACAGTGTGGCGGTGGTG 241
Qy 379 ThrAlaSerAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 242 ACAGCTTCAGCGCGCCCTACCGGGTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACA 301
Qy 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 302 CTGGCCCTCCCTCTACACCGGGAGAGCAGAGTGTCTCTGCCCAATACCGAGGGGACACT 361
Qy 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 362 GGAGGTGCTAGCAGTGAGGACAGCTGATGACCAAGCTTCTCTGCCAGGCCCTTAAGCCTTGA 421
Qy 439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProPro 458
Db 422 GCTCCCTTCCCTTAATGACACAGTGGGTGCTGGAGGCGATGGCTGCTCCCACTCCACCC 481
Qy 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
Db 482 CGCGCTCGGGGGCTCTGCGCTGTGTGTCTCCGTACGTGTGGTGGGGGAGCCCAACC 541
Qy 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 542 GAGGCCAGGGTGGTTCGGGGCGGGGATCTGCGCTGGACCTCGGCATCTCGATAGTGC 601
Qy 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnSerGln 518
Db 602 TTCCTGTGTCACAGGTGGCCCCATCCCTGTTATTGGGCTCCATTTGCCAGCTCAGCCAG 661

Qy 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 662 TCTGTCACTGCCTATATGTTCTGCCGAGCGCTGGTCTGGTGCCTATTACTTTGCT 721
Qy 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 722 ACACAGGTAGTATTGTACAAGAGCGACTTGGCCAATACTCAGCG 766
RESULT 28
LOCUS AR112294 AR112294 2143 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 15 from patent US 6130043.
ACCESSION AR112294
VERSION AR112294.1 GI:14092194
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2143)
AUTHORS Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N.,
Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D.,
Roberts-Rapp,L., Russell,J.C., Strope,S.D. and Yu,H.
TITLE Reagents and methods useful for detecting diseases of the prostate
JOURNAL Patent: US 6130043-A 15 10-OCT-2000;
FEATURES Location/Qualifiers

1. 2143
SOURCE
BASE COUNT 418 a 621 c 563 g 541 t
ORIGIN /organism="unknown"

Alignment Scores:
Pred. No.: 3,42e-74 Length: 2143
Score: 1270.00 Matches: 252
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.39% Indels: 0
DB: 6 Gaps: 0

US-09-593-793A-113 (1-553) x AR112294 (1-2143)

Qy 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal 321
Db 3 CAGGGCGTGCACAGCTGAGCGGGACCGGAGCGGAGACACTATGATGAAGCGCTT 62
Qy 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
Db 63 CGGATGGCAGCGTGGGCTGTCTCTCGAGTGGCCATCTCCCTGGTCTTCTCTGCTC 122
Qy 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
Db 123 ATGGACCGGCTGGTGCAGCGATTGGCAGTCTATTTGGCCAGTGTGGCAGCT 182
Qy 362 PheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSer 381
Db 183 TTCCTGTGGTGGCGGTGCCACATGCTGTGCCACAGTGTGGCGTGGTGACAGTTCA 242
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Db 243 GCCGCCCTCACCGGGTTACCTTCTAGCCCTGCAGATCTTGGCCCTACACACTGGCCCTCC 302
Qy 402 LeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAla 421
Db 303 CTCCTACACCGGGAGAGCAGCGTGTCTTCTGCCCAATACCGAGGGGACACTGGAGTGTCT 362
Qy 422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
Db 363 AGCAGTGAGGACAGCTGATGACCAAGCTTCTTCCAGGCCCTTAAGCCTGGAGCTCCCTTC 422
Qy 442 ProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeuCys 461
Db 423 CCTAATGGACACGGTGGTGTGGAGGCGAGTGGCTGCCCTCCACCTCCACCGCGCTTCG 482
Qy 462 GlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAlaArg 481

Db 483 GGGGCTCTGCGTGTGATGCTCTCCGTAGCTGTGGTGGGTGAGCCACCGAGGCCAGG 542
Qy 482 ValValProGlyArgGlyLeuCysLeuAspLeuAlaLeuLeuAspSerAlaPheLeuLeu 501
Db 543 GTGGTTCGGGGCGGGGATCTGCTGACCTGCGCATCTCCGTGATGAGTGCCTTCTGCTG 602
Qy 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521
Db 603 TCCAGGTGGCCCATCCCTGTTATGGCTCCATTGTCCAGCTCAGCCAGTCTGCTACT 662
Qy 522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaLeuTyrPheAlaThrGlnVal 541
Db 663 GCCTATATGGTGTCTGCGCGAGGCTGGTGTGTCGCGCATTTACTTTGCTACACAGTA 722
Qy 542 ValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 723 GTATTGTGACAGAGCGACTTGCCCAATACTCAGCG 758
RESULT 29
HSM804244 2477 bp mRNA linear PRI 10-JUL-2002
LOCUS Homo sapiens mRNA; cDNA DKEZp666D0110 (from clone DKEZp666D0110).
DEFINITION AL832933
ACCESSION AL832933.1 GI:21733520
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 2477)
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2002) 1. D-85764 Neuberberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKEZp666D0110) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/
FEATURES
source
1. .2477
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/tissue_type="stomach"
/clone_lib="666 (synonym: hsto2). vector pSport1; host
DH10B; sites NotI + SalI"
/dev_stage="adult"
polyA_signal 2425..2430
polyA_site 2447
BASE COUNT 505 a 713 c 634 g 625 t
ORIGIN
Alignment Scores:
Pred. No.: 3.28e-68 Length: 2477
Score: 1179.50 Matches: 258
Percent Similarity: 78.47% Conservative: 8
Best Local Similarity: 76.11% Mismatches: 29
Query Match: 41.23% Indels: 45
DB: 9 Gaps: 5
US-09-593-793A-113 (1-553) x HSM804244 (1-2477)
Qy 228 ProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArg 247
Db 142 CCTGGTTCACGGCGAGTGGCCCTCTCG-TCGCCACAGCAGCTTCCAAATAATCTCACC 200
Qy 248 LeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMet 267

Db 201 AGCGCTTTCAG-|||||:-CTCAGCGCT 221
Qy 268 ProArgThrLeuArgArg-LeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetTh 287
Db 222 CCTAGAAGCGTCTTGAAGCCTA-|||||:-TGCCAGCAGTGTCTTTGT 260
Qy 287 rPheThrLeu-|||||:-PheTyrThrAspPh 295
Db 261 GTTCCCTCTCACCCCGCTGTCTCTCACAGCTGAGACTCCACGAAACCTTCAGACTACCTT 320
Qy 295 eValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgAr 315
Db 321 CQTC-|||:-GCCTTCAGCAAGG-|||:-GCCTTGC 347
Qy 315 gHisTyrAspGluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSe 335
Db 348 CACATCTCTCTGCTGTCATGGACCGCTGTGTCAGCGATTTCGCGACTCGAGCAGTCTA 467
Qy 335 rLeuValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTy 355
Db 408 CCTGGTCTTCTCTCTGCTCATGGACCGCTGTGTCAGCGATTTCGCGACTCGAGCAGTCTA 467
Qy 355 rLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerVa 375
Db 468 TTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCCTGTCCACAGTGT 527
Qy 375 lAlaValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLe 395
Db 528 GGCCGTGTGTGACAGCTTCAGCCGCCCTCAGCGGGTTCACCTTCTCAGCCCTCAGCATCCT 587
Qy 395 uProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrAr 415
Db 588 GCCCTACACACTGGCTCCCTCTACCCCGGAGAGCAGGTGTCTCTGCCCAATACCG 647
Qy 415 gGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyPr 435
Db 648 AGGGACACTGGAGGTGTAGCAGTGAGGACAGCCCTGTATGACAGCTTCTCTGCCAGGCC 707
Qy 435 oLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuPr 455
Db 708 TAAGCTGGAGTCTCTCTCCCTTAATGACACGTGGGTGCTGGAGCAGTGGCTCTCTCC 767
Qy 455 oProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValAlaI 475
Db 768 ACCTCCACCGCGCTCTCGGGGGCTCTGCCTGTGATGCTCCGTACGTGTGGTGGG 827
Qy 475 yGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLe 495
Db 828 TGAGCCACCGAGGCGGTTCCGGGGCGGGGCGATCTGCCTGGACCTCGCCATCCT 887
Qy 495 uAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValI 515
Db 888 GGATAGTGCCTTCTCTGCTGTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTGTCCA 947
Qy 515 nLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaI 535
Db 948 GCTCAGCCAGTCTGTCACTGCCATATATGTTGTCGCCGAGGCCCTGGGTCTGGTGGCAT 1007
Qy 535 eTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1008 TTACTTGTCTACACAGTAGTAGTATTGTGACAAGAGCGACTTGGCCAAATACTCAGCG 1062
RESULT 30
AXI06229 789 bp DNA linear PAT 30-APR-2001
LOCUS AXI06229
DEFINITION Sequence 10 from Patent WO0125272.
ACCESSION AXI06229
VERSION AXI06229.1 GI:13921915
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 789)
AUTHORS Xu, J., Skeiky, Y.A., Reed, S.G. and Cheever, M.A.
TITLE Compositions and methods for therapy and diagnosis of prostate cancer

JOURNAL Patent: WO 0125272-A 10 12-APR-2001;

FEATURES CORIXA CORPORATION (US)
Location/Qualifiers

source

1. .789

/organism="Homo sapiens"

/db_xref="taxon:9606"

misc_feature /note="n = A,T,C or G"

BASE COUNT 122 a 250 c 221 g 182 t 14 others

ORIGIN

Alignment Scores:
Pred. No.: 1.04e-51 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 6 Gaps: 0

US-09-593-793A-113 (1-553) x AX106229 (1-789)

QY 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCTATWTGGCCAGCTGTGGCAGCTTCCCTGTGGCTGCCGTGCCATGCTGTGCCAC 62
QY 374 SerValAlaValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGCCGTGGTGACAGCTTTCAGCCGCCCTCACCCGGTTACCTTCTCAGCCCTGCAG 122
QY 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGlnLysGlnValPheLeuProLys 413
Db 123 ATCTGCGCTACACACTGGCTCCCTTACCACCCGGGAGAGCAGGTGTCTCCTGCCCAAA 182
QY 414 TyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
Db 183 TACCGAGGGGACACTGGAGGTGTAGCAGTGAGGACACGCTGTATGACAGCTTCTGCCA 242
QY 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeu 453
Db 243 GGCCCTAAGCCTGGAGCTCCCTTCCCTTAATGGACACGTGGGTCTGGAGGAGTGGCTG 302
QY 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
Db 303 CTCCACCTCCACCCGGCTCTGGGGGGCTCTGCCGTGTATGTCTCCGTACGTGTGTG 362
QY 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 493
Db 363 GTGGGTGAGCCACCGAGGAGGTGTTCGGGGCCGGGCATCTGCCGTGACCTGCC 422
QY 494 IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
Db 423 ATCTGTGATGATGC-TTCCCTGTCTCCANGTGGCCCATCCCTGTTTATGGGCTCCATT 481
QY 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuVal 533
Db 482 GTCCAGCTACGCCAGTGTCTACCTGCCTATATGTTGTCTGCCGAGGCTGGGTCTGGTG 541
QY 534 AlaTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 542 CC-ATTTACTTGTACACAGGTANTATTGACAAAGAACGANTTGGCCAAATACTCAGCG 600

RESULT 31

AX140520

LOCUS AX140520 789 bp DNA linear PAT 31-MAY-2001

DEFINITION Sequence 10 from Patent WO0134802.

ACCESSION AX140520

VERSION AX140520.1 GI:14280638

KEYWORDS

SOURCE

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
1 (bases 1 to 789)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Retter, M.W., Stolk, J.A., Day, C.H.,
Skeiky, Y.A. and Wang, A.

TITLE Compositions and methods for the therapy and diagnosis of prostate cancer

JOURNAL Patent: WO 0134802-A 10 17-MAY-2001;

FEATURES CORIXA CORPORATION (US)
Location/Qualifiers

source

1. .789

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 122 a 250 c 221 g 182 t 14 others

ORIGIN

Alignment Scores:
Pred. No.: 1.04e-51 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 6 Gaps: 0

US-09-593-793A-113 (1-553) x AX140520 (1-789)

QY 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCTATWTGGCCAGCTGTGGCAGCTTCCCTGTGGCTGCCGTGCCATGCTGTGCCAC 62
QY 374 SerValAlaValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGCCGTGGTGACAGCTTTCAGCCGCCCTCACCCGGTTACCTTCTCAGCCCTGCAG 122
QY 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGlnLysGlnValPheLeuProLys 413
Db 123 ATCTGCGCTACACACTGGCTCCCTTACCACCCGGGAGAGGAGGTGTCTCCTGCCCAAA 182
QY 414 TyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
Db 183 TACCGAGGGGACACTGGAGGTGTAGCAGTGAGGACACGCTGTATGACAGCTTCTGCCA 242
QY 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeu 453
Db 243 GGCCCTAAGCCTGGAGCTCCCTTCCCTTAATGGACACGTGGGTCTGGAGGAGTGGCTG 302
QY 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
Db 303 CTCCACCTCCACCCGGCTCTGGGGGGCTCTGCCGTGTATGTCTCCGTACGTGTGTG 362
QY 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 493
Db 363 GTGGGTGAGCCACCGAGGAGGTGTTCGGGGCCGGGCATCTGCCGTGACCTGCC 422
QY 494 IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
Db 423 ATCTGTGATGATGC-TTCCCTGTCTCCANGTGGCCCATCCCTGTTTATGGGCTCCATT 481
QY 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuVal 533
Db 482 GTCCAGCTACGCCAGTGTCTACCTGCCTATATGTTGTCTGCCGAGGCTGGGTCTGGTG 541
QY 534 AlaTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 542 CC-ATTTACTTGTACACAGGTANTATTGACAAAGAACGANTTGGCCAAATACTCAGCG 600

RESULT 32

AX200380

LOCUS AX200380 789 bp DNA linear PAT 29-AUG-2001

DEFINITION Sequence 10 from Patent WO0151633.

ACCESSION AX200380
VERSION AX200380.1 GI:15390176
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 10 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..789
Location/Qualifiers
BASE COUNT 122 a 250 c 221 g 182 t 14 others
ORIGIN
Alignment Scores:
Pred. No.: 1.04e-51 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 6 Gaps: 0
US-09-593-793A-113 (1-553) x AX200380 (1-789)
Qy 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCTATNTGGCCAGTGGCAGCTTCCCTGTGGGTGCGGTGCACATGCTGTCCAC 62
Qy 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGGCGGTGGTGCACAGCTTCAGCCGCTCAGCGGTTCCACCTTCAGCCCTGCAG 122
Qy 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
Db 123 ATCTGTCCTACACTGGCTTCCCTTACACCGGGAGAGCAGGTGTCTTCCGCCCAA 182
Qy 414 TyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
Db 183 TACCGAGGGACACTGGAGGTCTAGCAGTGGAGACGCTGATGACAGCTTCCTGCCA 242
Qy 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeu 453
Db 243 GGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGAGTGGCCTG 302
Qy 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
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Qy 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 493
Db 363 GTGGGTGAGCCACCGANGCCAGGGTGGTTCGCGGCGGGGCATCTGCTGGACTCGCC 422
Qy 494 IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
Db 482 GTCCAGCTCAGCCAGTCTGTCTACCTGATATGGTGTCTGCGGAGGCGCTGGGTCTGTC 541
Qy 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuVal 533
Db 423 ATCTCTGGATAGTGC-TTCCCTGTGTCCANGTGGCCCATCCCTCTTATGGGTCCATT 481
Qy 534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 542 CC-ATTACTTTGCTACACAGGTANTATTTCACAGACAGTNTGGCCAAATACTACGG 600
RESULT 33

AX267036
LOCUS AX267036 789 bp
DEFINITION Sequence 10 from Patent WO0173032.
ACCESSION AX267036
VERSION AX267036.1 GI:16515821
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 10 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..789
Location/Qualifiers
BASE COUNT 122 a 250 c 221 g 182 t 14 others
ORIGIN
Alignment Scores:
Pred. No.: 1.04e-51 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 6 Gaps: 0
US-09-593-793A-113 (1-553) x AX267036 (1-789)
Qy 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCTATNTGGCCAGTGGCAGCTTCCCTGTGGGTGCGGTGCACATGCTGTCCAC 62
Qy 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGGCGGTGGTGCACAGCTTCAGCCGCTCAGCGGTTCCACCTTCAGCCCTGCAG 122
Qy 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
Db 123 ATCTGTCCTACACTGGCTTCCCTTACACCGGGAGAGCAGGTGTCTTCCGCCCAA 182
Qy 414 TyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
Db 183 TACCGAGGGACACTGGAGGTCTAGCAGTGGAGACGCTGATGACAGCTTCCTGCCA 242
Qy 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeu 453
Db 243 GGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGAGTGGCCTG 302
Qy 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
Db 303 CTCCACCTCCACCGCGCTCTGCGGGGCTCTGCTGTGATGTCTCCGTACGTGTGGTG 362
Qy 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 493
Db 363 GTGGGTGAGCCACCGANGCCAGGGTGGTTCGCGGCGGGGCATCTGCTGGACTCGCC 422
Qy 494 IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
Db 423 ATCTCTGGATAGTGC-TTCCCTGTGTCCANGTGGCCCATCCCTCTTATGGGTCCATT 481
Qy 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuVal 533
Db 482 GTCCAGCTCAGCCAGTCTGTCTACCTGATATGGTGTCTGCGGAGGCGCTGGGTCTGTC 541
Qy 534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553

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Db      542 CC-ATTACTTGTACACAGGTANTATTTCACAGAAGCAGTTCGCCAAATCTACTACGG 600
RESULT 34
AC126523/C
LOCUS   AC126523              198037 bp    DNA        linear    HTG 14-JUL-2002
DEFINITION
Rattus norvegicus clone CH230-65F14, *** SEQUENCING IN PROGRESS
***, 65 unordered pieces.
ACCESSION
AC126523.1 GI:21700488
VERSION  HTG: HTGS_PHASE1.
KEYWORDS
Norway rat.
SOURCE  Rattus norvegicus
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
        Rattus.
REFERENCE
1 (bases 1 to 198037)
  Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
  Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayale,M., Banks,T.,
  Barbara,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
  Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
  Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
  Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
  Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
  Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
  Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
  Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinch,H.H.,
  Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
  Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
  Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
  Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
  Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
  Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
  Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B.E.,
  Homsif,F., Howard,S., Huber,J., Huiy,K.S., Hume,J., Jackson,L.E.,
  Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
  Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
  Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
  Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulsegad,H.,
  Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
  Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
  Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
  Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
  Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
  Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
  Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
  Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
  Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G.,
  Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
  Sodergren,E., Sonaika,T., Sparks,A., Stanley,H., Stone,H.,
  Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
  Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
  Usman,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,
  Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
  Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
  Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
  Weinstein,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 198037)
  Worley,K.C.
Direct Submission
Submitted (06-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 198037)
  Worley,K.C.
Direct Submission
Submitted (14-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine

```

Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GKBQ
Center clone name: CH230-65F14
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 149884 bases at least Q40
Consensus quality: 159599 bases at least Q30
Consensus quality: 166549 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: this is a 'working draft' sequence. It currently
* consists of 65 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1063: contig of 1063 bp in length
* 1064: gap of unknown length
* 1163: gap of unknown length
* 1164: contig of 1162 bp in length
* 2326: gap of unknown length
* 2425: gap of unknown length
* 2426: contig of 1131 bp in length
* 3557: gap of unknown length
* 3657: gap of unknown length
* 4752: contig of 1096 bp in length
* 4753: gap of unknown length
* 4853: gap of unknown length
* 5972: contig of 1120 bp in length
* 5973: gap of unknown length
* 6072: gap of unknown length
* 7818: contig of 1746 bp in length
* 7819: gap of unknown length
* 9266: contig of 1348 bp in length
* 9267: gap of unknown length
* 9367: gap of unknown length
* 10614: contig of 1248 bp in length
* 10715: gap of unknown length
* 10716: gap of unknown length
* 12014: contig of 1200 bp in length
* 11915: gap of unknown length
* 12015: gap of unknown length
* 14075: contig of 2061 bp in length
* 14076: gap of unknown length
* 14176: gap of unknown length
* 15601: contig of 1426 bp in length
* 15701: gap of unknown length
* 15702: gap of unknown length
* 17277: contig of 1576 bp in length
* 17278: gap of unknown length
* 17378: gap of unknown length
* 18658: gap of unknown length
* 18659: gap of unknown length
* 18758: gap of unknown length
* 20393: gap of unknown length
* 20492: gap of unknown length
* 20493: gap of unknown length
* 21642: contig of 1149 bp in length
* 21643: gap of unknown length
* 23412: contig of 1671 bp in length
* 23413: gap of unknown length
* 23512: gap of unknown length
* 25087: contig of 1575 bp in length
* 25088: gap of unknown length
* 25188: gap of unknown length
* 26859: contig of 1672 bp in length
* 26860: gap of unknown length
* 26959: gap of unknown length
* 28690: contig of 1739 bp in length
* 28699: gap of unknown length
* 28799: gap of unknown length
* 30717: contig of 1918 bp in length
* 30817: gap of unknown length
* 32509: contig of 1693 bp in length
* 32609: gap of unknown length
* 32610: contig of 1611 bp in length
* 34221: gap of unknown length
* 34320: gap of unknown length
* 34321: contig of 1240 bp in length
* 35561: gap of unknown length
* 35661: gap of unknown length
* 37669: contig of 2108 bp in length
* 37669: gap of unknown length
* 37869: contig of 1694 bp in length

* 39563	39662: gap of	unknown	length
* 39663	41676: contig of 2014	bp	in length
* 41677	41776: gap of	unknown	length
* 43658	43658: contig of 1882	bp	in length
* 43659	43758: gap of	unknown	length
* 43759	45824: contig of 1866	bp	in length
* 45725	45724: gap of	unknown	length
* 45725	48100: contig of 2376	bp	in length
* 48101	48200: gap of	unknown	length
* 48201	50489: contig of 2289	bp	in length
* 50490	50589: gap of	unknown	length
* 50590	52329: contig of 1740	bp	in length
* 52330	52429: gap of	unknown	length
* 52430	54544: contig of 2115	bp	in length
* 54545	54644: gap of	unknown	length
* 54645	56752: contig of 2108	bp	in length
* 56753	56852: gap of	unknown	length
* 56853	58339: contig of 1787	bp	in length
* 58640	58739: gap of	unknown	length
* 58740	60931: contig of 2192	bp	in length
* 60932	61031: gap of	unknown	length
* 61032	63481: contig of 2450	bp	in length
* 63482	63581: gap of	unknown	length
* 63582	66000: contig of 2419	bp	in length
* 66001	66100: gap of	unknown	length
* 66101	68760: contig of 2660	bp	in length
* 68761	68860: gap of	unknown	length
* 68861	71024: contig of 2164	bp	in length
* 71025	71124: gap of	unknown	length
* 71125	73169: contig of 2045	bp	in length
* 73170	73269: gap of	unknown	length
* 73270	76108: contig of 2839	bp	in length
* 76209	76208: gap of	unknown	length
* 76209	79687: contig of 3479	bp	in length
* 76688	79787: gap of	unknown	length
* 79788	82504: contig of 2717	bp	in length
* 82505	82604: gap of	unknown	length
* 82605	86873: contig of 4269	bp	in length
* 86874	86973: gap of	unknown	length
* 86974	91613: contig of 4640	bp	in length
* 91614	91713: gap of	unknown	length
* 91714	94992: contig of 3279	bp	in length
* 94993	95092: gap of	unknown	length
* 95093	97134: contig of 2042	bp	in length
* 97135	97234: gap of	unknown	length
* 97235	100423: contig of 3189	bp	in length
* 100424	100523: gap of	unknown	length
* 100524	104682: contig of 4159	bp	in length
* 104683	104782: gap of	unknown	length
* 104783	108313: contig of 3531	bp	in length
* 108314	108413: gap of	unknown	length
* 108414	113868: contig of 5455	bp	in length
* 113869	113968: gap of	unknown	length
* 113969	117789: contig of 3821	bp	in length
* 117790	117889: gap of	unknown	length
* 117890	120979: contig of 3090	bp	in length
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* 121080	123743: contig of 2664	bp	in length
* 123744	123843: gap of	unknown	length

Alignment Scores:

Pred. No.:	4.33e-33	Length:	198037
Score:	673.00	Matches:	208
Percent Similarity:	48.30%	Conservative:	34
Best Local Similarity:	41.52%	Mismatches:	147
Query Match:	23.52%	Indels:	113
DB:	2	Gaps:	17

US-09-593-793A-113 (1-553) x AC126523 (1-198037)

Qy 78 Trp---ArgGlyArgTyrGlyArgArg-----ArgProPhe 88

Db 60312 TGGCACAGGACGATATGGGCTGAGGCGCTTCTGTGCTTTCAGTTAGACACCCCGAGGC 60253

Qy	89	IleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrp	108
Db	60252	CGCTGGGGCTTGGGGTTGGGGTTGGGGTTG-----GGGTG	60217
Qy	109	LeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuLeuGly	128
Db	60216	TTCTCTAGTCTCAGGCGCTACAGGAAGAACTGAAAAATTTCA-----GGG	60169
Qy	129	ValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSer	148
Db	60168	TCAGGC-----AGCTGGGCTGCAGAGGTCCACAAAAA	60136
Qy	149	AspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIle	168
Db	60135	GATCTTCTGCTGCTCTCCCTTTTGACGGCCCAATTAC-----TGG	60094
Qy	169	SerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeu	188
Db	60093	GCTCTCCCTGGCAGAGGCCAAGCAGTCATCTCAGATGGTTTCTTCAGTCAGG	60034
Qy	189	Ala---ProTyrLeuGlyThrGln-GluGluCysLeuPheGlyLeuLeu-ThrLeuIleP	207
Db	60033	TCTGGACCTATAGGGGCGACAGTGAAGATCTATGAGAGGTCTCTCCCTATGGCCC	59974
Qy	207	he---LeuThrCysValAlaAlaThrLeuLeuValAlaGluAlaAlaLeuGlyProT	226
Db	59973	AGTGAAGAAAGTGTGTCAGGGGGTGTAGTCTGTCTGGAA-----	59930
Qy	226	hrGluProAlaGluGlyLeuSerAlaProSerLeuSer-----ProHisCysCysP	243
Db	59929	-----CTGGAGACCTTGCAATGCCCTCTTTTGGCACCCGCCCTCTCTGTGTCT	59878
Qy	243	roCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnL	263
Db	59877	CGCTTCTGTCTGTTCTACTCTTCTCTTCTTCTAGAGAGGTTCGCGCACTTTCTCAAC	59818
Qy	263	euCysCysArgMet-----ProArgThrLeuArgArgLeuPheV	276
Db	59817	C-TGTGGATTATGTGACTGACTTCTTATATATCTAGAGAAAGCTAGAACTTCA	59759
Qy	276	alAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheV	296
Db	59758	GGCTTCAAATTTGCTCCTTT-----	59739
Qy	296	alGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgH	316
Db	59738	-----CCTCCACCATGTTGAGGGGGG	59717
Qy	316	IsTyrAspGluGly---ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleS	335
Db	59716	AGCTGGGGGGGCTGAGGGAGGGGGTCTGTAGATCCACATCAAGTAGCCTTTCC	59657
Qy	335	erLeuValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValT	355
Db	59656	TCTTAGGTTT-----	59646
Qy	355	yrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeu---SerHis	374
Db	59645	-----GGATTTTCTTTTCCCTGAAAGCCAGTTGCCCTGTTTCATATA	59603
Qy	374	erValAlaValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnI	394
Db	59602	GCCTTGGTTAGGGCAGTGAAGGCCCTTCTGCATCCCGGAACCCCTGCATCTGAA-	59544
Qy	394	leLeuProTyrThr---LeuAlaSerLeuTyrHisArgGluGlyGlnValPheLeuProL	413
Db	59543	-----TACACACACCTTTGTTTCTTTTGTCCCCCACCCTCAGGTGTCTGCTGCCA	59492
Qy	413	ysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuP	433
Db	59491	AATACCGAGGGGACGCTGGAGGTGTAGCAGTGAAGACAGCAACACACCTTCTTCG	59432


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QY 433 roGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyL 453
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Db 59431 TAGGCCCTAAGCAGGAGCTCCCTTCCCAATGACACGCTGGCCCTGGCGCAGCAGCA 59372
QY 453 euLeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValV 473
::||| |||||
Db 59371 TCCTGGTGGCCCACTGCACCTCTGCGGCGCTCTGCCTGTGTATGCTCATCGAGTGG 59312
QY 473 alValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuA 493
|||||
Db 59311 TAGTGGGTGAGCCACTGAAGCAGAGTGTGTACTGGAGGGGCATTTGCCCTGGACCTTG 59252
QY 493 laileLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerI 513
|||||
Db 59251 CCATCCTGGACAGTGCCTTTCTGCTGTCCAGGTGGCTCCGTCCTGTTCATGGGCTCCA 59192
QY 513 leValGlnSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuV 533
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Db 59191 TTGTCCAGCTGAGCCACTGTGTCACTGGCTATATGTATGATCACTGACGCTTGGGTCTGG 59132
QY 533 alAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSer 552
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Db 59131 TCGCCATTACTTTGCTACACAGGTAGTGTTCACAAGANTGACTTGGCCAAATACTCA 59073

RESULT 35
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LOCUS Mus musculus, clone IMAGE:4984191, mRNA, partial cds.
DEFINITION BC024519
ACCESSION BC024519.1 GI:19353990
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

REMARK
COMMENT
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: gcapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shqc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAP Plate: 59 Row: p Column: 15
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.
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/note="Vector: pCMV-SPORT6"
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CDS

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FFPSALVILICFTIHLCSIPAPLRDAATPPSQDPPQSSLSASGMHEYSGIERVKN
GGADTEOPWENKPKPSQSORTSMKSLRLALNMPSHYRCLCVSHLIGWATFLSN
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REEKEKQGEAPGGPDNQRGVDFCAALTCMVLAQLILVGGGLFLVNMAGSVVVVV
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BASE COUNT 467 a 485 c 502 g 530 t 2 others
ORIGIN

Alignment Scores:

Pred. No.: 3,28e-23 Length: 1986
Score: 489.50 Matches: 146
Percent Similarity: 41.25% Conservative: 85
Best Local Similarity: 26.07% Mismatches: 228
Query Match: 17.11% Indels: 101
DB: 10 Gaps: 12

US-09-593-793A-113 (1-553) x AF360357 (1-1986)

QY 17 GlnLeuLeuValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIle 36
Db 104 AGCTTGTGTCATGCACAGCATGGCCATGTTGGCCGAGAGTTTGGCTATCGGTGGAGGCA 163
QY 37 ThrTyrValProLeuLeuLeuGluValGlyValGluLysPheMetThrMetVal 56
Db 164 GCATTGTGACTCCAGTCTGCTCAGCGTGGGCGTCCCTAAGAGCCGTGTACAGCATGGTG 223
QY 57 LeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAsp 76
Db 224 TGCCCTCCTAAGCCCATCTGGGATTCCTGCTCCAGCCCTGTGGTGGGATCAGCCAGTGT 283
QY 77 HisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIle 96
Db 284 CACTGCAGGCCCGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGT 343
QY 97 LeuLeuSerLeuPheLeuLeuProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAsp 116
Db 344 CTCTTGGGAATGCTCTGTACCTCAATGAGATGCGGTGCTATCAGCTTTGGTGTCTAAC 403
QY 117 ProArgPro-----LeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAsp 133
Db 404 CCAAGGCAGAGCGTATCTGGGCCCATTAAGCATCACATGGTAGGTGTCTCTTCGAT 463
QY 134 PheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAsp 153
Db 464 TTTTCTGCTGACTTATTGACGGGCCCATCAAGCCCTACTATTGATGTCGTGCTCCAC 523
QY 154 ProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyCys 173
Db 524 CAGGACAAG---GAGAAGGGCCCTCCACTACCATGCGCTTTCACAGGTTTGGAGGTGCC 580
QY 174 LeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGly 193
Db 581 CTGGGTACATTTTGGGTGCCATAGACTGGGTGCACTAGATCTGGGAAGGCTGTGGGC 640
QY 194 ThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAla 213
Db 641 ACAGAAATCCAGGTGATGTTCTTCTCTGCGCGGTGTTCTCATCTGTGCTTCATCACA 700
QY 214 ThrLeuLeuValAlaGluAlaAlaLeu-----GlyProThrGluPro----- 228
Db 701 CACCTGTGAGTATCCCTGAAGCTCCAGATGCTGCAACTGACCTCCCTCCCTCACAG 760
QY 229 -----AlaGluGlyLeuSerAlaProSerLeuSerProLisCysCysProCys 244
Db 244

Db 761 CAGGACCCCTCAGGGCTCGCTGCTGTCAGCCAGTGGGATGCATGAATAC----- 808
QY 245 ArgAlaArgLeuAlaPheArgAsnLeuGlyAla----- 255
Db 809 GGTTCATTATTCAGAAAGCTTAAAAATGAGGTGTCAGACACAGACAGCAGCAGTACAGGAATGG 868
QY 256 -----LeuLeuProArgLeuHisGln 262
Db 869 AAAAAACAAAAGCCTTCTGCCAGAGTCAGAGGACAATGTCGATGAAGTCACTCTCTCGG 928
QY 263 LeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrp 282
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Db 989 ACTGCCCTTCTGTCACCAACATGCTCTCTTCACAGATTTTCAGGACAGATGTTATACCAT 1048
QY 303 GlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyValArg 322
Db 1049 GGGGATCCCTACGGTGCACACAACTCCACGGAGTTCTTCATCTATCAAAAGAGGATTTGAG 1108
QY 323 MetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMet 342
Db 1109 GTCGGATGTTGGGCTTGGCATCAACTCTGTGTTTCTCAGTTTATTACTACTTCTCAG 1168
QY 343 AspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPhe 362
Db 1169 AAAGCTATGCTCTCTACATTTGATTTAAAGGCCCTTATTTTCATGGGATATTTGCTCTTT 1228
QY 363 ProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAla 382
Db 1229 GGCCTGGGAACAGGATTCATAGGACTCTTCCAAATGTCTACTCTCTGTCCTCTGT 1288
QY 383 AlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeu 402
Db 1289 TCTATGTTGGTGAATATCCAGACATTTGTACACTGTGCTCCCTTTAACCTCATGCTGAG 1348
QY 403 TyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSer 422
Db 1349 TACCACCGTGAAGAGAG-----AAAGAGAAGGCGCAGGAAGCG----- 1387
QY 423 SerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProphePro 442
Db 1388 -----CCAGGAGGCCCTGACAAC 1405
QY 443 AsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProAlaLeuCysGly 462
Db 1406 CAGGGGAGA-----GGCAAAAGCGTG-----GACTCGCGT 1435
QY 463 AlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAlaArgVal 482
Db 1436 GCTCTCACCTGGATGTCAGCTG-----GCTCAGATC 1468
QY 483 ValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuSer 502
Db 1469 TGGTGGAGGTGGC----- 1483
QY 503 GlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAla 522
Db 1484 -----CTGGGCTTCCCTGGTCAACATGGCTGGGAGTGGCTGCTG 1522
QY 523 TyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValVal 542
Db 1523 GTGGTGCATCAGCGTCTCGCGTCCCTGATAGGCTGTTGCTTTGGCGGCTCTTCGTA 1582
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LOCUS Mus musculus membrane-spanning transport protein 1 (Mstpl) mRNA,
DEFINITION complete cds.
ACCESSION AY034377
VERSION AY034377.1 GI:18252805

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QY 263 LeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerThr 282
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QY 283 MetAlaLeuMetThrPheThrAspPheValGlyGluGlyLeuTyrGln 302
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QY 303 GlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGlyValArg 322
Db 1062 GGGGATCCCTACGTCACACAACTCCACGGAGTTTCTCATCTATGAAAGAGAGTTGAG 1121
QY 323 MetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMet 342
Db 1122 GTCGGATGTTGGGGCTTGTGCATCACTCTGTGTTTCTTCTCACTTATTCATCTTTCAG 1181
QY 343 AspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPhe 362
Db 1182 AAAGCTATGCTCTCATGATGATTAAGGCCCTTATTTTCATGGGATATTGCTCTTT 1241
QY 363 ProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAla 382
Db 1242 GGCTCGGAACAGGATTCATAGGACTCTTTCCAAATGTCTACTCTACTGCTCTCTGT 1301
QY 383 AlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeu 402
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QY 403 TyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSer 422
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Db 1482 TTGGTTGGAGTGGC----- 1496
QY 503 GlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAla 522
Db 1497 -----CTGGGCTTCTCGTGGTCAACATGGCTGGGAGTGTGCTGTCGTC 1535
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DEFINITION Homo sapiens AIM-1 protein mRNA, complete cds.
ACCESSION AF172849
VERSION AF172849.1 GI:5802878
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SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1650)
AUTHORS Harada,M., Li,Y.F., El-Gamil,M., Rosenberg,S.A. and Robbins,P.F.

TITLE Use of an in vitro immunoselected tumor line to identify shared melanoma antigens recognized by HLA-A*0201-restricted T cells
JOURNAL Cancer Res. 61 (3), 1089-1094, (2001)
MEDLINE 21115844
PUBMED 11221837
... REFERENCE 2 (bases 1 to 1650)
AUTHORS Harada,M. and Robbins,P.F.
TITLE Direct Submission
JOURNAL Submitted (27-JUL-1999) Surgery Branch, National Cancer Institute,
9000 Rockville Pike, Bethesda, MD 20892, USA
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Pred. No.: 3,14e-23 Length: 1650
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Query Match: 17.07% Indels: 107
DB: 9 Gaps: 12
US-09-593-793a-113 (1-553) x AF172849 (1-1650)
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Db 122 ACCAGACTCATCATGCACAGCATGGCCATG-----TTCCGA 157
QY 28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProLeuLeuLeuGluValGly 47
Db 158 AGAGAGTTCTGCTACGCGGTGGAGCGCATGTGTGACCCCATGCTGTCTACGCGTAGT 217
QY 48 ValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuLeuValCys 67
Db 218 CTGCCCCAGAGCGCTGTACAGCATGTGTGGTTCCTCAGCCCCCATCTGGGATTCCTCGTG 277
QY 68 ValProLeuLeuGlySerAlaSerAspHisTyrArgGlyArgTyrGlyArgArgPro 87
Db 278 CAGCCCGTGTGGATCGGCCAGCCACCATCTCCGCGTCCAGGTGGGCGCCGGAGACCC 337
QY 88 PheIleThrAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGly 107
Db 338 TACATCTCACCCTCGGAGTCATGATGCTGCTGGGCATGGCTCTGTACCAATGGGGCT 397
QY 108 TrpLeuAlaGlyLeuLeuCysProAspProArg-----ProLeuGluLeuAlaLeu 124
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QY 125 LeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGlu 144
Db 458 ACCATGATAGGTGTCGTTCTCTTTGATTTTGTCTGCGGACTTCTCATGTCATGGCCCA 517
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Db 575 GCCCTCTTCACAGGTTTGGAGGTGCCCTGGTTACCTTTTGGGTGCTATAGACTGGGCC 634
Qy 185 ThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPheGlyLeuLeuThr 204
Db 635 CATCTGGAGCTGGGAAGACTGTTGGGTACAGAATTCAGGTCATGTTCTTCTCTGCA 694
Qy 205 LeuIlePheLeuThrCysValAlaAlaThrIleLeuValAlaGluGluAlaLeuGly 224
Db 695 TTGGTGCTCACTTTGTTGTTTACATCTGTGTCAGTATCTCTGAAGCCCCACTT--- 751
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ACCESSION AC018319
VERSION AC018319.1 GI:6552872
KEYWORDS HTGS, PHASE2.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.
REFERENCE 1. (bases 1 to 18567)
AUTHORS Adams, M. and Venter, J.C.
TITLE Direct Submission
JOURNAL Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT This sequence was identified as CDM:10214336 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
BASE COUNT 5705 a 3897 c 3763 g 5202 t
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Alignment Scores:
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Score: 458.50 Matches: 166
Percent Similarity: 37.39% Conservative: 101
Best Local Similarity: 23.25% Mismatches: 247
Query Match: 16.03% Indels: 200
DB: 2 Gaps: 19
US-09-593-793A-113 (1-553) x AC018319 (1-18567)
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Db 14261 CGGAAGACGGGTTCGAGATGTTTCGATTGTCGCCCATGCCCATGGAATTTGCC 14320
Qy 32 LeuAlaAlaGlyIleThrTyrValProLeuLeuGluValGlyValGluGluLys 51
Db 14321 TATCGCGGGAGACGAGATTTTCGTCCTCCGATTCTCTACAGATCGGTGGATCACAAA 14380
Qy 52 PheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeu 71
Db 14381 CACATGTCCATGACCTCGGGACTGTCGCCACTGATTGTTTATGTCCTCCGCTGCTG 14440
Qy 72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAla 91
Db 14441 GGAAGTATTAGCATCTCCTCAAGCTTCGTGGGTGCGCGACGCTCCAATTATCTCGATT 14500
Qy 92 LeuSerLeuGlyIleLeuLeuSerLeuPheLeuIlePro----- 104
Db 14501 CTATCATTTGGCATAATGTGCGGTTTTCGATTCTGTTGTCGATATGCAAGGATCTGGGTCG 14560
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Qy 105 -----Arg 105
Db 14561 CTGCTGGCGATGCGGATATCTATTGCAGAGTCAGCCTTGAATTTTCACATCTTCGTGC 14620
Qy 106 AlaGlyTrpLeuAlaGlyLeuLeuCys-----ProAspProArgPro 119
Db 14621 GGGGATCTGTGGCTGTCTTTCGGGTGAAGCGACGACGAGCACTTCGCATCCGAC 14680
Qy 120 LeuGluLeuAla-----LeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
Db 14681 TATAAGTTCGCGGTGATCCTTACGATTTTGGCATGGTCTTATGGATTCGATCCGGAT 14740
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Qy 158 ArgGlnAlaIleThrValAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
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Db 15485 TCCATTTACTCGCTGCTGGTGACCAAGTTAATGAAGTGGTTTCGGGTAAAGTCGGACACATA 15544
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Db 15605 AATAGATTATAAGACAATTCAGATCTTGGTATTAAACAAATAGAGTGTTCATTTGACT 15664
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Db 15665 GTTGCAACAGTGTACGAACCTTCTAGTTGCAACTGTCAAG----- 15706
Qy 386 GlyPheThrPheSerAlaLeu----- 392
Db 15707 --TTTACCTTTAAATTCCTTAAAGACAGTACGTTTGTATTAAACCACCTGAGCTATAATAT 15763
Qy 393 -----GlnIle-LeuProTyr----- 397
Db 15764 GTTGACGCTCTCTCCAAATCGAATATCTAAAGAAATCCAAATGATTTGATATATATAT 15823
Qy 398 -----ThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys----- 413
Db 15824 GTTAACCGTGATATCTCGCTCTTTTGTAGAACCAAGCGGGTTTACATTAGTGGAAATGAT 15883
Qy 414 -TyrArgGly-----AspThrGlyGlyAlaSerSerG1 424
Db 15884 TTAATCGTATCGGAATGCTTGTCTGGCTTGTGGCCAACTAAGTGGGAGTCTTGGT 15943
Qy 424 uAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe----- 441
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INSTITUTE Drosophila BAC Library) complete sequence.
AC010022
VERSION AC010022.8 GI:21328505
KEYWORDS HTG.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 165852)
Muzny,D., Scherer,S., Adams,M.D., Holt,R.A., Evans,C.A.,
Gocayne,J.D., Tabor,P., Williamson,A., Homsi,F.H.,
Dugan-Rocha,S.D., Sodergren,E.S., Hodgson,A.H., Chen,R.C.,
Ayele,M., Scott,G.S., Worley,K.W., Amaratides,P.G., Brandon,R.C.,
Rogers,Y., An,H., Baldwin,D., Beeson,K.Y., Brown,M., Buhay,C.,
Busam,D.A., Cencer,A., Chen,G., Chen,Z., Clerc-Blankenburg,K.,
Davenport,L.B., Dietz,S.M., Ding,Y., Dodson,K., Doup,L.E.,

Draper, H., Emery-Cohen, A., Ferriera, S., Garg, N.D.S., Houck, J., Hostin, D., Howland, T.J., Hume, J., Ibegwam, C., Jalali, M., Kovar, C., Liu, W., Mattei, B., McIntosh, T.C., Morgan, M., Moly, M., Murphy, B., Nelson, K.A., Ndassa, Y., Nguyen, N., Perez, L., Pittman, G.S., Puri, V., Scheeler, F., Shen, H., Strong, R., Tector, C., Wang, Q., Williams, S.M., Xiang, J., Zaveri, J.S., Zhou, J., Zorrilla, S., Smith, H.O., Wheeler, D., Weinstein, G., Gibbs, R. and Venter, J.C.

TITLE JOURNAL

Direct Submission

Unpublished

2 (bases 1 to 165852)

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AUTHORS

Worley, K.C., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amarutunge, H.C., Are, J.R., Banks, T., Barbarta, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hoques, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaik, T., Sparks, A., Stanley, H., Stone, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wlezyk, R., Wooden, S., Worley, K., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G. and Gibbs, R.

TITLE

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AUTHORS

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JOURNAL

Submitted (11-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

4 (bases 1 to 165852)

REFERENCE

AUTHORS

Worley, K.C., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amarutunge, H.C., Are, J.R., Banks, T., Barbarta, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,

Hernandez, J., Hernandez, O., Hodgson, A., Hoques, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Rolfe, M., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaik, T., Sparks, A., Stanley, H., Stone, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wlezyk, R., Wooden, S., Worley, K., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G. and Gibbs, R.

Direct Submission

Submitted (01-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

5 (bases 1 to 165852)

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REFERENCE

QY	386	GlyPheThrPheSerAlaLeu	-----	392	Unpublished		
Db	97755	-----TTTACCTTTAAATCTCTAAAGACAGTAGCTTTGATTAAACCACCTGAGCTATAATAT	97699	2 (bases 1 to 176929)	Worley, K.C., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbarella, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulsegued, H., Lozardo, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Mar, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoohtari, N., Sison, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.	4 (bases 1 to 176929)	Submitted (05-APR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
QY	393	-----GlnIle-LeuProTyr-----	397	3 (bases 1 to 176929)	Worley, K.C., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbarella, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulsegued, H., Lozardo, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoohtari, N., Sison, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.	3 (bases 1 to 176929)	Submitted (05-APR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
QY	393	-----GlnIle-LeuProTyr-----	397	3 (bases 1 to 176929)	Worley, K.C.		
QY	393	-----GlnIle-LeuProTyr-----	397	3 (bases 1 to 176929)	Worley, K.C.		
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VERSION		AE003552.2	GI:10728030
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ORGANISM		Drosophila melanogaster.	
REFERENCE			
AUTHORS			

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QY 518 nSerValThrAlaTyMetValSerAlaLaGlyLeuGlyLeuValAlaIleTyrrPheAl 538
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complete cds.
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VERSION AF332510.1 GI:15004312
KEYWORDS
SOURCE Oryzias latipes.
ORGANISM Oryzias latipes.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE
AUTHORS Fukumachi,S., Shimada,A. and Shima,A.
TITLE Mutations in the gene encoding B, a novel transporter protein,
reduce melanin content in medaka
JOURNAL Nat. Genet. 28 (4), 381-385 (2001)
MEDLINE 21372467
PUBMED 11479596
REFERENCE
AUTHORS Fukumachi,S., Shimada,A. and Shima,A.
TITLE Direct Submission
JOURNAL Submitted (26-DEC-2000) Integrated Biosciences, University of
Tokyo, Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
FEATURES
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ORIGIN
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Score: 456.00 Matches: 144
Percent Similarity: 39.77% Conservative: 95

Best Local Similarity: 23.96% Mismatches: 198
Query Match: 15.94% Indels: 164
DB: 5 Gaps: 17
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Db 349 CGACGCTTCTCGTGGTGGCTGATCCTCCACAGTATGTTATGTTGGTGGGAGTCTCG 408
QY 32 LeuAlaAlaGlyIleThrTyrrValProProLeuLeuLeuValGlyValGluGluLys 51
Db 409 TATGCGGTGGAAGCGGCATTTGTCACACGGTCTCTCAGCGTAGGTCTCCCGCCAGT 468
QY 52 PheMetThrMetValLeuGlyIleGlyProValLeuValCysValProLeuLeu 71
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Db 529 GGCTCAGCAAGTGACTACTGCTGGTCTCTCTGGGAAGGAGGAGCCCTACATC----- 582
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QY 103 -----IleProArgAlaGlyTrpLeuAlaGlyLeuLeuCys 114
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QY 193 GlyThrGlnGluCysLeuPhe-----GlyLeuLeuThrLeu 205
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Db	1882	TTC	1884
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LOCUS			
DEFINITION			
AB075229			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			

Past-A, a new class proton-associated sugar transport facilitator in the central nervous system

Unpublished
2 (bases 1 to 2256)
Shimokawa,N.
Direct Submission
Submitted (03-DEC-2001) Noriaki Shimokawa, Gunma University School of Medicine, Physiology 1st Division; 3-39-22 Showa-machi, Maebashi, Gunma 371-8511, Japan (E-mail:simokawa@med.gunma-u.ac.jp, Tel:81-27-220-7923, Fax:81-27-220-7926)

Location/Qualifiers
1. .2256
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/tissue_type="brain"
1. .2256
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/db_xref="GI:21321124"

gene

CDS

BASE COUNT 419 a 728 c 629 g 480 t

ORIGIN

Alignment Scores:
Pred. No.: 2,62e-20 Length: 2256
Score: 446.00 Matches: 160
Percent Similarity: 33.33% Conservative: 79
Best Local Similarity: 22.32% Mismatches: 206
Query Match: 15.59% Indels: 272
DB: 10 Gaps: 15

US-09-593-793A-113 (1-553) x AB075229 (1-2256)

Qy 17 GlnLeuLeuValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIle 36
Db 256 GAGCTGCTTCAATGCTGCTTCTGTTGGAATCGAGTTCAGCTAGCCATGAGACA 315
Qy 37 ThrTyrValProLeuLeuGluValGlyValGluLysPheMetMetVal 56
Db 316 GCGTACGTGACTCAGTACTCTCGCAATGCGCTGCTGACAGCTTACAGCTAGT 375
Qy 57 LeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAsp 76
Db 376 TGGTTCATCAGCCCATCTCGGATCTTGTGCGAGCTCTGTTGGTGGCTGAGTGCAC 435
Qy 77 HisTyrArgGlyArgTyrGlyArgArgArgProPheIleTyrAlaLeuSerLeuGlyIle 96
Db 436 CGATGTACTCAAGTGTGGAAGGAGAGCGCTTTCATCTTGTCTGCGCATAGGGCG 495
Qy 97 LeuLeuSerLeuPheLeuIleProArgAlaGlyTyrTrpLeuAlaGlyLeuCysProAsp 116
Db 496 TTGCTGGCCCTCTCGCTCTCTCTCAAT---GGAAGGGACATTTGATGGCCCTGGCTGAC 552
Qy 117 Pro-----ArgProLeuGluLeuAlaLeuLeuLeuLeuValGlyValGlyLeuLeuAsp 133
Db 553 ACAGCCACCAATCAAGTGGGCGATCTCTCTGAGCGGTATCGGGGTGCTGCTGATGCAC 612

Percent Similarity: 98.81% Conservative: 0
Best Local Similarity: 98.81% Mismatches: 1
Query Match: 15.38% Indels: 0
DB: 6 Gaps: 0

US-09-593-793A-113 (1-553) x AR112282 (1-255)

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DB	2	ACAGCTTCAGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACA	61
QY	399	LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr	418
DB	62	CTGGCTCCCTCTACCAACCGGAGAGCAGGTGTTCTGCCCAATACCGAGGGGACACT	121
QY	419	GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly	438
DB	122	GGAGGTGCTAGCAGTGAGACAGCCCTGATGACACAGCTTCCTGCCAGGCCCTAAGCCTGGA	181
QY	439	AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProPro	458
DB	182	GCTCCCTTCCCTAATGGACACGTTGGGTGCTGGGANGCAGTGGCTGCTCCACCTCCACCC	241
QY	459	AlaLeuCysGly	462
DB	242	GCGCTCTGCGGG	253

Search completed: February 19, 2003, 04:49:56
Job time : 3498 secs

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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 01:25:58 ; Search time 228 Seconds
(without alignments)
5462.084 Million cell updates/sec

Title: US-09-593-793a-113
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=100 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=45
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-WARN_TIMEOUT=30 -THRAD=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2861	100.0	1662	24	Human mast cell re
2	2861	100.0	2582	24	Prostate cancer-as
3	2861	100.0	3320	24	DNA encoding human
4	2861	100.0	3410	19	Full length cDNA s
5	2861	100.0	3410	19	Prostate tumour sp
6	2861	100.0	3410	21	cDNA sequence of h
7	2861	100.0	3410	21	Human immunogenic
8	2861	100.0	3410	22	Human prostate cDN
9	2861	100.0	3410	22	Human prostate tum
10	2861	100.0	3410	22	Human prostate-spe
11	2861	100.0	3410	22	Human prostate-spe
12	2861	100.0	3410	22	Prostate tumour an
13	2861	100.0	3410	24	Human LI-12 cDNA s
14	2861	100.0	3410	24	Human breast tumou
15	2716.5	94.9	4034	22	Human prostate cDNA
16	2716.5	94.9	4034	22	P553S cDNA splice
17	2716.5	94.9	4034	24	Human P553S splice
18	2601	90.9	2133	24	Thioredoxin-ubiqui
19	2538.5	88.7	4894	22	Human prostate cDNA
20	2538.5	88.7	4894	22	P553S cDNA splice
21	2538.5	88.7	4894	24	Human P553S splice
22	2400.5	83.9	3878	22	Human secreted pro
23	2144	74.9	6976	22	Human prostate cDNA
24	2144	74.9	6976	22	P553S cDNA splice
25	2144	74.9	6976	24	Human P553S splice
26	1920.5	67.1	2904	22	Human prostate cDNA
27	1920.5	67.1	2904	22	P553S cDNA splice
28	1920.5	67.1	2904	24	Human P553S splice
29	1696	59.3	1593	24	Thioredoxin-ubiqui
30	1604	56.1	1604	24	Human mast cell re
31	1403.5	49.1	1203	22	Human /M. tubercul
32	1403.5	49.1	1203	22	Ra12-P501S-E2 cons
33	1403.5	49.1	1203	22	Ra12-P501S-E2 cons
34	1287	45.0	2133	21	Human prostate-rel
35	1287	45.0	2133	22	Prostate gene PS10
36	1287	45.0	2152	20	Consensus sequence
37	1270	44.4	2124	21	Human prostate-rel
38	1270	44.4	2124	21	Prostate gene PS10
39	1270	44.4	2143	20	Clone 1711346IH t
40	1170.5	40.9	2462	21	cDNA sequence of a
41	919	32.1	789	19	3' cDNA sequence o
42	919	32.1	789	19	3' fragment of pro
43	919	32.1	789	21	Human immunogenic
44	919	32.1	789	22	Human prostate cDN
45	919	32.1	789	22	Human prostate tum
46	919	32.1	789	22	Human prostate-spe
47	919	32.1	789	22	Human prostate-spe
48	919	32.1	789	22	Prostate tumour an
49	919	32.1	789	24	Human LI-12 3' cDN
50	829	29.0	742	21	cDNA sequence of a
51	520.5	18.2	2052	23	Drosophila melanog
52	458.5	16.0	4437	23	Drosophila melanog
53	457.5	16.0	2476	22	Human polynucleoti
54	440	15.4	255	20	PS108 gene-specifi
55	440	15.4	255	21	Human prostate-rel
56	440	15.4	255	22	Prostate gene PS10
57	423	14.8	258	20	PS108 gene-specifi
58	423	14.8	258	21	Human prostate-rel
59	423	14.8	258	22	Prostate gene PS10
60	418	14.6	247	20	PS108 gene-specifi
61	418	14.6	247	21	Human prostate-rel
62	418	14.6	247	22	Prostate gene PS10
63	357	12.5	217	20	PS108 gene-specifi
64	357	12.5	217	21	Human prostate-rel
65	357	12.5	217	22	Prostate gene PS10
66	357	12.5	1885	20	Soybean sucrose tr
67	346.5	12.1	2135	24	Glycine max sucros

68 330 11.5 1548 22 AAI68588 S. tuberosum SUT1
69 328.5 11.5 1785 22 AAI68575 A. thaliana SUT2 e
70 326.5 11.4 2375 20 AAZ23128 Rice sucrose trans
71 325.5 11.4 2030 20 AAZ23135 Wheat sucrose tran
72 323.5 11.3 1803 21 AKA2576 Arabidopsis thalia
73 317.5 11.1 1977 20 AAZ23126 Corn sucrose trans
74 313.5 11.0 1818 22 AAI68593 S. tuberosum SUT2
75 313 10.9 2083 20 AAZ23133 Wheat sucrose tran
76 307.5 10.7 1503 22 AAI68574 L. esculentum SUT4
77 307.5 10.7 1503 22 AAI68592 S. tuberosum SUT4
78 306.5 10.7 2088 20 AAZ23124 Corn sucrose trans
79 306 10.7 1628 21 AAC53258 Arabidopsis thalia
80 300 10.5 1625 21 AAC54585 Arabidopsis thalia
81 300 10.5 2160 20 AAZ23134 Wheat sucrose tran
82 294.5 10.3 1533 22 AAI68573 A. thaliana SUT4 e
83 293.5 10.3 6918 21 AAC74763 Human ORFX ORF318
84 267 9.3 958 22 AAI61169 Human polynucleoti
85 247 8.6 231 20 AAV71170 PS108 gene-specifi
86 247 8.6 231 21 AAC63195 Human prostate-rel
87 247 8.6 231 22 AAS07591 Prostate gene PS10
88 235 8.2 1041 20 AAZ23130 Soybean sucrose tr
89 219.5 7.7 510 21 AAZ45681 cDNA sequence of a
90 203 7.1 828 24 ABK93112 Human prostate spe
91 197.5 6.9 1653 20 AAZ23127 Rice sucrose trans
92 197 6.9 432 22 AAD05262 Human secreted pro
93 195.5 6.8 1355 22 AAI68576 L. esculentum SUT2
94 192 6.7 435 20 AAX40506 Human secreted pro
95 191 6.7 34980 22 AAF86431 Pyrococcus abyssi
96 184.5 6.4 1249 21 AAC49139 Arabidopsis thalia
97 169 5.9 271 24 ABK93110 Human prostate spe
98 169 5.9 1251 21 AAC33335 Arabidopsis thalia
99 162 5.7 612 24 ABK93111 Human prostate spe
100 161 5.6 307 22 ABA11517 Human nervous syst

ALIGNMENTS

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ID ABN81324 standard; cDNA; 1662 BP.
XX AC ABN81324;
XX DT 30-AUG-2002 (first entry)
XX DE Human mast cell related splice variant gene MC14 SEQ ID NO 12.
XX KW Human; mast cell; MC; antiallergic; antinflammatory; antiasthmatic;
XX KW vasotrophic; dermatological; allergy; hypersensitivity; rhinitis; asthma;
XX KW gene; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS /*tag= a
XX FT /*product= "MC14 alternatively spliced variant"
XX PN WO200246389-A2.
XX PD 13-JUN-2002.
XX PF 07-DEC-2001; 2001WO-US46180.
XX PR 08-DEC-2000; 2000US-251835P.
XX PR 14-MAR-2001; 2001US-275479P.
XX PR 28-MAR-2001; 2001US-279115P.
XX PR 02-APR-2001; 2001US-280143P.
XX PA (UNIO) UCB SA.
XX PI Nocka K, Pirozzi G, Einstein R;
XX

DR WPI; 2002-508560/54.
DR P-PSDB; ABB77575.
XX Novel isolated nucleic acids that are differentially expressed in mast
PT cells in patients with allergic hypersensitivity, encoding proteins
PT associated with mast cell regranulation and allergic hypersensitivity
XX
PS Claim 1; Page 115-117; 119pp; English.
XX
CC The invention relates to isolated nucleic acid (ABN81319-ABN81324),
CC corresponding to genes differentially expressed in mast cells following
CC activation or in patients with allergic hypersensitivity disease, (I)
CC that encodes proteins (ABB77569-ABB77575) (II) or a protein fragment of
CC (II) if at least 6 amino acids. (II) is useful for identifying binding
CC partners. (I) or (II) is useful for diagnosing or treating a disease
CC state (e.g. allergic hypersensitivity, seasonal rhinitis, asthma,
CC urticaria or atopic dermatitis or mastocytosis) in a subject which
CC involves determining the level of expression of (I) or (II). A computer
CC system, comprising a database containing information identifying the
CC expression level in a tissue or at least one mast cell of (I), is useful
CC for presenting information to identify the relative expression level of
CC (I). (II) is used as a marker to detect, diagnose or identify an allergic
CC response in a patient. The protein can also serve as a target that
CC modulate gene expression or activity and as an antigen to raise
CC polyclonal or monoclonal antibodies. (II) is useful for identifying
CC agents that modulate expression of the protein or agents, such as
CC agonists or antagonists. The agonists or antagonists are useful for
CC modulating biological activity and function of (II) and thus are useful
CC for alleviating disease conditions such as allergic hypersensitivity,
XX seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis.
XX
SQ Sequence 1662 BP; 229 A; 551 C; 511 G; 371 T; 0 other;

Alignment Scores:

Pred. No.: Length: 1662
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
US-09-593-793a-113 (1-553) x ABN81324 (1-1662)
Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 1 ATGTGTCAGAGGCTGTGGGTGAGCCGCTGCTGGCGCAGCCGAGAGCCAGCTCTGTGCTG 60
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 61 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCCGAGGCATCACCTATGTGCGG 120
Qy 41 ProLeuLeuGluValGlyValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGly 60
Db 121 CCTCTGCTGCTGGAAGTGGGGTAGAGAGAGTTCATGACCATGGTGTGTCGGCATGTGT 180
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 181 CCAGTGTCTGGGCTGTGTCTGCTCCGCTCCTAGGCTCAGCCAGTGACCATGGCGTGA 240
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 241 CGCTATGGCCGCGCGGCCCTTCATCTGGGCACGTCTCTGGGCATCTCTGTGAGCCCTC 300
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 301 TTTCATCATCCCAAGGCCGCGCTGGCTAGCAGGGCTGCTGTCCCGCATCCAGGCCCTCG 360
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 361 GAGCTGGCACCTGCTCATCTCTGGCGGTGGGCTGCTGGACTTCTGTGGCCAGGTGCTTC 420
Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160

Db 421 |||||ACTCCACTGGAGGCGCTCTCTGACCTCTTCCGGGACCCGGACCACTGTGCGCAGGCC 480
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 481 TACTCTGTCTATGCTTCATGATCAGTCTTGGGGGCTGGCTGGGTACCTCTCGCTGCC 540
Qy 181 IleAspTyrAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 541 ATTGACTGGGACACCACTGCGCTGCGCCCTACCTGGGCACCCAGAGGAGTGCTCTTT 600
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 601 GGCCTGCTCACCTCATCTCTCCCTGCGTAGCAGCCACACTGCTGGTGGCTCAGGAG 660
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 661 CGAGCGCTGGGCCCCACCGAGCCACAGAGGCTGTGCGCCCTCTCTTGTGCGCCCA 720
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
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Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 781 CACCAGCTGTGCTGCGCATGCGCGCCACCTGCGCGCTCTCTGCTGAGCTGTC 840
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluLeu 300
Db 841 AGCTGATGGCACTCATGACCTTCACGCTTTCACGGATTCGTGGCGAGGGGCTG 900
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 901 TACCAGGCGGTGCCAGAGCTGAGCGGGCACCAGAGCGCCGAGACACTATGATGAGGC 960
Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 961 GTTCGGATGGGCGAGCTGGGGCTGTCTCTGTCAGTGGCGCATCTCCCTGCTCTCTCTG 1020
Qy 341 ValMetAspArgLeuValGluArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1021 GTCATGGACCGGCTGGTGACGGATTCGGCACTCGCAGCAGTCTATTTGGCCAGTGGCA 1080
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
Db 1081 GCTTTCCTGTGGTGGCGGTGCCACATGCTGTCCACAGTGTGGCGGTGGTACACT 1140
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1141 TCAGCGCGCTCACCGGTTTCACTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1200
Qy 401 SerLeuTyrHisArgGluGlyValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1201 TCCCTCTACCAACCGGGAAGAGGTGTCTCTGCCCAATACCGAGGGGACACTGGAGT 1260
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1261 GCTAGCACTGAGGACAGCTGATGACCACTTCTCTGCCAGGCCCTAAGCTGGAGCTCC 1320
Qy 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
Db 1321 TTCCCTAATGACACGTGGGTGCTGGAGGACGTGGCTCTCCCACTCCACCGCGCTC 1380
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480
Db 1381 TCGGGGCTCTGCTGTGTGATCTCCGTAGCTGTGGTGGGGAGCCACCGAGGCC 1440
Qy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1441 AGGGTGGTTCGGGGCGGGGATCTGCTGGACCTCGCATCTCTGGATAGTTCCTCTG 1500
Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
|||||

Db 1501 CTGTCCCCAGTGGCCCCCATCCCTGTTTATGGGCTCCATGTGCCAGTCCAGCAGTCTGTC 1560
Qy 521 ThrIlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1561 ACTGCTATATGGTGTCTGCGCAGGCCCTGGGTCTGGTGGCCATTACTTTGCTACACAG 1620
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1621 GTAGTATTGTACAGAGGCACTTGGCCAAATACTCAGCG 1659
RESULT 2
ABK92217
ID ABK92217 standard; DNA; 2582 BP.
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AC ABK92217;
XX
DT 15-AUG-2002 (first entry)
XX
DE Prostate cancer-associated DNA sequence #103.
XX
KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW gene therapy; gene; ds.
XX
OS Mammalia.
XX
PN WO200230268-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US32045.
XX
PR 13-OCT-2000; 2000US-0687576.
PR 08-DEC-2000; 2000US-0733288.
PR 08-DEC-2000; 2000US-0733742.
PR 24-JAN-2001; 2001US-263957P.
PR 16-MAR-2001; 2001US-276791P.
PR 16-MAR-2001; 2001US-276888P.
PR 06-APR-2001; 2001US-281922P.
PR 24-APR-2001; 2001US-286214P.
PR 30-APR-2001; 2001US-0847046.
PR 04-MAY-2001; 2001US-288589P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX
DR WPI; 2002-471335/50.
XX
PT p-PSDB; ABG61900.
XX
PT Detecting a prostate cancer-associated transcript in a cell in a
PT patient, useful for diagnosing prostate cancer (PC) or screening
PT modulators of PC, by determining if prostate cancer-associated genes
XX are expressed in a prostate tissue
PS Claim 22; Page 386; 436pp; English.
XX
XX The present invention relates to methods of detecting a prostate
CC cancer-associated transcript in a cell from a patient. The method
CC comprises contacting a biological sample from the patient with
CC prostate cancer-associated polynucleotides (designated PC genes) that
CC selectively hybridise to a sequence that is at least 80% identical
CC to them. The prostate cancer-associated polynucleotide sequences
CC are differentially expressed in prostate tumour tissue or in
CC prostate cancer and are derived from the tissues of various
CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
CC The methods of the invention are useful for diagnosing and treating
CC prostate cancer in mammals. The prostate cancer-associated genes are
CC useful for diagnosing or treating prostate cancer, as well as for
CC identifying modulators of prostate cancer or agents that inhibit
CC prostate cancer. The nucleic acid sequences are particularly useful
CC in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences.

XX Sequence 2582 BP; 407 A; 822 C; 785 G; 566 T; 2 other;

Alignment Scores:
Pred. No.: 1-le-218 Length: 2582
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-593-793a-113 (1-553) x ABK92217 (1-2582)

Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 310 ATGGTCCACAGGCTGTGGGTGAGCGCCTGCTGGGCACCGAAGCCAGCTCTGTGCTG 369
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 370 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCCGACGATCATCTATGTGCGG 429
Qy 41 ProLeuLeuLeuGluValGlyValGluLysPheMetThrMetValLeuGlyIleGly 60
Db 430 CCTCTGCTGCTGAAGTGGGGTAGAGGAAGTTTCATGACCATGTGTGGGCATGTGT 489
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlyLysAlaSerAspHisTrpArgGly 80
Db 490 CCAGTCTGGGCTGTCTGTCTGCCGCTCCTAGGCTCAGCCAGTGCACCTGGCGTGA 549
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 550 CCGTATGGCCGCGCGCGCCCTTCATCTGGGCACCTGTCTTGGGCATCTGTGAGCCCTC 609
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 610 TTTCATATCCCAAGGCCGCGCTGGCTAGCAGGGCTGCTGTGCCGGATCCACAGCCCTG 569
Qy 121 GluLeuAlaLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 670 GAGCTGGCACTGCTATCTGCGGCTGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTC 729
Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 730 ACTCCACTGGAGCCCTGTCTCTGACCTTTCCGGGACCCGACCTGTGCGCAGGCC 789
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 790 TACTGTGCTATAGCCCTTCATGATCATAGTCTTGGGGGCTGCTGGGCTACCTCTGCTGCC 849
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 850 ATTGACTGGGACACCAGTSCCTGCGCCCTACCTGGGCACCCAGGAGAGTGCCTCTTT 909
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 910 GGCCTGCTCACCTCTATCTCTCTGACCTGTAGCAGCCACACTGCTGTGTGCTGAGGAG 969
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 970 GCAGCGCTGGGCCCCACCAGGACGACAGAGGGCTGTGCGGCCCTCTCTGTGCGCCAC 1029
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1030 TGCTGTCCATGCGGCGCGCTGTGCTTTCGGGAACCTGGCGCCCTGTCTTCCCGCGCTG 1089
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1090 CACCAGCTGTGTGCGCATGCGCGCACCCCTGCGCGCGCTCTTGTGGCTGAGCTGTGC 1149
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1150 AGCTGGATGGCACTCATGACCTTCACGCTGTGTTTACAGGATTTCTGTGGGCGAGGGGCTG 1209

Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaAraArgHisTyrAspGluGly 320
Db 1210 TACCAGGGCGTCCAGAGACTGAGCGGGCAGCGAGCCGCGGACACTATGATGAAGGC 1269
Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1270 GTTCGGATGGGAGCGTGGGCTGTCTTCAGTGGCGCATCTCCCTGTCTCTCTCTG 1329
Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1330 GTCATGGACCGGCTGGTGAGCGATTCGGCACTCGAGCAGTCTATTGGCCAGTGGGCA 1389
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1390 GCTTTCCCTGTGCTGCCGTGCCACATGCCGTGTCCACAGTGTGGCCGTGGTACAGCT 1449
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1450 TCAGCGCGCCTCACCGGTTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1509
Qy 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1510 TCCTCTTACCACCGGAGAGCAGGTGTCTGCCAATACCGAGGGACACTGGAGGT 1569
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1570 GCTAGCAGTGAAGACAGCCTGATGACCACTTCTCTGCCAGGCCCTAAGCCTGGAGTCCC 1629
Qy 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeu 460
Db 1630 TTCCCTTAATGGACAGTGGGTGCTGGAGCAGTGGGCTCTCCACCTCCACCCGCGCTC 1689
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1690 TCGGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1749
Qy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1750 AGGGTGGTTCGCGGCGGGGCATCTGCTGGACCTGCGCCATCTGGATAGTGCCTTCCCTG 1809
Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1810 CTGTCCAGTGGCCCACTCCCTGTTTATGGGCTCATATGTCCAGTCCAGCCAGTCTGTC 1869
Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1870 ACTGCTATATGCTGCTGCCGAGCCCTGGTCTGGTGCCTATTTACTTTGCTACACAG 1929
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1930 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1968

RESULT 3
AAS14962
ID AAS14962 standard; cDNA; 3320 BP.
XX
AC AAS14962;
DT 14-FEB-2002 (first entry)
DE DNA encoding human PROST 03.
XX
KW Human; PROST 03; metastasis; prostate cancer; immune response;
cystostatic; vaccine; ss.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
CDS 282..1943
FT /*tag= a
FT /product= "PROST 03".
XX
PN W0200181577-A2.

XX 01-NOV-2001.
XX 26-APR-2001; 2001WO-US13323.
XX 27-APR-2000; 2000US-200065P.
XX 20-APR-2001; 2001US-0200065.
XX (SCHD) SCHERING AG.
XX
PI Lau T, Lin RJ, Parkes D, Parry G, Schneider DW, Steinbrecher R;
PI van Heuit PT, Wu J;
XX WPI; 2002-041404/05.
DR P-PSDB; AAU10324.
XX
PT Novel PROST 03 polypeptides and polynucleotides useful in research,
PT diagnosis and therapeutic applications, particularly for use in cancer
PT therapeutics -
XX
PS Claim 6; Fig 1; 77pp; English.
XX
CC The invention relates to an isolated PROST 03 polypeptide (I) and to
CC the polynucleotide (II) encoding PROST 03. Fragments of (I) were used
CC to generate antibodies (III) to PROST 03. (III) is useful for selectively
CC destroying a cell expressing (I), and for treating a disease-state
CC associated with expression of PROST 03 in a human patient. (III) is
CC useful for diagnosing metastasis associated with (I), in a subject.
CC (I) is also useful for diagnosing and treating diseases of cell
CC proliferation such as prostate cancers. (I) is also useful for generating
CC antibodies to PROST 03. (III) is useful in detecting the levels of PROST
CC 03 polypeptides in cells and tissues, and in targeting drugs to primary
CC and metastatic tumours. (I) is also useful for stimulating immune
CC response to PROST 03 containing cells. (II) is useful in diagnostic
CC assays for detecting the levels of polynucleotides encoding PROST 03 in
CC cells and tissues. (II) is useful as DNA probes, as targets for antisense
CC and ribozyme therapy, and as templates for the production of antisense
CC polynucleotides. (I) and (II) are useful in research, biological,
CC clinical and therapeutic purposes. The present sequence represents
CC the coding sequence of human PROST 03.
XX
SQ Sequence 3320 BP; 585 A; 1013 C; 944 G; 778 T; 0 other;

Alignment Scores:
Pred. No.: 1.53e-218 Length: 3320
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-593-793A-113 (1-553) x AAS14962 (1-3320)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db ATGGTCCAGAGGCTGGGTGAGCCGCTGCTGCGCACCGAAAGCCAGCTCTTGCTG 341
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCCGACAGGCATCACCTATGTGCGG 401
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAGTTTCATGACCATGGTGGGCAATTGGT 461
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db CCAGTGTGGGCTGTGCTGTCTCCCGCTCCCTAGCTCAGCCAGTACACCTGGCGTGA 521
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db CGCTATGGCCGCCGCCCTTCATCTGGGACATGCTCTGGGCATCTCTGTGACCTC 581

QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db TTTCTCATCCCAAGGCGGCTGGCTAGCAGGGCTGCTGCGCGATCCAGGCCCTG 641
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db GAGCTGGCACTGCTCATCTGGGCGTGGGGCTGCTGGACTTCTGTGGCAGGTGCTTC 701
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db ACTCCACTGGAGGCGCTGCTCTGACCTCTTCCGGGACCCGACACACTGTCGCAGGCC 761
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db TACTCTGTCTATGCTTTCATGATCAGTCTTGGGGCTGCTGGGCTACCTCCTGCTGCC 821
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db ATTGACTGGACACAGTGCCTGGCCCTTACCTGGGCGACCCAGAGGAGTGCCTCTT 881
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db GGCTCTGCTACCTCTCATCTCTACCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAG 941
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db GCAGGCGTGGGCGCCACCGAGCCAGAGAGGCTGTGGGCCCTCTCTTGTGCGCCAC 1001
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db TGCCTGTCCATGCGGCGCGCTGGCTTTCGGAACCTGGCGCCCTGCTCCCGGCTG 1061
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db CACCAAGCTGTGTCGCGCATGCGCGCACCTGCGCGGCTCTTCTGGCTGAGCTGTC 1121
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db ACCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGCGGAGGCTG 1181
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db TACCAGGCGTGCACAGAGCTGAGCGGCGCACCGAGGCGCGAGACACTATGATGAAGGC 1241
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db GTTCGATGGGCGAGCTGGGGCTGTTCCTGCGAGTGGCCATCTCCCTGCTCTCTCTG 1301
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db GTCATGGACCGGCTGGTGCAGCGATTGGCACTCCGACGAGTCTATTGGCCAGTGGCA 1361
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
Db GCTTTCCCTGTGGCTGGCGGTGCCACATGCTGCCACAGTGTGGCGCTGGTGCAGCT 1421
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db TCAGCGCGCTCACCGGTTTACCTTTCAGCCCTGCGAGATCTCCCTTACACACTGGCC 1481
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db TCCCTCTACCAACCGGAGAGAGGAGTGTTCCTGCCCAATAACCGAGGGGACACTGGAGT 1541
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db GCTAGCAGTGAAGCAGCCTGATGACCACTTCTTCCGCCAGGCCCTTAAGCCTGGAGCTCC 1601
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
Db TTCCCTAATGGACAGTGGGTGCTGGAGCAGTGGCGCTCCCGCTCCACCTCCACCGGCTC 1661
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480

Db 1662 TCGGGGCTCTCCCTGTGATGTCCTCGTAGCTGTGGTGGGTCAGCCACCGAGGCC 1721
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1722 AGGGTGTTCGGGGCGGGGCATCTGCTGGACCTGCCATCTGGATAGTGGCTTCCTG 1781
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1782 CTCTCCAGGTGGCCCATCTCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1841
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1842 ACTGCCTATATGTGCTGCCGAGGCTGGGTCTGGTGGCCATTTACTTGTGTACACAG 1901
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1902 GTAGTATTTGCAAGAGGACCTTGGCCAAATACTCAGCG 1940
RESULT 4
AAV61201
ID AAV61201 standard; cDNA; 3410 BP.
AC AAV61201;
XX
XX
DT 06-JAN-1999 (first entry)
XX Full length cDNA sequence of prostate tumour clone L1-12.
DE Prostate; cancer; tumour; vaccine; immunogen; clone; ss.
XX Homo sapiens.
XX
XX WO9837093-A2.
XX 27-AUG-1998.
PD
PF 25-FEB-1998; 98WO-US03492.
XX
XX 09-FEB-1998; 98US-0020956.
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
XX
XX (CORI-) CORIXA CORP.
XX
XX Dillon DC, Xu J;
XX WPI; 1998-609886/51.
DR P-PSDB; AAW71869.
XX
XX Polypeptides comprising immunogenic portions of prostate proteins -
PT used in a vaccine for the treatment of prostate cancer
PT
XX
PS Claim 3; Page 79-80; 130pp; English.
XX
CC The present sequence is a new DNA which encodes an immunogenic portion
CC of a prostate tumour protein. The encoded immunogen, or the DNA itself,
CC can be used as a vaccine for the treatment of prostate cancer. The DNA
CC was identified by analysis of a subtracted cDNA library obtained by
CC subtracting a prostate tumour cDNA expression library with a normal
CC tissue cDNA library.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;
Alignment Scores:
Pred. No.: 1.58e-218 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00 Conservative: 0
Best Local Similarity: 100.00 Mismatches: 0
Query Match: 100.00 Indels: 0
DB: 19 Gaps: 0
US-09-593-793A-113 (1-553) x AAV61201 (1-3410)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 284 ATGGTCCACGAGGCTGTGGGTAGCGCCCTGCTCGCGCACCGGAAGCCAGCTCTTGGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGTAACCTTTGGCCTGGAGGTGTGTTTGGCCGACGAGCATCACTATGTGCCG 403
QY 41 ProLeuLeuGluValGlyValGlyLeuGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAGTTTCATGACCATGCTGTGGCATTTGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisThrArgGly 80
Db 464 CCAGTCTGGGCTGCTGCTGTGCTCCGCTCCTAGGCTCAGCCAGTCACTGCGCTGGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCGGCTTCATCTGGGCATCTCCTTGGGCATCTCTGTAGGCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGCTGCTGTGCCCGGATCCAGGCCCTCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGTGGCATCTGCTCATCTGGCGTGGGCTGCTGGACTTCTGTGCCAGGTGCTCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCTGCTCTGACCTCTTCCGAGCCGCGGACCACTGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTATGCTTCATGATCATGTGGGGGCTGCTGGGCTACCTCTGCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
Db 824 ATTGACTGGGACACCATGTCCTGGCCCTACCTGGGACCCAGGAGGAGTGCCTCTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGCTGCTCACCTCATCTTCTCCTACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGGCTGGGCGCCACCAGGACGAGGAGGCTGTCGGGCCCCCTCTTGTGCCCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TCGTGTCCATGCGGCGCGCTTGGCTTTCGGAACCTGGCGGCTGCTTCCCGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuLeuArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCACTGTGCTGCGCATGCCCGCACCTGCGCGGCTCTTCTGTGGCTGAGTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTACGCTGTTTACCGGATTTCTGGGCGAGGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
Db 1184 TACCAGGCGCTGCCAGAGCTGAGCGGGCACCGAGGCCGAGGACACTATGATGAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGCAGCGTGGGCTGTCCCTGCGAGTGGCCATCTCCCTGGTCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGGACCGGCTGGTCAGCGATTCCGCACTTCGAGCAGTCTATTGTGCCAGTGTGGCA 1363

```
OY 361 AlapheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
Db 1364 GCTTTCCCTGTGGCTGCCGTCACATGCTGTCACAGTGTGGCTGTGACAGCT 1423
OY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCCCTCACCGGTTACCTCTCAGCCCTGCAGATCTCCTCCCTACACACTGGCC 1483
OY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCCTCTACCCAGGAGAGAGAGAGTGTTCCTGCCCAATACCGAGGGGACACTGGAGT 1543
OY 421 AlaSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGAGGACAGCTGATGACAGCTTCTCTGCCAGGCCCTAAGCCTGGAGCTCC 1603
OY 441 PheProAsnGlyHisValGlyAlaGlySerGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCCTAATGGACAGTGGGTGCTGGAGGCACTGGCCCTGCTCCACCTCCACCCGCGTC 1663
OY 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480
Db 1664 TCCGGGGCTCTGCTGTGATGTCCTCGTACGTGTGGTGGTGGGAGCCACACAGGCC 1723
OY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGGTGGTTCGGGGCGGGCATCTGCTGGACCTCGCCATCTCGATAGTGCCTTCCTG 1783
OY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCTCCAGGTGGCCCATCCCTGTTATGGGCTCCATGTGTCACGCTCAGCCAGTCTGT 1843
OY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGCTGTCTGCCAGGCTGGGCTGCTGGTCTGCTGCTTACTTGTCTACACAG 1903
OY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTGTGACAGAGGACTTGGCCAAATACTCAGCG 1942
RESULT 5
AAV58586
ID AAV58586 standard; cDNA; 3410 BP.
XX
AC AAV58586;
XX
DT 08-DEC-1998 (first entry)
XX
DE Prostate tumour specific gene clone L1-12.
XX
KW Prostate tumour specific gene; human; prostate cancer; detection;
KW therapy; ss.
XX
OS Homo sapiens.
FH
FH Key Location/Qualifiers
FT CDS 284..1945
FT /*tag= a
XX
PN WO9837418-A2.
XX
PD 27-AUG-1998.
XX
PF 25-FEB-1998; 98WO-US03690.
XX
PR 09-FEB-1998; 98US-0904809.
PR 25-FEB-1997; 97US-0806596.
PR 01-AUG-1997; 97US-0904809.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Xu J;
XX
```

WPI; 1998-480805/41.
P-PSDB; AAW69385.
Novel human prostate specific tumour protein and fragments - useful for detecting and treating prostate cancers
Claim 1; Page 84-85; 141pp; English.
This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate cancers.

Sequence 3410 BP; 657 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:
Pred. No.: 1,58e-218 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-593-793A-113 (1-553) x AAV58586 (1-3410)

OY 1 MetValGlnArgLeuTyrPheValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db 284 ATGGTCCAGAGCTGTGGTGTGGAGCGCTGTGCGGACCGAAAGCCAGCTCTGTCTG 343
OY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCGGCGGACCATCACCTATGTGCG 403
OY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGTGGAAAGTGGGGTAGAGGAGAGTTTCATGACCATGCTGCTGGGCATCTG 463
OY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGGCTGTGCTGTCTCCGCTCTAGCTCAGCCAGTGACCACTGGCGTGA 523
OY 81 ArgTyrGlyArgArgProPheIleThrPalaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCGCTTTCATCTGGGCACCTGTCTGGGCATCTGCTGAGCCTC 583
OY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGGCGGCTGGCTAGCAGGGCTGTGCGCCGGATCCAGGCCCTTG 643
OY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCAGCTGCATCTCTGGCGTGGGCTGTCTGGAGCTTCTGTGGCCAGGTGCTTC 703
OY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCGCTCTCTCTGACCTCTTCCGGGACCCGGACCACTGTGCCAGGCC 763
OY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTCTATGCTTTCATGATCAGTCTTGGGGGCTGCTGGGGTACTCTCTGCTGCC 823
OY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 824 ATTGACTGGGACACAGTGCCTGGCCCTTACCTGGGCGCCAGGAGGAGTGCCTCTTT 883
OY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db 884 GGCCTGCTCAGCCCTCATCTTCTCCTACCTGCGGTAGCAGCACACTGCTGCTGCTGAGGAG 943

```
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
|||
Db 944 GCAGCGCTGGGCCCCACCAGCAGCAGAGAGGCTGTGCGCCCTCTCTGTGCGCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
|||
Db 1004 TGCTGTCCATGCGCGCGCGCTGGCTTTCCGGAACCTGGCGCCCTGTCTCCCGGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
|||
Db 1064 CACCAGCTGTGTCGCGCATGCCCGCACCTGTGCGCGGCTCTCTGTGCTGAGCTGTGC 1123
QY 281 SerTyrMetAlaLeuMetThrPheThrLeuPheThrAspPheValGlyGluGlyLeu 300
|||
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCTGTGGCGAGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
|||
Db 1184 TACCAGGGCGTCCCGAGAGCTGAGCGGGCACCGAGGGCCGGAGACACTATGATGAAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
|||
Db 1244 GTTCGGATGGCAGCTGGGGCTGTCTTCAGTGCAGTGCCTCTCTGTCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
|||
Db 1304 GTCTGGACCGGCTGGTGCAGCGATTCGCGACTCGAGCAGTCTATTGGCCAGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
|||
Db 1364 GCTTTCCTGTGGCTGCCGTGCCACATGCCTGTCCACAGTGTGGCGCTGTGACAGCT 1423
QY 381 SerAlaAlaLeuThrClyPheThrPheSerAlaLeuGlnIleLeuProTyrThrIleuAla 400
|||
Db 1424 TCAGCGCGCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
|||
Db 1484 TCCTCTACACACCGGAGAGCAGGTGTCTTGCCCAATACCGAGGGGACACTGGAGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
|||
Db 1544 GCTAGCAGTGTAGGACAGCTGTATGCCAGCTTCTCTGCCAGGCCCTAAGCCTGGAGCTCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
|||
Db 1604 TTCCCTAATGGACAGCTGGGTGCTGGAGCAGTGGCTGCTCCCACTCCACCCCGGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
|||
Db 1664 TCGGGGGCTCTGCCTGTGATGCTCCGTACGTGTGGTGGTGAGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
|||
Db 1724 AGCGTGGTTCCCGGGCGGGGCACTCTGCCTGGACCTCGCCATCTCTGGATAGTCCCTC 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
|||
Db 1784 CTGTCCAGGTGGCCCACTCCCTGTTTATGGGCTCATTTGTCCAGCTCAGCCAGTCTGC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
|||
Db 1844 ACTGCTATATGTTGTCGCCCGAGCGCTGGGTCTGGTCTGCCATTTACTTTCTCTACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||
Db 1904 GTAGTATTTGACAGAGCGACTTGGCCAAATACTCAGCG 1942
RESULT 6
AAC79473
ID AAC79473 standard; cDNA; 3410 BP.
XX
```

```
AC AAC79473;
XX
DT 07-FEB-2001 (first entry)
XX
DE cDNA sequence of human breast tumour clone P501S.
XX
KW Human; breast tumour antigen; cytostatic; immunotherapy;
breast cancer; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200061756-A2.
XX
PD 19-OCT-2000.
XX
PF 10-APR-2000; 2000WO-US09688.
XX
PR 09-APR-1999; 99US-0288950.
PR 02-JUL-1999; 99US-0346327.
XX
PA (CORI-) CORIXA CORP.
PI Reed SG, Xu J, Dillon DC;
XX
DR WPI; 2000-638568/61.
DR P-PSDB; AAB28527.
XX
PT A novel isolated polypeptide comprising an immunogenic portion of a
breast cancer protein useful in the detection and treatment of breast
cancer -
XX
PS Claim 26; Page 91-92; 95pp; English.
XX
CC The present sequence was isolated from a breast tumour cDNA library. It
is provided in a specification relating to compounds for immunotherapy
and diagnosis of breast cancer. Breast tumour antigens and the
polynucleotides that encode them may be used in the production of a
pharmaceutical composition to be used in the treatment of breast cancer.
Proliferated T cells and incubated antigen presenting cells are also
required. The polypeptides and polynucleotides may also be used to
produce a vaccine.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:
Pred. No.: 1,58e-218 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-593-793a-113 (1-553) x AAC79473 (1-3410)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgGlyAlaGlnLeuLeu 20
|||
Db 284 ATGGTCCAGAGGCTGTGGGTGAGCGCGCTGTGCGCACCCGAAAGCCAGCTCTGTCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||
Db 344 CTCACACCTGCTAACCTTTGGCGCTGGAGGTGTGTTGGCGCGCAGGATCACCTATGTGCCG 403
QY 41 ProLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGly 60
|||
Db 404 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGTGGCATTTGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
|||
Db 464 CCAGTGTCTGGGCTGTGTGTCTGTCCTGCTCCGCTCTCTAGGCTCAGCCAGTGACCACTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
|||
Db 524 CGCTATGGCCCCCGCGCCCTTCATCTGGGCACGTGTCTCTGGGCATCTCTGTGAGCCTC 583
```

QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
|||||
Db 584 TTTCTCATCCCAAGGCGCGGTGGCTAGCAGGGCTGCTGCGCGGATCCAGGCCCTTG 643

QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
|||||
Db 644 GAGCTGGCACTGCTCATCTCGGGCTGGGGCTGCTGGACTTCTGTGGCAGGTGCTCTTC 703

QY 141 ThrProLeuGluAlaLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
|||||
Db 704 ACTCCACTGGAGGCCCTGCTCTCTGACCTTCCGGGACCCGACACACTGTGCCAGGCC 763

QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
|||||
Db 764 TACTCTGTATGCTTTCATGATGATGCTGTGGGGCTGCTGGGTACCTCTGCTGCTGCC 823

QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
|||||
Db 824 ATTGACTGGGACACAGTGCCTGCGCCCTTACCTGGGCACCCAGGAGGTGCTCTCTTT 883

QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
|||||
Db 884 GGCCTGCTCACCTCATCTTCTCAGCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAG 943

QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
|||||
Db 944 GCAGCGCTGGGCCCCACCGAGCCAGCAGAAAGGCTGTCGGCCCCCTCTTGTGCCCCAC 1003

QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
|||||
Db 1004 TGCTGTCCATGCGGGCGCGCTTGGCTTTCGCGAACCTGGGGCGCTGCTTCCCGGCTG 1063

QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
|||||
Db 1064 CACCAGCTGTGCTGGCGATGCCCCGACCCCTGCGCGGCTCTTCTGGCTGAGCTGTGC 1123

QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
|||||
Db 1124 ACCTGGATGGCACTCATGACCTTCACGCTGCTTTTACACGGATTCGTGGCGAGGGCTG 1183

QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
|||||
Db 1184 TACCAGGGCGTCCCGAGAGCTGAGCGGGCACCGGAGCCGAGACACTATGATGAAGGC 1243

QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
|||||
Db 1244 GTTCGGATGGGCGAGCTGGGGCTGTTCTCTGCAGTGGCGCATCTCCCTGGTCTCTCTG 1303

QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
|||||
Db 1304 GTCATGGACCGCTGCTGCAGGATTCGGCACTCCAGCAGTCTATTGGCCAGTGTGCA 1363

QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
|||||
Db 1364 GCTTTCCCTGTGGCTGCGGTGCCACATGCTGTCACAGTGTGCCGTGGTGACAGCT 1423

QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
|||||
Db 1424 TCAGCGCCCTACCGGGTTACCTTCTCAGCCCTGCAGATCTCCCTTACACACTGGCC 1483

QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
|||||
Db 1484 TCCCTCTACCCCGGAGAGCAGGTGTTCTTCGCCCAATACCGAGGGGACACTGGAGGT 1543

QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
|||||
Db 1544 GCTACAGTGGAGCAGCCTGATGACAGCTTCTTCCAGGCCCTTACGCTGGAGCTCC 1603

QY 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeu 460
|||||
Db 1604 TTCCCTAATGGACAGTGGGTGCTGGAGGAGTGGCTGCTCCACCTCCACCCCGGCTC 1663

QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
|||||
Db 1664 TCGCGGGCTCTGCGTGTGATGCTCTCCGTACGTGTGGTGGTGAGCCACCGAGGCC 1723

QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
|||||
Db 1724 AGGGTGGTTCGGGGCGGGCATCTCCCTGGACCTCGCCATCTCGATAGTGCCTTCCTG 1783

QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
|||||
Db 1784 CTGCTCCAGGTGGCCCATCTCCCTGTTATGGCTCCATGTCCAGCTCAGCAGTCTGTC 1843

QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
|||||
Db 1844 ACTGCTATATGCTGCTGCCGAGCGCTGGGTCTGGTCGCCATTTACTTTGCTACACAG 1903

QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||
Db 1904 GTAGTATTGACAGAGGACTTGGCCAAATACTCAGCG 1942

RESULT 7
AAA06349
ID AAA06349 standard; cDNA; 3410 BP.
AC AAA06349;
XX
XX 13-JUN-2000 (first entry)
XX Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:110.
XX Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
XX WO200004149-A2.
PN
XX 27-JAN-2000.
PD
XX 14-JUL-1999; 99WO-US15838.
PF
XX 14-JUL-1998; 98US-0115453.
PR 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 23-SEP-1998; 98US-0159822.
PR 15-JAN-1999; 99US-0232149.
PR 15-JAN-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.
XX
PA (CORI-) CORIXA CORP.
XX
XX Dillon DC, Harlocker SL, Yuqiu J, Xu J, Mitcham JL;
PI
XX WPI; 2000-171268/15.
DR
XX
XX New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein -
XX
XX Claim 1; Page 135-136; 263pp; English.
XX
CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (ptp). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AAA06241 to AAA06691 and
CC AAY82000 to AAY82020 represent sequences used in the exemplification of
CC the present invention.

XX SQ Sequence 3410 BP; 667 A; 1015 C; 945 G; 782 T; 1 other;

Alignment Scores:

Pred. No.: 1 58e-218 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-593-793a-113 (1-553) x AAA06349 (1-3410)

```
QY 1 MetValGlnArgLeuTrpValSerArgLeuArgHisArgLysAlaGlnLeuLeuLeu 20
DB 284 ATGGTCCAGAGGCTGTGGGTGAGCCGCTGCTGCGGCACCGGAAAGCCAGCTCTTGTGCT 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrValPro 40
DB 344 GTCACCTGCTAACCTTTGGCCCTGAGAGGTGTGTTTGGCCGACGATCACCCTATGTGCCG 403
QY 41 ProLeuLeuLeuGluValGlyValGluLysPheMetThrMetValLeuGlyIleGly 60
DB 404 CTTCTGCTGCTGAAGTGGGGGTAGAGGAGAGTTTATGACCATGGTGTGGGCATTGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
DB 464 CCAGTCTGGCCCTGCTGCTGCTGCCCTCCTTAGGCTAGCCAGTACCCACTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
DB 524 CGTATGGCGCGCGCGGCCCTTCATCTGGGCACCTGCTTGGGCATCTGCTGAGCCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
DB 584 TTTCTCATCCAGGCCCGGCTGGCTAGCAGGCTGCTGTGCCCGATCCAGGCCCTCG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
DB 644 GAGCTGGCACTGCTCATCTGGCGGTGGGCTGCTGGACTTCTGTGGCCAGGTGCTCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
DB 704 ACTCCACTGGAGCCCTGCTCTCTGACCTTTCCTGGGACCCCGACACACTGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
DB 764 TACTCTGTCTATGCCCTCATGATCAGTCTTGGGGGCTGGCTGGGCTACCTCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
DB 824 ATTGACTGGGACACCACTGCCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
DB 884 GGCTGCTCACCCCTCATCTCTCTACCTGCTAGCAGCCACACTGTGTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
DB 944 GCAGCCCTGGGGCCCCACCGAGCCAGAGAGGCTGTGGCCCCCTTGTGTGCCCCCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
DB 1004 TGCTGTCCATGGCGGCCCGCTTGGCTTTCGGAACCTTGGGCGCCCTGCTTCCCGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
DB 1064 CACCACCTGTGTGCCGCGCATGCCCGCACCTCGCCCGGCTCTCTGTGGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluLeuLeu 300
DB 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTGTTTACACGATTTTGTGGGCGAGGGGCTG 1183
```

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QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
DB 1184 TACCAGGCGCTGCCAGAGCTGAGCGCGGCACCGAGGCCCGGAGACACTATGATGAAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
DB 1244 GTTCGGATGGCAGCGCTGGGCTGTTCCTGCACTGGCCACTTCCCTGGTCTTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
DB 1304 GTCATGGACCGGCTGTGTGAGCGATTTCGCACTCGAGCAGTCTATTTGGCCAGTGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
DB 1364 GCTTTCCCTGTGGCTGCCGTGCCACATGCTCTGCCACAGTGTGGCCGTGGTGACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
DB 1424 TCAGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
DB 1484 TCCCTCTACCAACCGGAGAGCAGGTTCCTGCCCAATACCGAGGGCACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
DB 1544 GCTAGCAGTGAGACAGCTGATGACCACTTCTGCCAGGCCCTAAGCTGGAGCTCCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
DB 1604 TTCCCTTAATGGACACGTGGGTGCTGGAGCAGTGGGCTGCTCCCACTCCACCCGCGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
DB 1664 TCGGGGCGCTCTGCCCTGTGATGCTCCGTACGTGTGGTGGTGAGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
DB 1724 AGGGTGTTCGGGCGGGGCATCTGCCTGGACCTGCCATCCTGGATAGTGCCTTCTCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
DB 1784 CTGTCCAGGTGGCCCATCCCTCTGTTTATGGCTTCCAGCTCAGCCAGTCTGTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
DB 1844 ACTGCCATATGGTGTCTGCCGAGCCCTGGGTCTGTGTCGCCATTTACTTGTCTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
RESULT 8
AAS63557
ID AAS63557 standard; cDNA; 3410 BP.
XX
AC AAS63557;
XX
DF 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA sequence #109.
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX Homo sapiens.
XX WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
```

PR	09-MAY-2000;	2000US-0568100.	
PR	12-JUN-2000;	2000US-0570737.	
PR	13-JUN-2000;	2000US-0593793.	
PR	27-JUN-2000;	2000US-0605783.	
PR	10-AUG-2000;	2000US-0636215.	
PR	29-AUG-2000;	2000US-0651236.	
PR	06-SEP-2000;	2000US-0657279.	
PR	02-OCT-2000;	2000US-0679426.	
PR	10-OCT-2000;	2000US-0685166.	
XX			
PA	(CORI-) CORIXA CORP.		
XX			
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;		
PI	Fanger GR, Retter MW, Stolk JA, Day CH, Vedwick TS, Carter D;		
PI	Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;		
XX			
DR	WPI: 2001-639232/73.		
DR	P-FSDB: AAU69763.		
XX			
PT	New human prostate-specific polypeptides and polynucleotides useful for		
PT	the diagnosis and treatment of cancer, especially prostate cancer -		
XX			
PS	Claim 1; Page 267-268; 579pp; English.		
XX			
CC	The invention relates to isolated prostate-specific		
CC	polynucleotides, polypeptides, fusion proteins of the polypeptides,		
CC	antibodies raised against the polypeptides (or antigenic epitopes		
CC	derived from them) and antigen-presenting cells expressing the		
CC	polypeptides. The antibodies are useful for detecting the presence of		
CC	cancer, especially prostate cancer. The polypeptides, polynucleotides and		
CC	the antigen-presenting cells are useful for stimulating and/or expanding		
CC	T cells specific for a tumour protein, and for inhibiting the development		
CC	of cancer especially prostate cancer. Compositions comprising the		
CC	polynucleotide and/or polypeptide are useful for stimulating an immune		
CC	response, and for treating cancer. The oligonucleotide is useful for		
CC	detecting cancer. The present sequence is a prostate specific		
CC	polynucleotide of the invention.		
XX			
SQ	Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;		
	Alignment Scores:		
	Pred. No.:	1.58e-218	Length: 3410
	Score:	2861.00	Matches: 553
	Percent Similarity:	100.00%	Conservative: 0
	Best Local Similarity:	100.00%	Mismatches: 0
	Query Match:	100.00%	Indels: 0
	DB:	22	Gaps: 0
US-09-593-793A-113 (1-553), x AAS63557 (1-3410)			
Qy	1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20		
Db	284 ATGTGTCAGAGGCTGTGGGTGAGCGCCCTGCTGGCGCAGCCGAAAGCCAGCTCTTGCCTG 343		
Qy	21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAAlaGlyIleThrTrpValPro 40		
Db	344 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCCGAGGACATCACTATGTGCCG 403		
Qy	41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60		
Db	404 CCTCTGCTGCTGGAGTGGGGGTAGAGAGAAGTTTCATGACCATGTGTGGGCATTGGT 463		
Qy	61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80		
Db	464 CCAGTGTCTGGCCCTGGTCTGTGTCGCCCTCTAGGCTCAGCCAGTGACCACCTGGCGTGA 523		
Qy	81 ArgTrpGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100		
Db	524 CGCTATGGCCCGCCGCCCTTCATCTGGGCACCTGCTCTGGGCATCTCTGCTGAGCCCTC 583		
Qy	101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120		
Db	584 TTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGTGTCGCCGATCCAGGCCCTCC 643		

QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
|||||
Db 1724 AGGGTGGTTCCGGGGCGGCATCTGCTGGACCTCGCCATCTGGATAGTGCCTTCCTG 1783

QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
|||||
Db 1784 CTGTCCAGGTGGCCCAATCCCTGTTATGGGCTCCATTTGTCAGCTCAGCCAGTCTGTC 1843

QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuAlaGlyLeuValAlaIleTyrPheAlaThrGln 540
|||||
Db 1844 ACTGCCATATGGTGTCTCCCGCAGGCTGGTCTGGTGGCCATTACTTTCCTACACAG 1903

QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||
Db 1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942

RESULT 9

AAS10108
ID AAS10108 standard; cDNA; 3410 BP.

XX AAS10108;

XX DT 24-OCT-2001 (first entry)

XX DE Human prostate tumour cDNA L1-12.

XX KW Human; prostate tumour protein; prostate cancer; ss.

XX OS Homo sapiens.

XX XX US6262245-B1.

PN 17-JUL-2001.

XX 25-FEB-1998; 98US-0030607.

XX 25-FEB-1997; 97US-0806099.

PR 01-AUG-1997; 97US-0904804.

PR 01-FEB-1998; 98US-0020956.

PA (CORI-) CORIXA CORP.

XX Xu J, Dillon DC;

XX WPI; 2001-440862/47.

DR P-PSDB; AAU04961.

XX Novel polynucleotide encoding polypeptide comprising a portion of
PT prostate tumour protein useful for inhibiting development of prostate
PT cancer or for treating prostate cancer in a patient

XX Claim 3; Column 118-121; 105pp; English.

CC The sequence is a human prostate tumour cDNA which encodes a
CC partial tumour protein. The DNA is useful for inhibiting the development
CC of prostate cancer or for treating prostate cancer in a patient.

SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:

Pred. No.:	1.58e-218	Length:	3410
Score:	2861.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-593-793A-113 (1-553) x AAS10108 (1-3410)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20

Db 284 ATGGTCCAGAGGCTGTGGGTGAGCCGCTGTGCGGCACCGGAAAGCCAGCTCTTGTCTG 343

QY 21 ValAsnLeuLeuThrPheClyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||||
Db 344 GTCAACCTGCTAACCTTTGGCTTGGAGGTGCTTTTGGCCGAGGATCACTATGTGCGG 403

QY 41 ProLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGly 60
|||||
Db 404 CCTCTGCTGCTGGAGTGGGGGTAGAGAGAAGTTTCATACCATGGTGTGGGCATGTGT 463

QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTyrArgGly 80
|||||
Db 464 CAGTGTGGGGCTGGTGTGCTCCGCTCTAGGCTCAGCCAGTACACCACTGGCGTGA 523

QY 81 ArgTyrGlyArgArgProPheIleTyrAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
|||||
Db 524 CGCTATGGCCGCGCGGCTTCATCTGGGCACCTGCTCTGGGCATCTCTGCTGAGCCCTC 583

QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
|||||
Db 584 TTTTCTCATCCCAAGGCGGCTGGCTAGCAGGGCTGCTGTGCCGATCCAGGCCCTTG 643

QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
|||||
Db 644 GAGCTGGCAGCTGCTCATCTGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTCTTC 703

QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
|||||
Db 704 ACTCCACTGGAGGCTGCTCTGACCTCTTCCGCGGACCCGAGCACTGTGCCAGGCC 763

QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
|||||
Db 764 TACTCTGCTATGCTTTCATGATCAGTCTTGGGGGCTGCTGGGCTACCTCTCTGCTGCC 823

QY 181 IleAspTyrAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
|||||
Db 824 ATTGACTGGACACCACTGCTGCTGGCCCTTACCTGGGACCCAGGAGAGTGCCTCTTT 883

QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
|||||
Db 884 GGCCTGCTCACCTCATCTTCTCACCTGCTAGCAGCCACACACTGCTGGTGGCTGAGGAG 943

QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
|||||
Db 944 GCAGGCTGGGCCCCACCGAGCCAGAGAGGGCTGCGGCCCTCTCTCTGTGCCCCAC 1003

QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
|||||
Db 1004 TGCTGTCCATGCGCGCCGCTTGGCTTTCGGAACCTGGGCGCCCTGCTTCCCGGCTG 1063

QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
|||||
Db 1064 CACCAGCTGTGCTGCGCATGCCCGCACCCCTGCGCGGCTCTTCTGGCTGAGCTGTGC 1123

QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyLeu 300
|||||
Db 1124 AGCTGGATGGCACTCATACCTTCACGCTGTTTACAGGATTTCTGGCGCAGGGGCTG 1183

QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
|||||
Db 1184 TACCAGGCGGTGCCAGACTGAGCGGGACCCGAGGCCGAGACACTATATGATGAAGGC 1243

QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
|||||
Db 1244 GTTCGATGGCAGCGCTGGGGCTGTTCTGTGACAGTGGGCATCTCCCTGCTCTCTCTG 1303

QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
|||||
Db 1304 GTCATGGACCGGCTGTGTCAGCGATTGCGCACTCGAGCAGTCTATTTGGCCAGTGTGGA 1363

QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
|||||
Db 1364 GCTTTCCCTGTGGCTGCCGGTGCCACATGCCCTGTCCACAGTGTGGCGTGGTACAGCT 1423

QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400

|||||
Db 1424 TCAGCGCCCTCACGGGTTACCTTCTCAGCCCTGCAGATCCTCCCTACACACTGGCC 1483
Qy SerLeuTyrHisArgGluValPheLeuProLysTyrArgGlyAspThrGly 420
Db 1484 TCCCTCTACCCAGCGGAGAGGTGTCTTCCCAATACCGAGGGACACTGGAGGT 1543
Qy AlaSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGAGGACAGCTGATGACACAGCTTCTGCCAGGCCCTAAGCCTGGAGCTCC 1603
Qy PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCCTAATGACACAGTGGGTGCTGGAGGACGTGGCTTCCCTCCACCTCCACCCGCGTC 1663
Qy CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TCGGGGGCTCTGCGCTGTGATGTCTCCGTAGCTGTGGTGGTGGAGCCACCCAGAGCC 1723
Qy ArgValValProGlyArgGlyCysLeuAspLeuAlaLeuLeuAspSerAlaPheLeu 500
Db 1724 AGGTGGTTCGGGGCGGGGATCTGCTGGACCTCGGCATCTCGGATAGTGCCTTCCTG 1783
Qy LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCCCATCCTGTTTATGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1843
Qy ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGGTGTCTGCCGCGAGGCTGGGTCTGGTCGCATTTACTTTGCTACACAG 1903
Qy ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTTGACAGAGGACTTGGCCAAATACTCAGCG 1942
RESULT 10
AAH93465
ID AAH93465 standard; cDNA; 3410 BP.
XX AAH93465;
XX
XX
XX 04-OCT-2001 (first entry)
DE Human prostate-specific full length cDNA sequence L1-12.
XX
XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytostatic; gene therapy; metastasis; ss.
XX Homo sapiens.
XX
XX WO200151633-A2.
XX
XX 19-JUL-2001.
XX
XX 16-JAN-2001; 2001WO-US01574.
XX
XX 14-JAN-2000; 2000US-0483672.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX
XX WPI; 2001-425873/45.
XX
XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
XX
PS Claim 1; Page 265-266; 543pp; English.
XX
XX The present invention describes polynucleotide sequences (I) which encode

prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to AAH01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.

XX Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;
Alignment Scores:
Pred. NO.: 1.58e-218 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-09-593-793A-113 (1-553) x AAH93465 (1-3410)
Qy 1 MetValGlnArgLeuTyrValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 284 ATGGTCCAGAGGCTGTGGGTGAGCGCTGCTGGCGCACCGGAAAGCCAGCTCTTGGTG 343
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCGCAGGATCACCTATGTGCGG 403
Qy 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAAGTTTCATGACCATGGTCTGGGCAATTGGT 463
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTyrArgGly 80
Db 464 CCAGTGTGGCGCTGGTGTGTCCGCTCTAGCTCAGCCAGTGACCATGGCGTGGGA 523
Qy 81 ArgTyrGlyArgArgProPheIleThrAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCCGCGCGGCCCTTCATCTGGCACATGCTCTGGGCATCTCTGTGAGCCTC 583
Qy 101 PheLeuIleProArgAlaGlyTyrPheLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGGCGGCTGGCTAGCAGGGCTGTGTGCCCGGATCCCGAGGCCCTG 643
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACATGCTCATCTGGGCGTGGGGCTGTCTGGACTTCTGTGGCCAGGTGGCTTC 703
Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGACCCCGGACCATGTCTGCCAGGCC 763
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTCTATGCTTTCATGATCAGTCTTGGGGCTCCCTGGGCTACCTCTGCTGCC 823
Qy 181 IleAspTyrAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 824 ATTGACTGGGACACAGTGGCCCTTACCTGGGACCCAGGAGGAGTGGCTCTTT 883
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGCCTGCTCACCTTCATCTTCCCTACCTGCGTAGCAGCCACACATGCTGTGGCTGAGGAG 943
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGCGCTGGGCGCCACCGAGCCAGAGGGGTGTGGCGCCCTCTCTGTCGCCCCAC 1003

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QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
DB 1004 TGCTGTCCATGCGCGCCGCTTGCTTCGGAACCTGGCGCCCTGCTCCCGGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAlaGluLeuCys 280
DB 1064 CACCAGCTGTGCTGCGCATGCCCGCACCTGCGCCGGCTCTTCGTGGCTGAGCTGTC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
DB 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGCGAGGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
DB 1184 TACCAGGGCGTCCCGAGAGCTGAGCGCGGACCGAGCGGAGACACTATGATGAAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
DB 1244 GTTCGGATGGGAGCGCTGGGGCTGTCTCGCAGTCGCGCATCTCCCTGGTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
DB 1304 GTCATGGACGGCTGGTCAGGATTCGCGACTCGAGCAGTCTATTGGCCAGTGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
DB 1364 GCTTTCCTGCTGGCTGCCGGTGCCACATGCTGCTCCACAGTGTGGCGTGGTACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
DB 1424 TCAGCGCGCTTCACCGGGTTACCTTCTCAGCGCTTCAGAGTCTGCTCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
DB 1484 TCCCTCTACCAACCGGAGGAGGAGTGTCTTGCCCAATACCGAGGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
DB 1544 GCTAGCAGTGAAGACAGCTGATGACACAGCTTCCTGCCAGGCGCTAAGCCTGGAGCTCCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
DB 1604 TTCCCTAATGACACGTGGGTGCTGGAGGCACTGGCCCTGCCACCTCCACCGCGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480
DB 1664 TCGGGGGCTTGGCTGTGATGCTCCGTACGTGTGGTGGGTGAGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyLeuCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
DB 1724 AGGGTGGTTCCGGCGCGGGCATCTGCCTGGACCTCGCCATCTCTGATGCTTCCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
DB 1784 CTGTCCCAAGTGGCCCACTCCCTGTTTATGGCTCATTTGTCCAGCTCAGCAGCTGTCTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
DB 1844 ACTGCTATATGGGTGCTGCCGAGCGCTGGGTCTGGTGGCCATTACTTGTGTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 1904 GTAGTATTTGACAGAGCGACTTGGCCAAATACATCAGCG 1942
RESULT 11
AAH84779
ID AAH84779 standard; cDNA; 3410 BP.
XX
AC AAH84779;
XX
DT 25-SEP-2001 (first entry)
XX
```

```
DE Human prostate-specific cDNA sequence LI-12/P501S.
XX Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KW chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW prostate specific antigen; PSA; ss.
XX
OS Homo sapiens.
PN WO200134802-A2.
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US30904.
XX
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
XX
PA (CORI-) CORIXA CORP.
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;
XX WPI; 2001-308785/32.
XX
PT Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer.
XX
PS Claim 5; Page 164-165; 325pp; English.
XX
CC The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production.
CC The polypeptides, nucleic acids and antibodies from the present
CC invention are useful in the diagnosis and therapy of prostate cancer.
CC Prostate specific genes P704P, P712P, P775P, P774P, and B305D are located
CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC region. Prostate specific antigen (PSA) P501S was located on
CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
CC polynucleotide and polypeptide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:
Pred. No.: 1.58e-218 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-593-793A-113 (1-553) x AAH84779 (1-3410)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
DB 284 ATGTTCACAGAGCTGTGGTGTAGCGCCCTGCTGGCGCACCGGAAAGCCAGCTCTGTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaIleGlyIleThrTyrValPro 40
DB 344 CTCACCTCTAACCCTTTGGCTGGAGGTGTGTTGGCGCGGAGGATCACCTATGTGCGG 403
QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
DB 404 CCTCTGCTGGAGTGGGGGTAGAGGAGAGATTTCATGACCATGGTCTGGGCAATTGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
DB 464 CCAGTGTGGCGCTGGTGTGTGTCCTAGCTAGCTCAGCAGTACGACCTGGCGTGA 523
QY 81 ArgTyrGlyArgArgPropheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
```


Pred. No.:	1.58e-218	Length:	3410
Score:	2861.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0
US-09-593-793a-113 (1-553) x AAH02530 (1-3410)			
Qy	1	MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu	20
Db	284	ATGGTCCAGAGCGTGGGGTAGCCCGCTGCTGCCGACACCGGAAAGCCAGCTCTTGCTG	343
Qy	21	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro	40
Db	344	GTCACCTCTTAACCTTTGGCCCTGGAGGTGCTTTGGCCGACAGGCATCACCTATGTGCGG	403
Qy	41	ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly	60
Db	404	CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAGTTTCATGACCATTGCTGGGCATTGGT	463
Qy	61	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly	80
Db	464	CCAGTCTGGGCTGCTGTGTCCTGCCGCTCCTAGGCTCAGCCAGTGCACCTGGCGTGA	523
Qy	81	ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu	100
Db	524	CGCTATGGCCGCGCGGCCCTTCATCTGGGCACCTGCTCTTGGGCATCCTGCTGAGCCTC	583
Qy	101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu	120
Db	584	TTTCTCATCCCAAGGCCCGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCACAGGCCCTG	643
Qy	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe	140
Db	644	GAGCTGGCACTGCTATCCTGGCGTGGGGCTGCTGGACTTCTGGCCAGGTGTGCTTC	703
Qy	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160
Db	704	ACTCCACTGAGGCCCTGCTCTGACCTCTCCGGGACCCGACCACTGTCGCCAGGCC	763
Qy	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180
Db	764	TACTCTGTATGCTTTCATGATCATGCTTTGGGGCTGCTGGGTACCTCCTGCTGCC	823
Qy	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe	200
Db	824	ATTGACTGGGACACCACTGCTGCCCCCTACCTGGGCACCCAGAGGAGTGCCCTCTTT	883
Qy	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
Db	884	GCCCTGCTCACCCCTCATCTTCCTACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAG	943
Qy	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
Db	944	GCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTGCGCCCTCCTCTGTGCGCCCA	1003
Qy	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyValAlaLeuLeuProArgLeu	260
Db	1004	TCCTGTCCATGCGGGCCGCTTGGCTTTCCGGAACCTTGGGCGCCCTGCTTCCCCGGCTG	1063
Qy	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280
Db	1064	CACCACTGTGTGCGCATGCCCGACCCCTGCGCGGCTCTTCGTGGCTGAGCTGTGC	1123
Qy	281	SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu	300
Db	1124	AGCTGGATGGCACTCATGACCTTCACGCTGTTTACAGGATTTCTGTTGGCGAGGGGCTG	1183
Qy	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly	320
Db	1184	TACCAAGGCGCTGCCAGAGCTAGCGCGGACCCGAGGCCCGGAGACACTATGATGAAGC	1243

Qy	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340
Db	1244	GTTCGGATGGCAGCGCTGGGGCTGTTCCTGCAGTCCGCCATCTCCTGGTCTTCTCTTG	1303
Qy	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla	360
Db	1304	GTCATGGACCGGCTGGTCAGCGATTGGCACTTCGAGCAGTCTATTGGCCAGTGGCA	1363
Qy	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla	380
Db	1364	GCTTTCCCTGTCGCTGCCGTGCCACATGCCCTGTCCACAGTGTGCCGTGGTGCAGCT	1423
Qy	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400
Db	1424	TCAGCGGCCCTCACCGGTTACCTTCTCAGGCCCTGCAGATCCTGCCCTACACACTGGCC	1483
Qy	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	420
Db	1484	TCCCTCTACCAACCGGAGAACGAGGTTCCTGCCCAATACCGAGGGACACTGGAGT	1543
Qy	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440
Db	1544	GCTACAGTAGCAGCAGCCTGATGACAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTGCC	1603
Qy	441	PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu	460
Db	1604	TTCCCTAATGGACACGTGGGTGCTGGAGCAGTGGCTGCCACCTCCACCCGCGCTC	1663
Qy	461	CysGlyAlaSerAlaCysAspValSerValAtgValValValGlyGluProThrGluAla	480
Db	1664	TCGCGGGCTCTGCTGCTGATGTCCTCCATGCTGTGGTGGTGAGCCCAACCCAGGCC	1723
Qy	481	ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500
Db	1724	AGGGTGGTTCCGGCGCGGGCATCTGCCCTGGACCTGCCATCCTGGATAGTCCCTTCCTG	1783
Qy	501	LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
Db	1784	CTGTCCCAAGTGGCCCATCCCTGTTTATGGCTCCATTGTCCAGCTCAGCCAGTCTGTC	1843
Qy	521	ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	540
Db	1844	ACTGCTATATGGTCTGCCGACGGCTGGGTCTGGTCGCATTTACTTTGCTACACAG	1903
Qy	541	ValValPheAspLysSerAspLeuAlaLysTyrSerAla	553
Db	1904	GTAGTATTGACACAGGCACTTGGCCAAATACTCAGCG	1942
RESULT 13			
ABL94929			
ID	ABL94929	standard; cDNA; 3410 BP.	
XX	ABL94929;		
AC	ABL94929;		
DT	19-JUL-2002	(first entry)	
XX			
DE	Human L1-12	cdna sequence SEQ ID NO 110.	
XX			
KW	Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;		
KW	gene therapy; gene; ss.		
OS	Homo sapiens.		
XX			
PN	US200202248-A1.		
XX			
PD	21-FEB-2002.		
XX			
PF	12-JAN-2001; 2001US-0759143.		
XX			
PR	25-FEB-1997; 97US-0806099.		
PR	01-AUG-1997; 97US-0904804.		
PR	09-FEB-1998; 98US-0020956.		
PR	25-FEB-1998; 98US-0030607.		

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PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
(XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
XU J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
WPI; 2002-255649/30.
XX
New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer -
XX
Claim 1; SEQ ID NO 110; 87pp; English.
PS
The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Alignment Scores:
Pred. No.: Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-593-793a-113 (1-553) x ABL94929 (1-3410)
QY 1 MetValGlnArgLeuTyrValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 284 ATGGTCCAGAGCGCTGGGGTGAGCCGCTGCTGGCGCACCGGAAAGCCAGCTCTTGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGCTTTGGCGCGCAGGCATCACCTATGTGCGG 403
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QY 41 ProLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGGTGTGGCATGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGGCTGGTCTGTCTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCGGCTTCATCTGGGCACCTGCTTGGGCATCTGCTGAGCCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGCGGCTGGCTAGCAGGGCTGCTGCCCCGATGCCAGGCCCTG 643
QY 121 GluLeuAlaLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTGGCGGTGGGCTGCTGGACTTCTGTGGCCAGGTGCTTTC 703
QY 141 ThrProLeuGluAlaLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCGCTGCTCTGACCTCTTCCGGGACCCGACACTGTGCGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGCTCATGCTTCATGATCAGTCTTGGGGGCTGCTGGGCTACCTCTGCTGCTCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 824 ATTGACTGGGACACAGTCGCCCTACCTGGGCGCACCCAGGAGAGTGCCTCTTT 883
QY 201 GlyLeuLeuThrIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluLeu 220
Db 884 GGCTGCTCACCTCATCTTCTCCTCCTGCTAGCAGCCACACTGCTGCTGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGGCGTGGGCGCCCGCCAGCGAGGAGGCTGTGCGGCCCTCTCTTGTGCGCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATGCGGGCGCGCTTGGCTTTCGGAACCTGGGCGCGCTGCTCCCGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGCTGCCGATGCCCGCACCTGCGCGCGCTTCTGCTGCTGAGTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCAGCGTGTTCACACGGATTTCGTGGCGGAGGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTrpAspGluGly 320
Db 1184 TACCAGGGGCTGCCAGAGCTGAGCGGCGCACCGAGGCCCGGAGACACTATGATGAAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGCGAGCTGGGGCTGTTCCTGTCAGTGGCGCATCTCCCTGCTTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGGACCGGCTGGTGCGAGGATTCGGCACTCGAGCAGTCTATTGGCCAGTGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCCTGTGGCTGCCGTCACATGCTTCCCACAGTGTGCCGCTGTGTGACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCCTCACCGGGTTACCTTCTCAGCCCTGCAGATCCTGCCCTTACACACTGGCC 1483
```



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Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGTCGGCATGCGCCGACCCCTGCGCGGCTCTTCTGGCTGAGCTGTC 1123
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrLeuPheValGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTGTTTACAGGATTCGTGGCGAGGGGTG 1183
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCGTCCAGAGCTGAGCGCGGACCCGAGGCGGAGACACTATGATGAAGC 1243
Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGGAGCGCTGGGGCTGTCTCTGAGTCGCGCATCTCCCTGCTCTCTCTG 1303
Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGGACCGGCTGGTCAGCGATTCGCGCACTCGAGCAGTCTATTGGCCAGTGTGCA 1363
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCTGTGGCTGCGGGTCCACATGCTCCACAGTGTGGCGTGGTGACACT 1423
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCTCACCGGTTCACTTCACGCTTCAGCCCTGCAGATCTCCCTACACACTGGCC 1483
Qy 401 SerLeuTyrHisArgGluGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCCTCTACCAACCGGAGGAGCGGTGTCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCT 1543
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 CTTAGCACTGAGGACGCTGATGACAGCTTCTGTCAGGCGCTTCCAGGCTGAGGCTGCC 1603
Qy 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCCTAATGGACAGCTGGGTGCTGGAGGACGTGGCTCCACCTCCACCGCGCTC 1663
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480
Db 1664 TCGGGGCTCTGCTGTGTGTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1723
Qy 481 ArgValValProGlyArgGlyLeuCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1783
Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGGCGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1843
Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1903
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTGACAGAGCGACTTGCCCAATACTCAGCG 1942
RESULT 15
ID AAS64040
XX AAS64040 standard; cDNA; 4034 BP.
XX AC AAS64040;
XX DE
XX DT 29-JAN-2002 (first entry)
XX DE
XX KW Human prostate cDNA P553s splice variant #3.
XX OS Human; prostate cancer; ss: cytostatic; immunostimulant; tumour.
XX OS Homo sapiens.
```

XX WO200173032-A2.

XX 04-OCT-2001.

XX 27-MAR-2001; 2001WO-US09919.

XX 27-MAR-2000; 2000US-0536857.

XX 09-MAY-2000; 2000US-0568100.

XX 12-MAY-2000; 2000US-0570737.

XX 13-JUN-2000; 2000US-0593793.

XX 27-JUN-2000; 2000US-0605783.

XX 10-AUG-2000; 2000US-0636215.

XX 29-AUG-2000; 2000US-0651236.

XX 06-SEP-2000; 2000US-0657279.

XX 02-OCT-2000; 2000US-0679426.

XX 10-OCT-2000; 2000US-0685166.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

XX Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;

XX Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;

XX WPI; 2001-639232/73.

XX New human prostate-specific polypeptides and polynucleotides useful for

XX the diagnosis and treatment of cancer, especially prostate cancer -

XX Claim 1; Page 483-484; 579pp; English.

XX The invention relates to isolated prostate-specific

XX polynucleotides, polypeptides, fusion proteins of the polypeptides,

XX antibodies raised against the polypeptides (or antigenic epitopes

XX derived from them) and antigen-presenting cells expressing the

XX polypeptides. The antibodies are useful for detecting the presence of

XX cancer, especially prostate cancer. The polypeptides, polynucleotides and

XX the antigen-presenting cells are useful for stimulating and/or expanding

XX T cells specific for a tumour protein, and for inhibiting the development

XX of cancer especially prostate cancer. Compositions comprising the

XX polynucleotide and/or polypeptide are useful for stimulating an immune

XX response, and for treating cancer. The oligonucleotide is useful for

XX detecting cancer. The present sequence is a prostate specific

XX polynucleotide of the invention.

XX Sequence 4034 BP; 721 A; 1226 C; 1141 G; 946 T; 0 other;

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Alignment Scores:

Pred. No.: 6,72e-207 Length: 4034

Score: 2716.50 Matches: 553

Percent Similarity: 70.09% Conservative: 0

Best Local Similarity: 70.09% Mismatches: 0

Query Match: 94.95% Indels: 236

DB: 22 Gaps: 1

US-09-593-793A-113 (1-553) x AAS64040 (1-4034)

Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20

Db 281 ATGTCCAGAGGCTGTGGGTGAGCGGCTGCTGGCGGACCGGAAAGCCAGCTCTTGTCTG 340

Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40

Db 341 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCCGCGGACATCACCATTGTGCGG 400

Qy 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60

Db 401 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAAGTTCATGACCATGCTGGCGATTGGT 460

Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80

Db 461 CCAGTGTGGGCGCTGGTGTGTGTCCTGCTAGGCTCAGCCAGTGGACCTGGCGGTGA 520

QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuSerLeu 100
|||||
Db 521 CGTATGGCGCGCGGCCCTTCATCTGGGCACTCTCTTGGGCATCTCTGAGCCTC 580
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTCTCATCCCAAGGCGCGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCAGGCCCTTG 640
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 641 GAGCTGGCACTGCTCATCTGGCGTGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTC 700
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGGCCCTGCTCTGTACCTCTTCGSGGACCCGACACCTGTGCCAGGCC 760
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrIleLeuProAla 180
Db 761 TACTCTGTCTATGCCCTTCATGATCATGTCTTGGGGCTGGCTGGGCTACCTCTGCTGCC 820
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 821 ATTGACTGGGACACCACTGCCCTGGCCCCCTACCTGGGGACCCAGGAGAGTGCTCTTT 880
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 881 GGCCCTGCTCACCTCATCTTCTCACCTGCTAGCAGCCACACTGCTGTGTGGCTGAGGAG 940
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 941 GCAGCCCTGGGCCCCACCAGGACAGAGAGGGCTGTCCGCCCTCTCTTGTGCCCCAC 1000
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1001 TGCTGTCCATGCGGCGCGCTTGGCTTCCGGAACCTGGGCGCCCTGCTTCCCGGCTG 1060
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1061 CACCAGCTGTGTGCCGATGCCCGCACCCCTGCGCGGCTCTTCTGTGGCTGAGCTGTGC 1120
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1121 AGCTGATGGCACTCATGACCTTCAGCTGTGTTTACCGGATTTCTGTGGCGAGGGGCTG 1180
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGlu--- 319
Db 1181 TACCAGGGCTGCCAGAGCTGAGCGGGCACCGAGGCCGAGACACTATGATGAAGT 1240
QY 319 ----- 319
Db 1241 AAGGCCCTGGCAGCCAGCAGAGGCTGGTGTGGGAGCGCGCCACCAGACGACACTCGGG 1300
QY 319 ----- 319
Db 1301 GCTGTCTGGGCTGGTGCCTCTCCATCCTGCGCCCGACTTCTCTGTACAGAAAGTGGGG 1360
QY 319 ----- 319
Db 1361 ATGGAGCCCATCTGCATACACGGCTTCTCATGGGTGTGGAACACTCTGCTTGGGTTTC 1420
QY 319 ----- 319
Db 1421 AGGAAGCCCTCTGGTGTCTTAGGAGTCTGATCAGAGTGGTGTGCCCTAGTTTGACAGAAG 1480
QY 319 ----- 319
Db 1481 GAAAGCGGAGCTTATTCAAAGCTTAGAGGGAGTGGAGAGTTAAGGCTGGATTTCAGAT 1540
QY 319 ----- 319
Db 1541 CTGGCTGGTTCCAGCGGAGTGTGCCCTGTCTCCCCACACACTTTCCAAATAATCTCA 1600
QY 319 ----- 319

Db 1601 CCAGCGCCTTCCAGCTCAGGCGTCTTAGAAGGCTCTTGAAGCCTATGGCCAGCTGTCTTT 1660
QY 319 ----- 319
Db 1661 GTGTTCCTCTTCAACCGCCTGTCTCACAGCTCCAGAAACCTTCAGACTACC 1720
QY 319 ----- 319
Db 1721 TTCTCTGCTTTCAGCAAGGGGCTTGCCACATCTCTGAGGGTCACTGGAGAACCTTA 1780
QY 319 ----- 319
Db 1781 GACTCCCATTTGCTAGAGGTAGAAAGGAGGTGTGGGAGCAGGGCTGTCCACAGC 1840
QY 319 ----- 319
Db 1841 AGGTCTGCTGCAGCAGGTACCTGTGGTTCGCGCTTCTCATCTCCCTGAGACTGCTCCGAC 1900
QY 320 ----- GlyValArgMetGlySe 325
Db 1901 CCTTCCCTCCAGGCTCTGTCTGTATGGGCCCTTCTCCCTGTGAGGGCTTCGGATGGCAG 1960
QY 325 rLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLe 345
Db 1961 CCTGGGGCTGTTCCTGCACTGCGCATCTCCCTGTCTCTCTGCTCATGGACGGCT 2020
QY 345 uValGlnArgPheGlyThrArgAlaValTyrLeuAlaLeuSerValAlaPheProValAl 365
Db 2021 GGTGAGCGATTCGGCACTCGAGCAGTCTATTGTGCCAGTGTGGCAGCTTCCCTGTGGC 2080
QY 365 aAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuTh 385
Db 2081 TGCCGGTGCCACATGCTTCCACAGTGTGCCGTGGTGACAGCTTCAGCCGCCCTCAC 2140
QY 385 rGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisAr 405
Db 2141 CGGGTTACCTTCTCAGCGCTGCAGATCTTCCCTACACACTGGGCTTCCCTTACACCG 2200
QY 405 gGluGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAs 425
Db 2201 GGAGAGCAGGGTTCTCTGCCCAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGA 2260
QY 425 pSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHi 445
Db 2261 CAGCCTGATGACCACTTCTTCCAGGCCCTAAGCCTGAGCTCCCTTCCCTTAATGGACA 2320
QY 445 sValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAl 465
Db 2321 CGTGGGTGCTGGAGCAGTGGCTGCTCCCACTCCAGCCGCGCTCTGCGGGCGCTCTGC 2380
QY 465 aCysAspValSerValArgValValValGlyGluProThrGluAlaArgValValProGl 485
Db 2381 CTGTGATGTCTCCGTACGTGTGGTGGGTGAGCCACCGAGGCCAGGGTGGTTCGGGG 2440
QY 485 yArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAl 505
Db 2441 CCGGGCATCTGCCTGGACCTGCGCATCTCGATAGTGCCTTCTCTGCTTCCAGGTGGC 2500
QY 505 aProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVa 525
Db 2501 CCCATCCCTGTTATGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCTATATGCT 2560
QY 525 lSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLy 545
Db 2561 GTCTCCCGCAGGCCCTGGGTGCTGGTCGCATTTACTTTGCTACACAGGTAGTATTTGACAA 2620
QY 545 sSerAspLeuAlaLysTyrSerAla 553
Db 2621 GAGCCACTTGGCCAATACTACGCG 2645
RESULT 16
AAH93868


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QY 319 ----- 319
Db 1541 CTGCTGTTCAGCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCAAAATAATCTCA 1600
QY 319 ----- 319
Db 1601 CCAGCGCCTTCCAGCTCAGCGCTCCTAGAGCGCTTGAAGCCTATGGCCAGCTGTCTTT 1660
QY 319 ----- 319
Db 1661 GTGTTCCCTCTCACCGCGCTGTCTCACAGCTGAGACTCCCAAGAAACCTTCAGACTACC 1720
QY 319 ----- 319
Db 1721 TTCTCTTGCTTTCAGCAAGGGCGTGTGCCACATTTCTCTGAGGTCAGTGAAGAACCTA 1780
QY 319 ----- 319
Db 1781 GACTCCCATGTAGAGGTAGAAAGGGAGGGGTGCTGGGGAGCAGGGCTGTCTCCACAGC 1840
QY 319 ----- 319
Db 1841 AGGTCTCGTGACAGGTACCTGTGGTTCGGCTTCTCATCTCCCTGAGACTGCTCCGAC 1900
QY 320 -----GlyValArgMetGlyse 325
Db 1901 CCTTCCCTCCAGGCTCTGTCTGATGGGCCCTCTCCCTCTGCAGGCGTTCCGATGGCAG 1960
QY 325 rleuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLe 345
Db 1961 CTTGGGGCTGTTCCTGCAGTGGCGCATCTCCCTGTCTCTCTGTCATGTGACCGGCT 2020
QY 345 uValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAl 365
Db 2021 GGTGAGCAGATTCCGACATCGACAGTCTATTGGCCAGTGTGGCAGCTTCCCTGTGGC 2080
QY 365 aAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuTh 385
Db 2081 TGCCGGTGCCACATGCTGTCCACAGTGTGGCCGTGTGACAGCTTCAGCGCGCCTCAC 2140
QY 385 rGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisAr 405
Db 2141 CGGGTTCACCTTCTCAGCCCTGCATGCTGCCCTACACACTGGCCTCCCTTACACCG 2200
QY 405 gGlyLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAs 425
Db 2201 GGAGAGCAGGTGTCTCCGCCCAATACGAGGGACACTGGAGGTGCTAGCAGTGAGGA 2260
QY 425 pSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHI 445
Db 2261 CAGCCTGATGACCACTTCTCCAGGCCCTAAGCCTGGAGTCCCTTCCCTAATGGACA 2320
QY 445 sValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAl 465
Db 2321 CGTGGGTGCTGAGCAGTGGCCTGCTCCCACTCCACCGCGCTCTCGGGGCGCTTCGC 2380
QY 465 acYaspValSerValArgValValValGlyGluProThrGluAlaArgValValProGl 485
Db 2381 CTGTGATGTCTCCGTACGTGGTGGTGGTGAGGCCACCGAGGCCAGGGTGGTTCCGGG 2440
QY 485 yArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuSerGlnValAl 505
Db 2441 CCGGGGCATCTGCCCTGGACCTCGCCATCTTGATAGTGCCTTCTCTGCTGCCAGGTGC 2500
QY 505 aProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVa 525
Db 2501 CCATCCCTGTTATGGGCTCATGTGTCAGCTCAGCCAGTGTGTCAGTGCCTATATGGT 2560
QY 525 lSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLy 545
Db 2561 GTCCTCCGCGAGCGCTGGTGTGGTGGCCATTACTTTCCTACACAGGTAGTATTGGAA 2620
QY 545 sSerAspLeuAlaLysTyrSerAla 553
```

```
Db 2621 GAGCGACTTGGCCAAATACTACGCG 2645
RESULT 17
ABL95411
ID ABL95411 standard; cDNA; 4034 BP.
AC ABL95411;
XX
XX 19-JUL-2002 (first entry)
XX
XX Human P553S splice variant SEQ ID NO 704.
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX US2002022248-A1.
XX
XX 21-FEB-2002.
XX
XX 12-JAN-2001; 2001US-0759143.
XX
XX 25-FEB-1997; 97US-0806099.
XX 01-AUG-1997; 97US-0904804.
XX 09-FEB-1998; 98US-0020956.
XX 25-FEB-1998; 98US-0030607.
XX 14-JUL-1998; 98US-0115453.
XX 23-SEP-1998; 98US-0159812.
XX 15-JAN-1999; 99US-0232149.
XX 09-APR-1999; 99US-0288946.
XX 13-JUL-1999; 99US-0352616.
XX 12-NOV-1999; 99US-0439313.
XX 18-NOV-1999; 99US-0443686.
XX 14-JAN-2000; 2000US-0483672.
XX 27-MAR-2000; 2000US-0536857.
XX 09-MAY-2000; 2000US-0568100.
XX 12-MAY-2000; 2000US-0570737.
XX 13-JUN-2000; 2000US-0593793.
XX 27-JUN-2000; 2000US-0605783.
XX 10-AUG-2000; 2000US-0636215.
XX 29-AUG-2000; 2000US-0651236.
XX 06-SEP-2000; 2000US-0657279.
XX 02-OCT-2000; 2000US-0679426.
XX 10-OCT-2000; 2000US-0685166.
XX
XX (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler, WT, Henderson RA;
XX
XX WPI; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
```

PT progression of cancer

XX
XXXXX-00000-6877

PS Claim 1; SEQ ID NO 704; 87pp; English.
XX
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.

Sequence 4034 BP; 721 A; 1226 C; 1141 G; 946 T; 0 other;

Alignment Scores:

Pred. No.:	6, 72e-207	Length:	4034
Score:	2716.50	Matches:	553
Percent Similarity:	70.09%	Conservative:	0
Best Local Similarity:	70.09%	Mismatches:	236
Query Match:	94.95%	Indels:	1
DB:	24	Gaps:	

US-09-593-793A-113 (1-553) x ABL95411 (1-4034)

QY	1	MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu	20
DB	281	ATGGTCCAGAGGTGTGGGTGAGCCGCTGCTGCGCACCGAAAGCCAGACTGTGCTG	340
QY	21	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaCyltIleThrTrValPro	40
DB	341	GTCAACTGCTAACTTTGGCTTGGAGGTGTGTTTGGCCGAGGCATCACCTATGTGGCG	400
QY	41	ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly	60
DB	401	CCCTCTGCTGCGAAGTGGGGGTAGAGGAGAAGTTTCATGCCATGGTGGTGGCATTGGT	460
QY	61	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly	80
DB	461	CCAGTGTGGGCTGTGCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACCTGGGCTGGA	520
QY	81	ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu	100
DB	521	CGCTATGGCCGCGCCGCGCCCTTCATCTGGGCACCTGTCTTGGGCATCTGCTGAGCCCTC	580
QY	101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu	120
DB	581	TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTCTGTGCCGGATCCCAGGCCCTGT	640
QY	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe	140
DB	641	GAGCTGGCACTGCTCATCTCTGGCGGTGGGGTCTGTGGACTTCTGTGGCCAGAGTGTCTC	700
QY	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160
DB	701	ACTCCACTGGAGCCCTGCTCTCTGACCTTCTCCGGGACCCGACACCTGTCTGCCAGGCC	760
QY	161	TyrSerValTrpAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrTrLeuLeuProAla	180
DB	761	TACTCTGTCTATGCCCTCATGATCAGTCTTGGGGCTGCTTGGGTACCTCTGCTGCTGCC	820
QY	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe	200
DB	821	ATTGACTGGGACACCAAGTGCCTTGGCCCTTACCTTGGGACCCAGAGAGTGCCTCTTT	880
QY	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
DB	881	GGCTCTGCTACCCCTCATCTTCTTCACTCGGTAGCAGCCACACTGCTGGTGGCTGAGGAG	940
QY	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
DB	941	GCAGCGCTGGGCCCCACCGAGCCAGAGAAGGGCTGTCTGCGCCCTCTCTTGTCTGCGCCCA	1000
QY	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260
DB	1001	TGCTGTCCATGCGCGCCGCTTGGCTTTTCCGAACTGGGCGCTGCTCTCCCGGGTGT	1060

Db 2141 CCGGTTACCTTCTCAGCCCTCAGATCCTGCCCTACACACTGGGCTCCCTTACACCG 2200
Qy 405 gGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAs 425
Db 2201 GGAGAACGAGGTCTCTGCCCAATACGAGGGGACACTGAGGTGTAGCAGTGAGA 2260
Qy 425 pSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHi 445
Db 2261 CAGCCTGATGACCACTTCTCTCCAGGCCCTTAAGCCTGGAGCTCCCTTCCCTAATGGACA 2320
Qy 445 sValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeuCysGlyAlaSerAl 465
Db 2321 CGTGGGTGTGAGGAGCAGTGGCTCTCCACCTCCACCGCGCTCTCGGGGCTCTGC 2380
Qy 465 acYasPValSerValArgValValValGlyGlyProThrGluAlaArgValValProGl 485
Db 2381 CTGTGATGTCTCCGACGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2440
Qy 485 yArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAl 505
Db 2441 CCGGGGCATCTGCCTGGACCTCGCCATCTCGATAGTGCCTTCTCTCCAGGTGGC 2500
Qy 505 aProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVa 525
Db 2501 CCATCCCTGTATTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCCTATATG 2560
Qy 525 lSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLy 545
Db 2561 GTCTGCCGAGCCCTGGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2620
Qy 545 sSerAspLeuAlaLysTyrSerAla 553
Db 2621 GAGCGACTTGGCCAAATACTCAGCG 2645
RESULT 18
ABA91283
ID ABA91283 standard; DNA: 2133 BP.
XX ABA91283;
XX
XX
DT 08-APR-2002 (first entry)
XX
DE ThioRedoxin-ubiquitin-P501S(aa55-553)His triple gene fusion.
XX
KW ThioRedoxin; trxA; ubiquitin; P501S; tumour; prostate; antigen;
KW cancer; vaccine; therapy; human; gene; ds.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Escherichia coli.
PN WO200200892-A1.
XX
PD 03-JAN-2002.
XX
PF 19-JUN-2001; 2001WO-EP06952.
XX
PR 26-JUN-2000; 2000GB-0015619.
PR 30-OCT-2000; 2000GB-0026484.
XX
PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Cabezon Silva TEV, Delisse AEF;
XX
DR WPI; 2002-147888/19.
DR P-PSDB; AAM50661.
XX
PT Novel DNA sequence encoding triple fusion protein comprising ubiquitin
PT fused between thioRedoxin and polypeptide of interest, useful for
PT producing recombinant polypeptide of interest suitable for medicinal
PT use
XX
PS Example 5; Fig 9a; 87pp; English.

XX The present sequence is that of a triple gene fusion comprising,
CC from the 5' end, the trxA thioRedoxin gene from Escherichia coli,
CC the human ubiquitin coding sequence, the prostate antigen P501S
CC (amino acids 55-553) coding sequence, and DNA encoding a histidine
CC tail. The triple fusion was constructed in plasmid pRIT15063,
CC which included the Saccharomyces cerevisiae CUP1 promoter and
CC yeast alpha prepro signal sequence. The triple fusion protein
CC (see AAM50661) was produced in E. coli G1724 transformants. This
CC is an example of the production of triple fusion proteins of the
CC invention comprising ubiquitin fused between thioRedoxin and a
CC protein of interest, in this case P501S(aa55-553). A claimed method
CC of producing a recombinant protein of interest involves: culturing
CC a host cell (preferably E. coli) under conditions which allow
CC for co-expression of the triple fusion and a ubiquitin-specific
CC endoprotease (especially UBPI from Saccharomyces cerevisiae);
CC and recovering the recombinant protein directly from the bacterial
CC cells after it has been subjected to the action of the
CC ubiquitin-specific endoprotease in vivo. In the present case,
CC a p501-like protein of 509 amino acids is generated. The
CC recombinant protein can used as a vaccine for cancer therapy.
XX
SQ Sequence 2133 BP; 384 A; 656 C; 614 G; 479 T; 0 other;

.. Alignment Scores:
Pred. No.: 4.89e-198 Length: 2133
Score: 2601.00 Matches: 501
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 90.91% Indels: 0
DB: 24 Gaps: 0

US-09-593-793A-113 (1-553); x ABA91283 (1-2133)
Qy 53 MetThrMetValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGly 72
Db 604 ATGACCATGGTGTGGGCAATTGGTCCAGTGTGGGCTGGTGTGTGCCGCTCTAGGC 663
Qy 73 SerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAlaLeu 92
Db 664 TCAGGCAGTGACCACTGGCGTGGAGCGCTATGCGCGCGCGCGCCCTTCATCTGGGCACTG 723
Qy 93 SerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeu 112
Db 724 TCCTTGGGCATCTCTGCTGAGCCTCTTCTCATCCCAAGGCGCGGCTGTAGCAGGCTG 783
Qy 113 LeuCysProAspProArgProLeuGluLeuAlaLeuLeuLeuGlyValGlyLeuLeu 132
Db 784 CTGTGCCCGGATCCAGGCGGCTGGAGCTGGCAGTGCATCTCTGGGCGTGGGCTGCTG 843
Qy 133 AspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArg 152
Db 844 GACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCGCTGCTCTCTGACCTCTTCGG 903
Qy 153 AspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGly 172
Db 904 GACCGGACCACTGTGCCAGCGCTACTCTGTCTATGCTTTCATGATCAGTCTTGGGCGC 963
Qy 173 CysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeu 192
Db 964 TCCTTGGGCTACCTCTGCTGCCATTGACGGGACACAGTGGCGCTGGCGGCTTACCTG 1023
Qy 193 GlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAla 212
Db 1024 GGCACCCAGGAGGAGTGGCTCTTTCGCTGCTCACCTCATCTTCTCACCTGCCTAGCA 1083
Qy 213 AlaThrLeuLeuValAlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeu 232
Db 1084 GCCACACTGCTGGTGCCTGAGGAGGAGCGCTGGGCGGCGCCACCGACGACGAGGCGGTG 1143
Qy 233 SerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsn 252
Db 1144 TCGGCCCCCTCTCTTGTGCCCCACACTGCTGTCCATCGCGGCGCGCTGGCTTTCCGGAAC 1203

QY 253 LeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArg 272
|||||
Db 1204 CTGGGGCCCTGCTCCCGGGTGCACACAGTGTCTGCCGATGCCCGCACCTGGCG 1263

QY 273 ArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyr 292
|||||
Db 1264 CGGCTCTTCGTGGCTGAGCTGTGACAGTGGATGGCACTCATCACCTTCACGCTGTTTAC 1323

QY 293 ThrAspPheValGlyGluLeuTyrGlnGlyValProArgAlaGluProGlyThrGlu 312
|||||
Db 1324 ACGGATTTCGTGGCGAGGGCTGTACCAAGGCGTGCACAGAGCTGAGCGGGCACCCGAG 1383

QY 313 AlaArgArgHisTyrAspGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCys 332
|||||
Db 1384 GCCCGGAGACACTATGATGAAGCGCTCGGATGGCAGCGCTGCTTCCTCGAGTGC 1443

QY 333 AlaIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArg 352
|||||
Db 1444 GCATCTCCCTGCTTCTCTCTGTCATGGACCGGCTGGTGCAGCGATTTCGGCACTCGA 1503

QY 353 AlaValTyrLeuAlaSerValAlaPheProValAlaAlaGlyAlaThrCysLeuSer 372
|||||
Db 1504 GCAGTCTATTGGCCAGTGTGCAGCTTTCCTGTGGCTGGCGGTGCCACATGCGCTGCC 1563

QY 373 HisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeu 392
|||||
Db 1564 CACAGTGTGGCGTGTGCACAGCTTCAGCGCGCTTCACCGGGTTCACCTTCACGCCCTG 1623

QY 393 GlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuPro 412
|||||
Db 1624 CAGATCCTGCCCTACACACTGGCCTCCCTCTACCAACCGGAGACAGGTGTTCTGCCC 1683

QY 413 LysTyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeu 432
|||||
Db 1684 AAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAAGACAGCCTGATCACCAGTTCCTG 1743

QY 433 ProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGly 452
|||||
Db 1744 CCAGCCCTAAGCTGGAGTCCCTCCCTAATGACACAGTGGGTGTGGAGGCAAGTGGC 1803

QY 453 LeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgVal 472
|||||
Db 1804 CTGCTCCCACTCCACCCCGCGCTCTGCGGGGCTCTGCTGTGATGTCTCCGTACGTGTG 1863

QY 473 ValValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeu 492
|||||
Db 1864 GTGGTGGGTGAGCCACCGAGGCCAGGGTGGTTCGCGGCGCGGGGATCTGCTGGACCTC 1923

QY 493 AlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySer 512
|||||
Db 1924 GCCATCCTGGATAGTCCCTTCTGCTGTCCAGGTGGCCCATCCCTCTTTATGGGCTCC 1983

QY 513 IleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeu 532
|||||
Db 1984 ATTGTCCAGCTCAGCCAGTGTCTACTGCTATATGTTGTCTGCCGAGCGCTGGGCTGTG 2043

QY 533 ValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSer 552
|||||
Db 2044 GTCCGCATTACTTTGCTACACAGGTAGTATTTGACAGAGCGACTTGGCCAAATACTCA 2103

QY 553 Ala 553
|||
Db 2104 GCG 2106

RESULT 19
AAS64038
ID AAS64038 standard; cDNA; 4894 BP.
XX
AC AAS64038;
XX
DT 29-JAN-2002 (first entry)
XX

DE Human prosate cDNA p53s splice variant #1.
XX
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US099919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX
XU Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2001-639232/73.
DR N-PSDB; AAU69874, AAU69875.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Claim 1; Page 480-482; 579pp; English.
XX
CC The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
SQ Sequence 4894 BP; 928 A; 1448 C; 1354 G; 1163 T; 1 other;

Alignment Scores:
Pred. No.: 1.39e-192 Length: 4894
Score: 2538 50 Matches: 551
Percent Similarity: 51.11% Conservative: 0
Best Local Similarity: 51.11% Mismatches: 2
Query Match: 88.73% Indels: 526
DB: 22 Gaps: 2

US-09-593-793A-113 (1-553) x AAS64038 (1-4894)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
|||||
Db 274 ATGGTCCAGAGGCTGTGGCTGAGCGCTGCTGCGGACCGAAAGCCAGCTCTTGCTG 333

QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||||
Db 334 GTCAACCTGCTAACTTTGGCTTGGAGGTGTGTTGGCGCGCAGCATCATGTGCGCG 393

QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeu----- 57
|||||

Db 394 CCTCTGCTCTGGAAGTGGGGTAGAGGAGAAAGTTTCATGACCATGGTGCT-GGGTGAGTC 452
QY 57 ----- 57
Db 453 ACTACATCCTCCTTCTTCCAGATACATGCCACCTGGCATGTGGGACAGAGTA 512
QY 57 ----- 57
Db 513 CCTCTGCCCTGGGAGCTGCTTGGAGGGAGAGGTGGTCTGCTGGGAAGGCATTGCTGGGCA 572
QY 57 ----- 57
Db 573 GGAGGGTGACCTTGGGCTGAGGGGGCACACCAAGAGAAAGAGAAATACCAAGGACATA 632
QY 57 ----- 57
Db 633 CCCAGTCACCTCTGGATCCCTGGTCTCCACAGAGCCTGGCTCATAGGAGACATGGAG 692
QY 57 ----- 57
Db 693 AAATGCTCTAAACCTTTGGCTAGCCCTTTTATAATTTATAGCGATTATCTCATTTAATGC 752
QY 57 ----- 57
Db 753 TTACAAACCACCATTTGAGGTGATCCATTTACAGAGAAAGAGAGCGCTTTTAAGAGG 812
QY 57 ----- 57
Db 813 TTAGGTAGTCTTAGCCAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCA 872
QY 57 ----- 57
Db 873 GGTCTCCAGCGGAGCTTGCTCTACCCCTAGGACAAAGGGGTGGACTCCTGACTGCA 932
QY 57 ----- 57
Db 933 GATAAATTTACAAAAGCCACAGAGGCAAGTAGTAACCATTTGTGTGACAAACCCCTCACC 992
QY 57 ----- 57
Db 993 CCCAGGAAGGGGCCCTGTGAGGATTGCAGGCTCGAGCTGAGCTCACACTGCTTTGTAAC 1052
QY 57 ----- 57
Db 1053 GCTGCTCTTACCCCTCCCTAGGTCTCGGCTTTTGAATAAGTATCACCTTCTTAGTGTCTCC 1112
QY 57 ----- 57
Db 1113 ATGCTCAGTTTGTCCATCTGAAATGGGGGCATCTGTAAATGCCTGTGTATGAGAGTA 1172
QY 57 ----- 57
Db 1173 AATTACAGCATCCCTGTGAAGACGTAGCACAGTGTGAGTACGGAATGTTATTTCATCC 1232
QY 57 ----- 57
Db 1233 TTCTCAGGAGCTTGGTTCCTCCCTTGCCCTTTACTTTGCTCCAGCCATTGACTCAT 1292
QY 58 -----GlyIleGlyProValLeuGlyLeuValIcysValProLeuLeu 71
Db 1293 ACTACTTCCCTTTCTGACGGCATTGGTCCAGTGTGGGCTGGTGTGTCCCGCTCCTA 1352
QY 72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyValArgArgProPheIleTrpAla 91
Db 1353 GCCTCAGCCAGTGACCACTGGGCTGGAGCTATGCCCGCCGCGCCCTTCATCTGGGCA 1412
QY 92 LeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly 111
Db 1413 CTGTCTTGGGCATCTGTGTAGCTCTTCTCTCATCCCAAGGCGGCTGGCTAGCAGGG 1472
QY 112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu 131
Db 1473 CTGCTGTGCCCCGATCCCAAGGCCCTGGAGCTGGCACTGCTCATCTCTGGGCGTGGGGCTG 1532

QY 132 LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151
Db 1533 CTGGACTTCTGTGGCCAGGTGCTTCACTCCACTGGAGGCCCTGCTCTCTCACTCTTC 1592
QY 152 ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
Db 1593 CGGGACCCGGACCACTGTGCCAGGCCCTACTGTCTATGCTTCTATGATCATGTGGG 1652
QY 172 GlyCysLeuGlyTyrLeuLeuProAlaIleAspTTrpAspThrSerAlaLeuAlaProTyr 191
Db 1653 GGCTGCTTGGGCTACTCTCTGCTGCCATTGACTGGGACACAGTGCCTGGCCCCCTTAC 1712
QY 192 LeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
Db 1713 CTGGGACCCAGGAGGTGCTCTTGGCCTGCTCACCTCATCTCTCTCACTACCTGCGTA 1772
QY 212 AlaAlaThrLeuLeuValAlaGluAlaLeuGlyProThrGluProAlaGluGly 231
Db 1773 GCAGCACACTGCTGGTGGCTGAGGAGCGCGCTGGGCCCCACCGAGCCAGCAGAAGG 1832
QY 232 LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg 251
Db 1833 CTGTCGGCCCCCTCTCTGTGCCCCACTGCTGTCCATGCCGGGCCCTGTGGCTTTCCGG 1892
QY 252 AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271
Db 1893 AACCTGGGGCCCTGCTTCCCGGCTGCACCACTGCTGCTGCATGCCCGCACCTCG 1952
QY 272 ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291
Db 1953 CGCCCGCTCTTCTGGTGGCTGAGCTGTGCAGCTGGATGGCACTCATGACCTTTCACGTT 2012
QY 292 TyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr 311
Db 2013 TACACGATTTCTGGGGCAGGGGCTGTACAGGGCTGCCAGAGCTGAGCGGGGCACC 2072
QY 312 GluAlaArgArgHisTyrAspGlu----- 319
Db 2073 GAGGCCCGAGACACTATGATGAAGCTTAAGGCTTTGGCAGCCAGCAGAGCTGGTGGG 2132
QY 319 ----- 319
Db 2133 AGCCCCCACCAGACAGACACTCGGGCTGTGTCTGGGCTGGTGCCTTCCATCCTGCG 2192
QY 319 ----- 319
Db 2193 CCCGACTTCTCTGTTCAGGAAGTGGGATGGACCCCATCTGCATACACGGCTTCTCATGG 2252
QY 319 ----- 319
Db 2253 GTGTGGAACATCTCTGCTTGGGTTTTCAGGAAGGCTCTGTGGCTGTCTAGGAGTCTGATC 2312
QY 319 ----- 319
Db 2313 AGAGTCGTTGCCCACTTTTGACAGAAAGGCGGAGCTTATTCAAAAGTCTAGAGGGAG 2372
QY 319 ----- 319
Db 2373 TGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCCGAGTGTGCCCTCTGCT 2432
QY 319 ----- 319
Db 2433 CCCCACACGACTTTCCAAATATCTCACAGCGCCTTCCAGCTCAGGCTCCTAGAAAGG 2492
QY 319 ----- 319
Db 2493 TCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCTCTCACCCGCTGTCTCTACAGCTG 2552
QY 319 ----- 319
Db 2553 AGACTCCAGGAACCTTCAGACTACCTTCTCTGCTTCCAGCAAGGGCGGTGGCCACA 2612


```
QY 319 ----- 319
Db 2613 TTCTCTGAGGTCAGTGAAGAACCTAGACTCCCATTCCTAGAGGTAGAAAGGGGAGGG 2672
QY 319 ----- 319
Db 2673 TGCTGGGAGCAGGCTGGTCCACAGCAGGTCCTGTCGAGCAGGTACCTGTGTTCGCC 2732
QY 319 ----- 319
Db 2733 TTCTCATCTCCTGAGACTGCTCGACCCCTCCCTCCAGGCTCTGTCTGATGGCCCTC 2792
QY 320 -----GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe 336
Db 2793 TCCCTCTCAGGCGTTCCGATGGCAGCGCTGGGGCTGTCTCGAGTCGCCCATCTCCCT 2852
QY 336 uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe 356
Db 2853 GGCTCTCTCTGGTCAATGGACCGCTGGTGCAGCGATTCGGCATCTCGAGCAGTCTATT 2912
QY 356 uAlaSerValAlaAlaPheProValAlaAlaGlyValAlaThrCysLeuSerHisSerValAl 376
Db 2913 GGCCAGTGGCAGCTTCCCTGTGGCTGGCTGGCGGTGCCACATGCCCTGCCACAGTGTGC 2972
QY 376 aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 396
Db 2973 CGTGTGACAGCTTCAGCGCGCTCACCGGGTTCACCTTCTCAGCGCTGCAGATCCTGCC 3032
QY 396 oTyrThrLeuAlaSerLeuTyrHisArgGlnGlyValPheLeuProLysTyrArgG1 416
Db 3033 CTACACACTGGCCCTCCCTTACCACCGGAGAGCAGGTGTCTCGCCCAATACCGAGG 3092
QY 416 yAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLy 436
Db 3093 GGACACTGGAGGTGCTAGCAGTGAGGACAGCGCTGATGACACAGCTTCTGCCAGGCCCTAA 3152
QY 436 sProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProPr 456
Db 3153 GCCTGGAGCTCCCTTCCCTAATGGACACAGTGGGTGTGGAGGCAGTGGCCTGCTCCACC 3212
QY 456 oProProAlaLeuGlyAlaSerAlaCysAspValSerValArgValValGlyG1 476
Db 3213 TCCACCGCGCTCTCGCGGGCTCTGCCTGTGATGTCTCCGTAGCTGTGTGGGTGA 3272
QY 476 uProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAs 496
Db 3273 GCCCAGCAGGCCAGGTTGGTTCCGGCCGGGGCATCTGCCGTGGACCTCGCCCATCTGGA 3332
QY 496 pSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLe 516
Db 3333 TAGTGCCTTCCCTGCTGCCAGGTGGCCCATCCCTGTTTATGGCTCCATTGTCCAGCT 3392
QY 516 uSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTy 536
Db 3393 CAGCAGTCTCTCACTGCCTATATGGTGTCTCGCGCGAGCGCTGGGTCTGTGGCGCAITTA 3452
QY 536 rPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 3453 CTTTGTACACAGGTAGTATTGTGACAGAGCGACTTGGCCCAATACTCAGCG 3504
RESULT 20
AAH93866
ID AAH93866 standard; cDNA; 4894 BP.
XX AC AAH93866;
XX AC
XX 04-OCT-2001 (first entry)
XX DE
XX DE P553S cDNA splice variant P553S-14.
XX KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
XX KW cytosstatic; gene therapy; metastasis; ss.
XX XX
```

```
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX
XX WPI; 2001-425873/45.
DR
XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines.
XX
PS Claim 1; Page 457-459; 543pp; English.
XX
XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC cells prepared using (I) or (II) are used to treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 4894 BP; 928 A; 1448 C; 1354 G; 1163 T; 1 other;

Alignment Scores:
Pred. No.: 1.39e-192 Length: 4894
Score: 2538.50 Matches: 551
Percent Similarity: 51.11% Conservative: 0
Best Local Similarity: 51.11% Mismatches: 2
Query Match: 88.73% Indels: 526
DB: 22 Gaps: 2

US-09-593-793A-113 (1-553) x AAH93866 (1-4894)

QY 1 MetValGlnArgLeuTyrPValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db 274 ATGTCACAGAGGCTGTGGGTGAGCGCTGCTGCGGCACCGAAAGCCAGCTTGTG 333
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 334 GTCACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCGCAGGCATCACCATTGTGCG 393
QY 41 ProLeuLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeu----- 57
Db 394 CCTCTGCTGTGGAAGTGGGGGTAGAGAGAAGTTCATGACCATGGTGCT-GGGTGAGTC 452
QY 57 ----- 57
Db 453 ACTACATCCCTCTTCCCTTCCTGTTCCAGATACATGCCACCTGGCATGTGGACAGAGTA 512
QY 57 ----- 57
Db 513 CCTCTGCCCTGGGAGCTGCTTGGAGGAGAGAGGTGCTGCTGGGAAGGCATTGCTGGCA 572
QY 57 ----- 57
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Db 573 GGAGGTTGACCCCTGGCTGAGGGGCGACACCAAGAGAAAGAGAAATACCAAGGACATA 632
QY 57 ----- 57
Db 633 CCCAGTCACTCTGGATCCCTGGTCCTGCACAGAGCCTGGCTCATAGGAGACACTGGAG 692
QY 57 ----- 57
Db 693 AAATGCTCTAACCCTTGGCTAGCCCTTTTATAATTTATAGGATTATCTCATTTAATGC 752
QY 57 ----- 57
Db 753 TTACAACCACCATTGAGGTGATCCATTTTACAGAGAAAGAGAGAGGCTTTTAAAGAG 812
QY 57 ----- 57
Db 813 TTAGTAAAGTCTTAGCCAAAGCCAATAGCAGCTCAACAGTAGAGCTGGACTCCATCAA 872
QY 57 ----- 57
Db 873 GGTCTCCAGCGGAGCTTGCTTCCTACCCTAGGACAAGGGGTGGACTCTGACTTGCA 932
QY 57 ----- 57
Db 933 GATAAATTTACAAAAGCCACAGAAGGCAAGTAGTAACCATTTGTGACAAACCCCTCAC 992
QY 57 ----- 57
Db 993 CCCAGGAAGGGGCCCTGTGAGGATTCCAGGCTCTGGAGTCACACTCTGTTGTAAC 1052
QY 57 ----- 57
Db 1053 GCTGCTCTTTACCCCTCCCTAGGTCTCGCGCTTTGAATAGTATCACTCTTAGTTGCTCC 1112
QY 57 ----- 57
Db 1113 ATGCCTCAGTTTGTCCATCTGAATAATGGGGCATCTGTAATGCCCTGTATTAGGAGTA 1172
QY 57 ----- 57
Db 1173 AATTACAGCATCCCTGTGNAGAGCTAGCACAGTGTGAGTAGCGGAATGTTATTTCCATCC 1232
QY 57 ----- 57
Db 1233 TTCTCAGGAGCTTGTTCCCTCCCTTCCCTTTACTTTGCTCCAGCATTGACTCAT 1292
QY 58 -----GlyIleGlyProValLeuGlyLeuValCysValProLeuLeu 71
Db 1293 ACTACTTCCCTTTTGCAGGCATTGGTCCAGTGTGGGCGCTGGTGTGTCCTCCCTCTTA 1352
QY 72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAla 91
Db 1353 GGCTCAGCCAGTGACCACTGGGCTGGAGCTATGCGCGCGCGCCCTTCATCTGGSCA 1412
QY 92 LeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly 111
Db 1413 CTGTCTTGGGCATCTGCTGAGCCTTTCTCATCCCAAGGGCGGCTGGCTAGCAGG 1472
QY 112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu 131
Db 1473 CTGTGTGCCCGGATCCAGGGCCCTGGAGCTGGACATGCTCATCTGGGCGTGGGGCTG 1532
QY 132 LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151
Db 1533 CTGGACTTCTGTGGCAGAGTGTCTCACTCCACTGGAGGCCCTGCTCTCTGACCTCTTC 1592
QY 152 ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
Db 1593 CGGACCCCGGACCACTGTCCGACGCTTACTCTGTCTATGCTTATGATCATGATCAGTCTTGG 1652
QY 172 GlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyr 191
Db 1653 GGCTGCCCTGGGCTACCTCTGCTGCCATTTGACTGGGACACCAAGTGGCCCTGGCCCTTAC 1712

QY 192 LeuGlyThrGlnGluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
Db 1713 CTGGSCACCCAGGAGAGTGTCTTTGGCTGTGCACCTCATCTTCTCACTTCCGCTA 1772
QY 212 AlaAlaThrLeuLeuValAlaGluAlaLeuGlyProThrGluProAlaGluGly 231
Db 1773 GCAGCACACTGCTGTGGCTGAGGAGCAGCGCTGGGCCCCACGAGCCAGCAGAAAGG 1832
QY 232 LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg 251
Db 1833 CTGTGGGCCCCCTCTTGTGCCCCACTGTGTCTCCATCGGGGCCCTTGGCTTTCCGG 1892
QY 252 AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271
Db 1893 AACCTGGGGCCCTCTTCCCGGCTGCACAGCTGTGTCGCATGCCCGCACCTCG 1952
QY 272 ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291
Db 1953 CGCCGGCTCTTCTGTGGCTGAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTT 2012
QY 292 TyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr 311
Db 2013 TACACGGATTTCGTGGCGCAGGGCTGTACCAGGGCTGCCAGAGCTGAGCCGGGGCACC 2072
QY 312 GluAlaArgArgHisTyrAspGlu----- 319
Db 2073 GAGGCCCGAGACACTATGATGAAGGTAAAGGCTTTGGCAGCGCAGAGGCTGTGTGGG 2132
QY 319 ----- 319
Db 2133 AGCCCCCACCAGACAGACACACTCGGGCTGTGTCTGGGCTGGTGCCTTCCATCCTGGC 2192
QY 319 ----- 319
Db 2193 CCCGACTTCTCTGTCCAGAAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGG 2252
QY 319 ----- 319
Db 2253 GTGTGAACATCTCTGCTTGGGTTTCAGGAAGGCTCTGGCTGTCTAGGAGTCTGATC 2312
QY 319 ----- 319
Db 2313 AGAGTCGTTGCCCCAGTTTGTACAGAAAGGCGGAGCTTATTCAAAGTCTAGAGGAG 2372
QY 319 ----- 319
Db 2373 TGGAGGAGTTAAGGCTGGATTTCAGATCTGCTGGTTCCAGCCGAGTGTGCCCTCTGCT 2432
QY 319 ----- 319
Db 2433 CCCCCACGACTTTCCTCAATAATCTCACAGCGCTTCCAGCTCAGGCTCTCTAGAAAGC 2492
QY 319 ----- 319
Db 2493 TCTTGAAGCCTATGSCCAGCTGTCTTTGTGTCCCTCTCACCCGCTGTCTCTACAGGTG 2552
QY 319 ----- 319
Db 2553 AGACTCCAGGAAACCTTCAGACTACCTTCCTCTGCCTTCAGCAAGGGCGTTGCCACA 2612
QY 319 ----- 319
Db 2613 TTCTCTGAGGTCAGTGGGAAGAACCTAGACTCCCATTTGCTAGAGTAGAAGGAAGG 2672
QY 319 ----- 319
Db 2673 TGCTGGGAGCAGGCTGGTCCACAGAGGTCCTGTGCAGCAGGTACCTGTGTTCGCC 2732
QY 319 ----- 319
Db 2733 TTCTCATCTCCTGAGACTGTCTCCGACCCCTTCCCTCCAGGCTGTGTCTGATGGCCCTC 2792

QY 320 -----GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe 336
Db 2793 TCCCTCTGCAGCGTTCCGATGGCAGCTGGGGCTGTTCTTCGATGGCCATCTCCCT 2852
QY 336 uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrIle 356
Db 2853 GGTCTCTCTCTGGTATGACCGCTGGTGCAGGATTCGGCAGCTCGAGCAGTCTATT 2912
QY 356 uAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl 376
Db 2913 GCCCAGTGGCAGCTTTCCCTGTGGCTGCCGTTCCACATGCCCTGCCAGAGTGGC 2972
QY 376 aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 396
Db 2973 CGTGTGACAGCTTCAGCGGCCCTCACCGGTTCCACCTTCCTCAGCCCTGCAGATCCTGCC 3032
QY 396 oTyrThrLeuAlaSerLeuTyrHisArgGlnLysGlnValPheLeuProLysTyrArgG1 416
Db 3033 CTACACACTGGCCTCCCTCTACACCGGAGAGAGGTGTTCCTGCCCAATACCGAGG 3092
QY 416 vAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLy 436
Db 3093 GGACACTGGAGTGTAGCAGTGAGGACAGCCTGATGACCACTTCCTGCCAGGCCCTAA 3152
QY 436 sProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProPr 456
Db 3153 GCCTGGAGCTCCCTTCCCTAATGACACGTGGGTGTGGAGCAGTGGCCTGCTCCAC 3212
QY 456 oProProLaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyG1 476
Db 3213 TCCACCGCGCTCTCGGGGCTCTGCCTGTGATGCTCCGTACGTGTGGTGGTGA 3272
QY 476 uProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAs 496
Db 3273 GCCCACCGAGCGGGGTGTTCCGGCGGGGCAATCTGCCGTGGACCTCGCCATCTGGA 3332
QY 496 pSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnIle 516
Db 3333 TAGTGCTCTCTGCTGCTCCAGGTGCCCATCCCTGTTATGGGCTCCATTTGTCAGCT 3392
QY 516 uSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyr 536
Db 3393 CAGCCAGCTGTGCTACTGCTATATGGTGTCTGCCGAGGCCCTGGGTCTGGTGCATTTA 3452
QY 536 rPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 3453 CTTTGCTACACAGGTAGTATTGACAGAGGACTTGGCCAAATACTCAGCG 3504
RESULT 21
ABL95409
ID ABL95409 standard; cDNA; 4894 BP.
XX
AC ABL95409;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human p53S splice variant SEQ ID NO 702.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US200202248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.

PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
XX (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SREI/) SREIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2002-255649/30.
XX
PT New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer -
XX
PS Claim 1; SEQ ID NO 702; 87pp; English.
XX
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
SQ Sequence 4894 BP; 928 A; 1448 C; 1354 G; 1163 T; 1 other;
Alignment Scores:
Pred. NO.: 1.39e-192 Length: 4894
Score: 2538.50 Matches: 551
Percent Similarity: 51.11% Conservative: 0
Best Local Similarity: 51.11% Mismatches: 2
Query Match: 88.73% Indels: 526
DB: 24 Gaps: 2
US-09-593-793A-113 (1-553) x ABL95409 (1-4894)
Qy 1 MetValGlnArgLeuTyrPheValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db 274 ATGGTCCAGAGCTGTGGCTGAGCGCTGCTGGCGCACCGAAGCCACCTCTTGTG 333
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 334 GTCAACCTGCTAACTTTGGCCTGGAGGTGTGTTGGCGCGGCGCATCACCTATGTGCG 393

Qy	41	ProLeuLeuGluValGlyValGlyGluGlyPheMetThrMetValLeu	57
Db	394	CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGGTCT -GGGTGAGTC	452
Qy	57	-----	57
Db	453	ACTATACCTCCTTCCTTCCTGTTCCAGATACATGCCACCTGGCATGTGGACAGGAGTA	512
Qy	57	-----	57
Db	513	CCTCTGCCCTGGGAGCTGCTTGGAGGGAGAGTGTCTGCTGGGAAGGCATTGCTGGGCA	572
Qy	57	-----	57
Db	573	GGAGGGTGACCTTGGGCTGAGGGGGCACACCAAGAGAAAGAGAATACCAAGGACATA	632
Qy	57	-----	57
Db	633	CCCAGTCACCTCTGGATCCCTGCTGTCACAGAGCCTGGCTCATAGGAGACACTGGAG	692
Qy	57	-----	57
Db	693	AAATGCTCCTAACTTTGGCTAGCCCTTTTATATTTATAGCGATATCTCATTTAATGC	752
Qy	57	-----	57
Db	753	TTACAACCACCATTTGAGGTGATCCATTTTACAGAGAAGGAGCAGAGGCTTTTAAGAGG	812
Qy	57	-----	57
Db	813	TTAGGTAAGTCTTAGCCAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA	872
Qy	57	-----	57
Db	873	GGTCTCCACGCGAGCTTGTCTTACCCTTAGSACAAGGGTGGACTCTGACTCTGCA	932
Qy	57	-----	57
Db	933	GATAAATTTACAAAAGCCACAGAGGCAAGTAGTAACCATTTGTGACAAACCCTCACC	992
Qy	57	-----	57
Db	993	CCCAGAAAGAGGGCCCTGTGAGGATTCGAGGCTCTGGAGTCCACACTGCTTGTGAAAC	1052
Qy	57	-----	57
Db	1053	GCTGCCCTTTACCTCCTTAGTCTGCGCTTTGAATAGTATCACCTTCTTAGTGTCTCC	1112
Qy	57	-----	57
Db	1113	ATGCTCAGTTTGTCCATCTGAANAATGGGGGCATCTGTAATGCCCTGTGTATGAGGAGTA	1172
Qy	57	-----	57
Db	1173	AATTACAGCATCCTCTGTGAAGAGCTAGCACAGTCTGAGTACGGAATGTTATTTCCATCC	1232
Qy	57	-----	57
Db	1233	TTCTCAGGAGCTTGGTTCCCTTCCCTTGGCCCTTTACTTGTCCCAGCCATTGACTCAT	1292
Qy	58	-----GlyIleGlyProValLeuGlyLeuValCysValProLeuLeu	71
Db	1293	ACTACTTCCCTTCTTGAGAGCATTTGTCAGTGTGGGCTGGTCTGTGTCCCGCTCCTA	1352
Qy	72	GlySerAlaSerAspHisTrpArgGlyArgTyrglyArgArgArgPropheIleTrpAla	91
Db	1353	GGCTCAGCCAGTCACCACTGGCGTGGACGCTATGCGCCGCCGCCCTTCATCTGGGCA	1412
Qy	92	LeuSerLeuGlyIleLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly	111
Db	1413	CTGTCTTGGGCATCTGTCTGAGCCTCTTCTCATCCCAAGGGCGGCTGGCTAGCAGGG	1472

QY	112	LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu	131
DB	1473	CTGCTGTGCGCGATCCAGCGCCCTGGAGCTGGCACTGCTCATCTCGGCGCTGGGCGT	1532
QY	132	LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe	151
DB	1533	CTGGACTCTGTGGCCAGGTGCTTCACTCCACTGGAGCCCTGCTCTGTGACCTCTTC	1592
QY	152	ArgAspProAspHisCysArgGlnAlaIleThrSerValIleAlaPheMetIleSerLeuGly	171
DB	1593	CGGGACCCGACCACTGTCCCGAGCCCTACTCTGTCTATGCTTTCATGATCAGTCTTGG	1652
QY	172	GlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyr	191
DB	1653	GGCTGCTGGGTACCTCCTGCTGCTGCAITGACTGGGACACCACTGCTGGCCCTTAC	1712
QY	192	LeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal	211
DB	1713	CTGGGCACCCAGAGAGTGCCTTCTTGGCGCTGCTCACCTCATCTTCCTCACTCGGTA	1772
QY	212	AlaAlaThrLeuLeuValAlaGluGluAlaLeuLeuGlyProThrGluProAlaGluGly	231
DB	1773	GCAGCCACACTGCTGTGTGCTGAGGAGGACGCTGGGCCCCACCCAGCCAGAGGG	1832
QY	232	LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg	251
DB	1833	CTGTCGGCCCCCTCTGTGTCGCCCACTGCTGTCCATGCGGGCCGCTTGGCTTTCCGG	1892
QY	252	AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu	271
DB	1893	AACCTGGGCGCCTGCTTCCCGGCTGCACCACTGCTGTGCGCATGCCCCACCCCTG	1952
QY	272	ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe	291
DB	1953	CGCCGGCTCTCTGTGCTCAGCTGTGCAGTGGATGGCACTCATGACCTTCAGCTGTTT	2012
QY	292	TyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr	311
DB	2013	TACACGGATTCTGTGGCGAGGGCTGTACCAAGGGCTGCCACAGACTGAGCGGGCACC	2072
QY	312	GluAlaArgArgHisTyrAspGlu	319
DB	2073	GAGGCCCGAGACACTATGATGAAGGTAAGGCCTTGGCAGCCAGCAGAGCTGGTGGG	2132
QY	319	-----	319
DB	2133	AGCGCCCAACAGACAGACACTCGGGGCTGTGTCTGGGCTGGTGCCTTCTCCATCTCGC	2192
QY	319	-----	319
DB	2193	CCCGACTTCTGTCTAGGAAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGG	2252
QY	319	-----	319
DB	2253	GTGTGGAAACATCTCTGTTGCGGTTTCAGGAAGGCCTCTGGCTGCTTAGAGTCTGATC	2312
QY	319	-----	319
DB	2313	AGAGTCGTTGCCCACTTTGACAGAAGAAAGCGGGAGCTTATTCAAAGTCTAGAGGGAG	2372
QY	319	-----	319
DB	2373	TGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCGGCACTGTGCCCTTGCT	2432
QY	319	-----	319
DB	2433	CCCCAACGACTTTCCAAATAATCTCACCAAGCGCCTTCCAGCTCAGGCGCTCTAGAAGCG	2492
QY	319	-----	319
DB	2493	TCTTGAAGCCTATGCGCACTGTCTTTGTGTTCCTCTCACCGCGCTGTCTTCACAGCTG	2552
QY	319	-----	319

Db 2553 AGACTCCAGGAAACCTTCAGACTACCTTCCTCTGCTTTCAGCAAGGGCGTGGCCACA 2612
QY 319 ----- 319
Db 2613 TTCTCTGAGGGTCAGTGAAGAACCTTAGACTCCCATTTCTAGAGGTAGAAAGGGGAAGG 2672
QY 319 ----- 319
Db 2673 TGCTGGGAGCAGGGCTGGTCCACAGCAGGTCTCGTGCAGCAGGTACCTGTGTTCGGCC 2732
QY 319 ----- 319
Db 2733 TTCTCATCTCCCTGAGACTGCTCCGACCTTCCTCCAGGCTCTGTCTGATGGCCCTC 2792
QY 320 -----GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe 336
Db 2793 TCCTCTCGAGGCGTTCGGATGGCAGCTGGGGCTGTTCCTCGCATGGCCATCTCCCT 2852
QY 336 uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe 356
Db 2853 GGTCTCTCTCTGGTCATCGACCGGCTGTGCAGCGATTCGGCACTCGAGCAGTCTATT 2912
QY 356 uAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl 376
Db 2913 GGCCAGTGTGGCAGCTTTCCTCTGGCTGCCGTGCCACATGCTGTCCACAGTGTGGC 2972
QY 376 aValValThrAlaSerAlaAlaThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 396
Db 2973 CGTGGTGACAGCTTTCAGCGCCCTCACCGGGTTTCACCTTCTCAGCGCTCGCATCTGCC 3032
QY 396 oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgG 416
Db 3033 CTACACACTGGCTCCCTCTACACCGGGAGAGCAGGTGTTCTGCCCAATACCGAGG 3092
QY 416 yAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProly 436
Db 3093 GGACACTGGAGGTGTAGCAGTGAGCAGCAGCTGATGACCACTCTCCAGGCGCTAA 3152
QY 436 sProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProPr 456
Db 3153 GCCTGGAGTCTCCCTTCCCTTAATGGACACGTGGGTGTGGAGGACGTGGCTGCTCCAC 3212
QY 456 oProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGly 476
Db 3213 TCCACCGCGCTCTGGGGGCTCTGCCCTGTGATGCTCTCCGTACGTGTGGTGGGTGA 3272
QY 476 uProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAs 496
Db 3273 GCCACCGAGGCGCAGGGTGTTCGGGGCGGGCATCTGCCGTGGACCTCGCCATCTGGA 3332
QY 496 pSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLe 516
Db 3333 TAGTCCCTTCTCCGTGTCCAGGTGGCCCATCCCTGTTTATGGGCTCATTTGTCCAGCT 3392
QY 516 uSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyr 536
Db 3393 CAGCCAGTCTGCTACTGCTATATGGTGTCTGCCAGGCGCTGGGTCTGGTCCCATTTA 3452
QY 536 rPheAlaThrGlnValValPheAspLysSerAspLeuAlaIleTyrSerAla 553
Db 3453 CTTTGTACACAGCAGTAGTATTTGACAAGAGCAGCTTGGCCAAATACTCAGCG 3504
RESULT 22
AAD05230
ID AAD05230 standard; cDNA: 3878 BP.
XX
AC AAD05230;
XX
DT 18-JUL-2001 (first entry)
XX
DE Human secreted protein-encoding gene 11 cDNA clone HWBARI4, SEQ ID NO:21.
XX

KW Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
KW inflammation; neurological disorder; Alzheimer's disease; food additive;
KW angionenic disorder; kidney disorder; gastrointestinal disorder; allergy;
KW pregnancy-related disorder; endocrine disorder; infection; wound healing;
KW cell culture; chemotaxis; vulnerability; binding partner identification;
KW gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 152..1267
FT /*tag= a
FT /product= "Human secreted protein"
FT /transl_except= (pos:209..211, aa:xaa)
FT /note= "Xaa corresponds to any of the naturally occurring
FT L-amino acids"
FT sig_peptide 152..295
FT /*tag= b
FT mat_peptide 296..1264
FT /*tag= c
FT /product= "Mature human secreted protein"
XX
PN WO200134629-A1.
XX
PD 17-MAY-2001.
XX
PF 08-NOV-2000; 2000WO-US30654.
XX
PR 12-NOV-1999; 99US-0164835.
PR 27-JUL-2000; 2000US-0221142.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Komatsoulis GA, Wei P, Fiscella M, Baker KP;
XX
DR WPI: 2001-308779/32.
DR P-PDB: AAE01362.
XX
PT New nucleic acid encoding one of 21 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions,
PT such as autoimmune disease and cancer, and used as a food additive or
PT preservative -
XX
PS Claim 1; Page 388-389; 490pp; English.
XX
CC AAD05220-AAD05282 represent cDNAs corresponding to 21 human secreted
CC protein genes, and AAE01352-AAE01413 represent the proteins they encode.
CC AAE01415-AAE01433 represent human secreted protein fragments or variants.
CC The secreted proteins and their genes are useful for preventing, treating
CC or ameliorating medical conditions, e.g., by protein or gene therapy.
CC Pathological conditions can be diagnosed by determining the amount of the
CC new protein in a sample or by determining the presence of mutations in
CC the new genes. Specific uses are described for each of the 21 genes,
CC based on the tissues in which they are most highly expressed, and include
CC developing products for the diagnosis or treatment of proliferative
CC disorders, cancer, tumours, foetal and developmental abnormalities,
CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC angionenic disorders, kidney disorders, gastrointestinal disorders,
CC pregnancy-related disorders, endocrine disorders, and infections. The
CC proteins can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues, to identify their cognate ligands or binding
CC partners, and in chemotaxis, and can be used as a food additive or
CC preservative to modify storage properties. Antibodies specific for a

CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
CC The present sequence represents a human secreted protein-encoding cDNA of
CC the invention.

XX
SQ Sequence 3878 BP; 709 A; 1164 C; 1044 G; 951 T; 10 other:

Alignment Scores:
Pred. No.: 1 07e-181 Length: 3878
Score: 2400.50 Matches: 493
Percent Similarity: 67.39% Conservative: 3
Best Local Similarity: 66.98% Mismatches: 4
Query Match: 83.90% Indels: 237
DB: 22 Gaps: 1

US-09-593-793a-113 (1-553) x AAD05230 (1-3878)

QY 54 ThrMetValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySer 73
DQ 233 TCCTCTTTCAGAGCATTTGCTCCAGTGTGGGCTGTTGTCCTCCGCTCCTAGGCTCA 292
QY 74 AlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAlaLeuSer 93
DQ 293 GCCAGTGACACTGGCGWGGAGCGCTATGGCGCGCGCGCGCTTCATCTGGGCACTGTCC 352
QY 94 LeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeu 113
DQ 353 TTGGGCACTCTGCTGAGCCTTTCTTCATCCCAAGGCGCGGCTGGCTAGCAGGGCTGCTG 412
QY 114 CysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAsp 133
DQ 413 TGCCCGGATCCCAAGGCCCTGGAGCTGGCACGTCTCATCTGGGCGTGGGCTGTGGAC 472
QY 134 PheCysGlyClnValCysPheTrpProLeuGluAlaLeuLeuSerAspLeuPheArgAsp 153
DQ 473 TTTCTGGGCGAGGTGTCTTCTACCTCCACCTGGAGGCGCTCTCTGACCTCTTCCGGGAC 532
QY 154 ProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCys 173
DQ 533 CCGGACCACTGTGGCAGGCGCTACTCTGTCTATGCTTTCATGATCATCTTTGGGGGCTGC 592
QY 174 LeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGly 193
DQ 593 CTGGGCTACTCTGCTGCTGCATTGACTGGACACAGTGCCTGGCCCTACCTGGGCG 652
QY 194 ThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAla 213
DQ 653 ACCAGGAGGAGTGCCTTTTGGGCTGCTCAGCCCTCATCTCTCACCCTGCTAGCAGCC 712
QY 214 ThrLeuLeuValAlaGluAlaLeuLeuGlyProThrGluProAlaGluGlyLeuSer 233
DQ 713 ACACCTGCTGGTCTGAGGAGGCGGCTGGGCGCCACAGCCAGCAGCAGGCTGTGCG 772
QY 234 AlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeu 253
DQ 773 GCCCCCTCTTGTGGCCCACTGCTCTCCATGCGGGCGCGCTTGGCTTTCCGGAACCTG 832
QY 254 GlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArg 273
DQ 833 GGGCGGCTGCTTCCCGGCTGCACAGCTGTGCTGCGGATGCCCGCACCTTGGCGCGG 892
QY 274 LeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThr 293
DQ 893 CTCTCTGCTGGCTGAGCTGTGACGTGGATGGCACTCATGACCTTCACGCTGTTTACAGC 952
QY 294 AspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAla 313
DQ 953 GATTTCGTGGGCGAGGGGCTGTACAGGGCGTGCACAGCTGAGCGGGCACCGAGGCC 1012
QY 314 ArgArgHisTyrAspGlu----- 319
DQ 1013 CGGAGACACTATGATGAAGGTAAAGGCTTTGGGCGCAGCAGAGGCTGGTGGGAGCGCG 1072

QY 319 ----- 319
DQ 1073 CCACCAGACGACACTCGGGCTGTGTGGGCTTGGCTTCCATCTTCCATCTTGGGCTGG 1132
QY 319 ----- 319
DQ 1133 TTCTCTGTCCAGAAAGTGGGATGGACCCCATCTGCATACAGGCTTCTCATGGGTGG 1192
QY 319 ----- 319
DQ 1193 AACATCTCTGCTTGGGTTTCAGGAAGGCTTGGGCTGTCTAGGAGTGTGATCAGAGTC 1252
QY 319 ----- 319
DQ 1253 GTTGCCCACTTTGACAGAAGGAAGCGGAGCTTATTCAAAGCTTAGAGGAGTGGAG 1312
QY 319 ----- 319
DQ 1313 AGTTAAGGCTGGATTTTCAGATCTGCTGTTCAGCGCGAGTGTGCCCTCTGCTCCCCA 1372
QY 319 ----- 319
DQ 1373 ACGACTTTCCAAATAATCTCACAGGCGCTTCAGCTCAGGCGTCTTAGAAGGCTTGA 1432
QY 319 ----- 319
DQ 1433 AGCCTATGGCCAGCTCTCTTTGTGTTCCTCTCACCCGCTGTCTCTACAGCTGAGACTC 1492
QY 319 ----- 319
DQ 1493 CCAGGAACCTTCAGACTACCTTCCTCTGCTTCAGAAAGGGCGTTGCCACATCTCT 1552
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QY 319 ----- 319
DQ 1613 GGAGCAGGCTGTCCACAGCAGGTCTCGTGACAGAGGTACCTGTGTTCGCCCTCTCA 1672
QY 319 ----- 319
DQ 1673 TCTCCTGAGACTGCTCCGACCTTCCCTCCAGGCTCTGTGTATGGCCCTCTCCCCTC 1732
QY 320 ---- GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPh 338
DQ 1733 TCGAGCGTTCGGATGGGCGCTGGGCTGTTCCTGCAAGTGGCCATCTCCTGTGTCTT 1792
QY 338 eSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSe 358
DQ 1793 CTCTCTGGTCATGGACCGGCTGGTGCAGCGATTTCGSCACTCGAGCAGTCTATTGGCCAG 1852
QY 358 rValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVa 378
DQ 1853 TGTGGCAGCTTTCCCTGTGGCTGCCGTCACATGCTCTGCCACAGTGTGGCGCTGT 1912
QY 378 lThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
DQ 1913 GACAGCTTCAGCGGCTCACCAGGTTACCTTCAGCCCTGCAGATCCTGCCCTTACAC 1972
QY 398 rLeuAlaSerLeuTyrHisArgGluGlyGlnValPheLeuProLysTyrArgGlyAspThr 418
DQ 1973 ACTGGCTCCCTCTACCAACCGGAGAGCAGGTGTTCCTGCCCAATAACCGAGGCGAC 2032
QY 418 rGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
DQ 2033 TGGAGTGTAGCAGTGGAGCAGCGCTGATGACCACTCTCTGCCAGGCGCTTAAGCCTGG 2092
QY 438 yAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
DQ 2093 AGCTCCCTTCCCTAATGGACAGTGGGCTGCTGGAGCAGTGGCTGCCCTGCCCTCCACC 2152

QY 57 ----- 57
Db 1004 ATGCTCAGTTTGTCCATCTGAAATGGGGGCATCTCTAATGCTGTGTTATGAGGAGTA 1063
QY 57 ----- 57
Db 1064 AATTACAGCATCCCTGTGTGAAGACGTAGCACAGTGTGAGTACGGAATGTTATTTCATCC 1123
QY 57 ----- 57
Db 1124 TTCTCAGGAGCTTGGTTCCCTTCCCTTCCCTTTACTTGTGCCAGCCATTGACTCAT 1183
QY 58 -----GlyIleGlyProValLeuGlyLeuValCysValProLeuLeu 71
Db 1184 ACTACTTCCCTTCTGCAGGCATTGGTCCAGTGTGGCCCTGTGTGTGCCGCTCCTA 1243
QY 72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAla 91
Db 1244 GGCTCAGCCAGTGACCACTGGCGTGGACGTATGGCGCGCGCGGCTTCATCTGGCA 1303
QY 92 LeuSerLeuGlyIleLeuLeuSerLeuPheLeuLeuProArgAlaGlyTrpLeuAlaGly 111
Db 1304 CTGTCTTGGCATCTTGTGAGCCCTTCTTCTCATCCAAAGGCGCGCTGGCTAGCAGGG 1363
QY 112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu 131
Db 1364 CTGCTGTGCCCGGATCCACAGGCCCTGGAGCTGGCACTGCTCATCTGGGCGTGGGCTG 1423
QY 132 LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151
Db 1424 CTGGACTTCTGTGCCAGGTGTGCTTACATCCACTGGAGGCCCTGTCTCTGACCTCTTC 1483
QY 152 ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
Db 1484 CGGGACCCGAGCACCTGTGCCAGGCCCTACTGTCTATGCCCTTCATGATCAGCTTGGG 1543
QY 172 GlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyr 191
Db 1544 GGCTGCTGGCTACCTTCCTGCCCTGGCATGACTGGGACACCACTGCCCTGGCCCCCTAC 1603
QY 192 LeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
Db 1604 CTGGGACCCAGAGAGTGCCTTGTGGCTGTCTCACCTCATCTTCTCACCTGCCTA 1663
QY 212 AlaAlaThrLeuLeuValAlaGluAlaLeuGlyProThrGluProAlaGluGly 231
Db 1664 GCAGCCACACTGTGTGGTGTGAGGAGCGACGCTGGGCCCCACCGAGCCAGCAAGGG 1723
QY 232 LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg 251
Db 1724 CTGTGGGCCCTTCTTGTGCCCCACTGTGTCCATGCGGGCCGCTTGGCTTCCGG 1783
QY 252 AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271
Db 1784 AACCTGGGCCCTTGTCTCCCGGCTGCACAGCTGTGTGGCGCATGCGCCGACCCCTG 1843
QY 272 ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291
Db 1844 CGCGGCTCTCTGTGGCTGAGCTGTGCAGTGGATGGCATCATGACCTTCACGCTGTGT 1903
QY 292 TyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr 311
Db 1904 TACACGGATTTCTGGCGGAGGGGCTGTACCAGGGGCTGCCAGAGCTGAGCGCGGCACC 1963
QY 312 GluAlaArgArgHisTyrAspGlu----- 319
Db 1964 GAGGCCGGAGACACTATGATGAAGGTAAAGGCTTGGCAGCCAGCAGAGGCTGGTGTGGG 2023
QY 319 ----- 319
Db 2024 AGCGGCCACAGAGACACTCGGGGCTGTCTCGGGCTGTGTGGGCTGTCTCCATCTCTGGC 2083

QY 319 ----- 319
Db 2084 CCCGACTTCTCTGTAGAAAGTGGGATGGACCCCATCTGCATACACGGCTTCTCATGG 2143
QY 319 ----- 319
Db 2144 GTGTGAACATCTCTCTGTGGGTTTCAGGAAGGCCTCTGGTGTCTTAGAGCTGTGATC 2203
QY 319 ----- 319
Db 2204 AGAGTCGTTCCCCAGTTTGACAGAGAAGGCGGAGCTTATTCAAAGTCTAGAGGGAG 2263
QY 319 ----- 319
Db 2264 TGGAGGAGTTAAGGCTGGATTTCAGATCTGCCGTGTTCACAGCGCAGTGTGCCCTCTGCT 2323
QY 319 ----- 319
Db 2324 CCCCCAACGACTTTCAAAATAATCTCACCAGCGCCTTCCAGCTCAGCGGTCTTAGAAGCG 2383
QY 319 ----- 319
Db 2384 TCTTGAAGCCTATGGCCAGCTGTCTTGTGTTCCTCTCACCCGCTGTCTTCACAGCTG 2443
QY 319 ----- 319
Db 2444 AGACTCCCAGAAACCTTCAGACTACCTTCTGCTTTCAGCAAGGGCGTTGCCACA 2503
QY 319 ----- 319
Db 2504 TTCTCTGAGGTCAGTGGAGAACCTTAGACTCCATTGCTAGAGGTAGAAAGGGAAGG 2563
QY 319 ----- 319
Db 2564 TGCTGGGAGCAGGGCTGGTCCACACAGAGTCTCTGTGCAGCAGGTACCTGTGTTCCGCC 2623
QY 319 ----- 319
Db 2624 TTCTCATCTCCCTGAGACTGCTCCGACCCCTTCCCTCCAGGCTCTCTGTATGGCCCCTC 2683
QY 320 -----GlyValArgMetClySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe 336
Db 2684 TCCTCTGCAGGGCTTCGGATGGGACGCTGGGGCTGTTCCTGCACTGGCCATCTCCCT 2743
QY 336 uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe 356
Db 2744 GGTCTTCTCTGTGTCATGGACCGGCTGGTGCAGCGATTTCGGCACTCGAGCAGTCTATT 2803
QY 356 uAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl 376
Db 2804 GGCCAGTGTGGCAGCTTCCCTGTGGCTGCCGTGCACATGCTGTCCACAGTGTGGC 2863
QY 376 aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 396
Db 2864 CGTGGTGACAGCTTCAGCGGCCCTTCACGGGTTTCACCTTCTCAGCCCTGCAGATCTGCC 2923
QY 396 oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnVal----- 409
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Db 3103 GGGCCAGAGGCTTGGCTGCAGAACAGTGTAGATTAGATTCTGGGAATGACTTCTCTGGGG 3162
QY 409 ----- 409

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Qy 409 ----- 409
Db 3223 TCCCGAAGGTCAGGCCAGCAGGAGCCCTAGCCTTCTAGGCTGGTTGTCTATGGAGAGG 3282
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Db 3283 CAGGCGCTGAATCAGATGACCCCTGGGCCATTACAGCCTCAGCAGACGGAGTGGGAATG 3342
Qy 409 ----- 409
Db 3343 GTCCAGCCTTAGCAACACCTTTCTTCAGGGAGCAGCAACCTGACTTAGCCTATCCTAC 3402
Qy 409 ----- 409
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Qy 409 ----- 409
Db 3523 TCCCTTCCCTTCCCTGTGGCAGATATCTAGCTTGACACCTGACCCACTCACTTGGG 3582
Qy 409 ----- 409
Db 3583 CACTGTGTAAGTTGTGGGACCTCCTTCTTGGTTGGCCCTACACTAACCCGCCCTCCAG 3642
Qy 409 ----- 409
Db 3643 GGGCCCTTTCTTGGGAAGCCACTAACCCAGGTAGTGTGTCATCTTGTCCCTCCA 3702
Qy 409 ----- 409
Db 3703 CTGACCTCACTGAGCTACAAACCTGGGTGCTGGACTCTGCTTGAGGGGCATGAAGTGG 3762
Qy 409 ----- 409
Db 3763 GGTGTCCCAAGGGAGGAGAGATGCAAGACTGCTCTCATAGAGCTCTCAGACTGAGGA 3822
Qy 409 ----- 409
Db 3823 AGACCTGCCCTGCGTCTCTAGCATTGAGGAGGAGTAGTAAAGTTCTAGCTGAGA 3882
Qy 409 ----- 409
Db 3883 GCCTGGTTAACTGAGTAGGTAGCTGCAGGGGTGAGAGTAGGAGGGAGGGGCTAAGGT 3942
Qy 409 ----- 409
Db 3943 TTTGGTTGGGGAGCCTGGTTCCTTGAGACCCCTGTTAGCCCACTGATAACCTTCTTCAGC 4002
Qy 409 ----- 409
Db 4003 CTTCACTCTTCTGCTTGCTGGCTGGGGCAGGGGCTGGCATCAGGGGCCAGGCCTGA 4062
Qy 409 ----- 409
Db 4063 GTATGTGCTGTCTGCCAGGAAGTTCTTGGGGCTAGCCATCTTCTCCAGATGGAGGAGC 4122
Qy 409 ----- 409
Db 4123 ATGCTGTCTCGGACCCTCCAGACTCCAGACTCCAACTCAGCGGACATTCCTGGGGTGGCAGGC 4182
Qy 409 ----- 409
Db 4183 AGGAGGAGAAAGTCTCTGGGAGCCCCCTTCTTAACAGCAGCTGATGGCAGACTTGGCACTG 4242
Qy 409 ----- 409

Db 4243 CACGCTGTCTCCCTTCTTCCCTTTGCCCCACTTCTTGAGCTGCATGTGTAGCCCTGGGCTTCC 4302
Qy 409 ----- 409
Db 4303 CTGGTGTCAAGTTTGTAGCTCTGCCATCGCTCCACCTCGCAATGCAGCCAACTCAACTC 4362
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Db 4363 TTCTGGCATGGGACAAATGTTGGATAAGACCTGGCCTTGTCTTAAATAGGAGGCTCTGG 4422
Qy 409 ----- 409
Db 4423 GCCATCAAGGCAGGGGTTGGGGGATGGTGTCCACAGTCACTCTGATCTAAGTCAAGA 4482
Qy 409 ----- 409
Db 4483 CAGCAGGAAGAAGTGAGAGCCTTCAACATTAGCACAGCTGGGGCTGGGGAGGTGGGA 4542
Qy 409 ----- 409
Db 4543 AGGGGACATTCTCCTGCTTGGGTCTACTGGATTCTCCCTGCCCAAGGCTGGGGACA 4602
Qy 409 ----- 409
Db 4603 AGGAGCTCATGGCAGGSCAGCTACCTTAGTGCATCTGGGACCCAGAGAGCAGAGCT 4662
Qy 409 ----- 409
Db 4663 TCTCTGACCCGGCAATGAGGATTTCCAGATGTGCGAGTGGAGGCGAGGAGGAAG 4722
Qy 409 ----- 409
Db 4723 GTTAGGAGAGCCTCGTGGGTTTGGGCCATCAGGGGCCCTGCCCTTGGCTTTTGTCTCCTC 4782
Qy 409 ----- 409
Db 4783 TGTCTGTGCATCTCTTACCACCGCTCTCATTCGCCCTGTCTCTTTTCTTACCTTGGAG 4842
Qy 409 ----- 409
Db 4843 CTCTGTCTCTCTCATCTGTGATATATGAGTTTGTCTGCTTACCTGTCTTAAGAGGCT 4902
Qy 409 ----- 409
Db 4903 AGAGGAGACCTAGACTTCTGGGTTCACATTTGTCCCCCCCCCTACCCGCTTACCCCTTCC 4962
Qy 409 ----- 409
Db 4963 CACTCCTGAGGAAGGTCCTGTTAGACTTGGACCAAGTAGGGTCTCCATCTTCTCTCCT 5022
Qy 409 ----- 409
Db 5023 GCTCCTGATTCTCATGAAAGTCCCATTTGCCCTGGGATGGAGGCAAGGTCGTGTTCTCACA 5082
Qy 409 ----- 409
Db 5083 GCTGGGTGGTCCAGTCTGGGTACACACTGTCTCTTCCCCCTTTCTTACCCCTCT 5142
Qy 410 -----PheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAspSe 426
|||||
Db 5143 GCCTTAGGTGTCTCTGCCCAAATACCGAGGGGACACTGGAGGTCTAGCAGTAGGACAG 5202
Qy 426 rLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisVa 446
|||||
Db 5203 CCTATGACCAGCTTCTTCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTATGACACAGT 5262
Qy 446 lGlyAlaGlySerGlyLeuLeuProProProProAlaLeuCysGlyAlaSerAlaCy 466
|||||
Db 5263 GGTGTCTGGAGCAGTGGCCTGCTCCACCTCCACCCGGGCTCTGCGGGGCTCTGCTG 5322
Qy 466 sAspValSerValArgValValValGlyGluProThrGluAlaArgValValProGlyAr 486
|||||
Db 5323 TGATGTCTCGTACGTGTGTGGTGGTGGAGCCACCGAGGCAAGGTGTTCCGGGCGC 5382

QY 486 gGlylleCysLeuAspLeuAlaileLeuAspSerAlaPheLeuLeuSerGlnValAlaPr 506
|||||
Db 5383 GGCATCTCGCTGGACCTCGCCATCTGGATAGTCCCTTCCTGGCTGCCAGGTGGCCCC 5442
QY 506 oSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSe 526
|||||
Db 5443 ATCCCTGTTTATGGGCTCCATTTGTCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTC 5502
QY 526 rAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSe 546
|||||
Db 5503 TGCCCGAGCCCTGGGTCTGGTGGCCATTACTTTGCTACACAGGTAGTATTTGACAAGAG 5562
QY 546 rAspLeuAlaLysTyrSerAla 553
|||||
Db 5563 CGACTTGGCCAAATACTCAGCG 5584
RESULT 24
AAH93869
ID AAH93869 standard; cDNA; 6976 BP.
XX
AC AAH93869;
XX
DT 04-OCT-2001 (first entry)
XX
DE P553s cDNA splice variant P553s-6.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX
DR WPI; 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
PS Claim 1; Page 461-463; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I). (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
SQ Sequence 6976 BP; 1312 A; 1996 C; 1961 G; 1706 T; 1 other;
Alignment Scores:
Pred. No.: 6.81e-161 Length: 6976

Score: 2144.00 Matches: 551
Percent Similarity: 30.48% Conservative: 0
Best Local Similarity: 30.48% Mismatches: 2
Query Match: 74.94% Indels: 1257
DB: 22 Gaps: 3
US-09-593-793A-113 (1-553) x AAH93869 (1-6976)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 165 ATGGTCCAGAGCTGTGGGTGACCGCTGCTGCGCGCACCGGAAAGCCAGCTCTGTGTG 224
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGlyIleThrTyrValPro 40
Db 225 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCGCAGGCATCACCTATGTGCGG 284
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeu----- 57
Db 285 COTCTGCTGTGGAAGTGGGGTAGAGGAGAAAGTTTCATGACCATGGTGCT-GGGTGAGTTC 343
QY 57 ----- 57
Db 344 ACTACATCCTCCTTCCTTCCTGTTCCAGATACATGCCACCTGGCATGTGGGACACAGTA 403
QY 57 ----- 57
Db 404 CCTCTGCCCTGGGAGCTGCTTGGAGGAGAGGTGCTCTCTGGGAAGGCATTGCTGGGCA 463
QY 57 ----- 57
Db 464 GGAGGTGACCCCTGGGCTGAGGGGGGCACACCAGAGAAGAAGAGAAATACCAGGACATA 523
QY 57 ----- 57
Db 524 CCCCAGTCACCTCTGGATCCCTGGTCTGCACAGAGACCTGGCTCATAGGAGACACTGGAG 583
QY 57 ----- 57
Db 584 AAATGCTCTAACCTTTGGTAGCCCTTTTATAAATTTATAGCGATTATCTCATTTAATGC 643
QY 57 ----- 57
Db 644 TTACAACCAACCATTTGAGGTGATCCATTTTACAGAGAAGAGAGAGAGGCTTTTAAAGAG 703
QY 57 ----- 57
Db 704 TTAGTAAGTCTTAGCCAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 763
QY 57 ----- 57
Db 764 GGTCTCCAGCGGAGCTTGTCTCTACCCCTAGGACAAGGGGTGGACTCCTGACTCTGCA 823
QY 57 ----- 57
Db 824 GATAAATTTACAAAAGCCACAGAGGCAAGTAGTAACCATTTGTGTGACAAACCCCTCAC 883
QY 57 ----- 57
Db 884 CCCAGGAAGAGGGGCCCCCTGTGAGGATTTCAGAGCTCTGGAGTCACACTGCTTGTGAAAC 943
QY 57 ----- 57
Db 944 GCTGCTCTTACCCCTCCCTAGTGTCTGCGCCCTTTGAATAAGTATCACTTMTTAGTTGCTCC 1003
QY 57 ----- 57
Db 1004 ATGCCTCAGTTTGTCCATCTCAAAATGGGQCATCTGTAATGCCCTGTGTTATGAGAGTA 1063
QY 57 ----- 57
Db 1064 AATTACGCATCCCTGTGAAGACGTAGCACAGTGTGAGTAGGAAATGTTATTTCATCC 1123
QY 57 ----- 57

Db 1124 TTCTCAGGAGCTTGGTTCCCTTCCCTTGCCTTTACTTGTCCAGCAATTGACTCAT 1183
Qy 58 -----GlyIleGlyProValLeuGlyLeuValCysValProLeuLeu 71
Db 1184 ACTACTTCCCTTCTTGCAGGCAATTGGTCCAGTGTGGGCCCTGGTCTGTGCCCCGCTCTTA 1243
Qy 72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAla 91
Db 1244 GGCTCAGCAGTACCACTGGCGTGGACGCTATGCCCGCGCGCCCTTCATCTGGGCA 1303
Qy 92 LeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly 111
Db 1304 CTGTCTTGGGCATCTCTGCTGAGCCTCTTCTCATCCCAAGGCGCGCTGGCTAGCAGG 1363
Qy 112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuIleLeuGlyValGlyLeu 131
Db 1364 CTGCTGTGCCGGATCCCAAGGCCCTGGAGCTGGACATGCTCATCTGGGGGTGGGGGTG 1423
Qy 132 LeuAspPheCysGlyGlnValCysPheTrpProLeuGluAlaLeuLeuSerAspLeuPhe 151
Db 1424 CTGGACTTCTGTGGCCAGGTGTCTCACTCCACTGGAGGCCCTGCTCTCTGACCTCTTC 1483
Qy 152 ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
Db 1484 CGGACCGGGACCACTGTCCGAGGCCCTACTGTGTCTATGCTTTCATGATCAGTCTTGGG 1543
Qy 172 GlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspTrpSerAlaLeuAlaProTyr 191
Db 1544 GGCTGCCCTGGGGCTACTCTGCTGCCATTTGACTGGGACACAGTGCCTGGCCCCCTTAC 1603
Qy 192 LeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
Db 1604 CTGGCACCCAGGAGGAGTGCCTTTTGGCTGTCTACCCCTCACTTCTCTCACCTGCGTA 1663
Qy 212 AlaAlaThrLeuLeuValAlaGluGluAlaLeuGlyProThrGluProAlaGluGly 231
Db 1664 GCAGCCACACTGTGCTGGCTGAGGAGCAGCGCTGGGCGCCACCGAGCCAGCAGAGGG 1723
Qy 232 LeuSerAlaProSerLeuSerProHisCysProCysArgAlaArgLeuAlaPheArg 251
Db 1724 CTGTGGCGCCCTCTGTGCGCCCACTGTCTCATGCCGGCGCGCTGGCTTTCGG 1783
Qy 252 AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271
Db 1784 AACCTGGCGCCCTGTCTCCCGGCTGCACCACTGTCTGCGCATGCCCGCACCCCTG 1843
Qy 272 ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291
Db 1844 CGCCGGCTCTTCTGCTGGCTGTGCAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTT 1903
Qy 292 TyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr 311
Db 1904 TACAGGATTTCTGTGGCGAGGGGTGTACCAGGGCGTGTACCAGGGCGTGGCCAGAGCTGAGCGGGCAC 1963
Qy 312 GluAlaArgArgHisTyrAspGlu----- 319
Db 1964 GAGGCCCGGAGACACTATGATGAAGGTAAGGCTTGGCGAGCCAGCAGAGGCTGTGTGGG 2023
Qy 319 ----- 319
Db 2024 AGCCGCCACCAGACGACACTCGGGGCTGTGTCTGGGCTGGTGGCTCTCCATCCTGGC 2083
Qy 319 ----- 319
Db 2084 CCCGACTTCTCTGTAGGAAAGTGGGATGGACCCCACTCTGCATACAGGCTTCTCATGG 2143
Qy 319 ----- 319
Db 2144 CTGTGGAACATCTCTGCTTGGGTTTCAGGAAGGCTCTGGCTGCTCTAGGAGTCTGATC 2203
Qy 319 ----- 319

Db 2204 AGAGTCTGTTGCCCAAGTTTGCACAGAAGGAAGCGGAGCTTATTCAAAGTCTAGAGGAG 2263
Qy 319 ----- 319
Db 2264 TGGAGGAGTTAAGGCTGGATTTTCAGATCTGCCTGTGTTCCAGCCGCACTGTGCCCTCTGCT 2323
Qy 319 ----- 319
Db 2324 CCCCCAAGCACTTTCAAAATAATCTCACAGCGCCTTCCAGCTCAGGCGTCTCTAGAAGCG 2383
Qy 319 ----- 319
Db 2384 TCTTGAAGCCTATGGCCAGCTGTCTTTGTGTCTTCCCTCTCACCCGCTCTCTCACAGCTG 2443
Qy 319 ----- 319
Db 2444 AGACTCCCAAGNAACCTTCAGACTACCTTCTCTGCCCTTCAGCAAGGGGCGTTGCCACA 2503
Qy 319 ----- 319
Db 2504 TTCTCTGAGGTCAGTGGGAAGAACCTAGACTTCCATTGCTAGAGGTAGAAAGGGGAAGGG 2563
Qy 319 ----- 319
Db 2564 TGCTGGGAGCAGGCGTGGTCCACAGCAGGTCTCGTGCAGCAGGTACCTGTGTTCCGCC 2623
Qy 319 ----- 319
Db 2624 TTCTCATCTCCTCTGAGACTGTCTCCAGCCCTTCCCTCCAGGCTCTGTCTGATGGGCCCTTC 2683
Qy 320 -----GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerIle 336
Db 2684 TCCCTCTCAGCGCGTTCGATGGGCAGCTGGGGCTGTTCCTGCAGTGGCCATCTCCCT 2743
Qy 336 uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValIle 356
Db 2744 GGTCTTCTCTCTGCTGTCATGGACCGCGCTGTGCAGCGATTCGCGCACTCGCAGCAGTCTATTT 2803
Qy 356 uAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl 376
Db 2804 GGCCAGTGTGGCAGCTTTCCTGTGGCTGCCGGTGCACATGCTGTCCACAGTGTGGC 2863
Qy 376 aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 396
Db 2864 CGTGTGTACAGCTTCAGCGCGCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCC 2923
Qy 396 oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnVal----- 409
Db 2924 CTACACACTGGCTTCCCTCTACCCACGGGAGAGCAGGT-ACTCATTTGGCCAGTGGGTGG 2982
Qy 409 ----- 409
Db 2983 AGTCAGGTTGGAGGGTGGTCTGGGTTTGTGGAGGCCAACTAGCTCAGAACCTGGTAT 3042
Qy 409 ----- 409
Db 3043 CTGGCAAGCAACTTTGGAGAGTGTCTTCTTGAATCAGAGAAGAGCTTATCCTAGCCCA 3102
Qy 409 ----- 409
Db 3103 GGGCCAGAGGCTTGGGCTGCAGAACAGTGTAGATTAGATTCTTGGGAATGACTTCTCTGGG 3162
Qy 409 ----- 409
Db 3163 TCAGGACTGTGTAGCAGCTTGAATGGATGATTGCAGGAATATGCAAAATACGATAGTGGAA 3222
Qy 409 ----- 409
Db 3223 TCCGGAAGGGTCAGCCAGCAGGAGCCCTAGGCTTCTAGGCTGTGTTGTTCTATGGAGG 3282
Qy 409 ----- 409
Db 3283 CAGGCGCTGAATCAGATGACCCCTTGGGCCATTTACGCTCAGCAGACGGGAGTGGGAATG 3342

QY 409 ----- 409
Db 3343 GTCCAGCCTTAGCAACACCTTTCTTCAGGGAGCAGCAACCTGACTTAGCCTGTATCCTAC 3402
QY 409 ----- 409
Db 3403 TCTGCTCTGAGATGGGCGAGGCTCCTTCTACCCCTTTCTTCTGCTTATTTTCT 3462
QY 409 ----- 409
Db 3463 TTTCTGTCTAATTCCCTTTTCTTCTGCATCCCTCTTGGCTCTTCCCTTTCTCTCT 3522
QY 409 ----- 409
Db 3523 TCCCCTTCCCTTCCCTCTGGCAGATATCTGAGCTTGACACCTGACCCACCTCACITGGG 3582
QY 409 ----- 409
Db 3583 CACTGTGTAAGTTGTGGGACCTCTCTTCTTCTGCATCCCTCTTGGCTCTTCCCTTTCTCTCT 3642
QY 409 ----- 409
Db 3643 GGGCCCTTTCTTGGGAAGCCACCTAACCCAGGTAGTGTGCTCATCTTGTCCCTCCA 3702
QY 409 ----- 409
Db 3703 CTGACCTCACTGAGCTACAAACCTGGGTCTGACTCTGCCTTGAGGGGCATGAAGTTGG 3762
QY 409 ----- 409
Db 3763 GGTGTCCCAAGGAGGAGGAGATGCAGGACTGCTCTCATAGAGCTCTCAGACTGTAGGGA 3822
QY 409 ----- 409
Db 3823 AGACCTGCCCTTCGCTAGCACTTGAGGAGAGGAGTAGGTAAAGTTCTGAGCTGAGA 3882
QY 409 ----- 409
Db 3883 GGCTGGTTAACTGAGTAGGTAGCTGCAGGGGTGAGAGGTATGGAGGGAGGGCTAAGGT 3942
QY 409 ----- 409
Db 3943 TTTGGTTGGGGAGCCTGCTCCTGAGACCCCTGTTAGCCCACTGATAACCTTCTTCAGC 4002
QY 409 ----- 409
Db 4003 CTTCACTCTTCTGCTGGCTGGGTGGGGCAGGGGGCTGGGCATCAGCGCCAGGCCTGA 4062
QY 409 ----- 409
Db 4063 GTATGTGCTGCTGCCAGGGAACGTTCTGGGGCTAGCCATCTTCTCCAGATGGAGGAGC 4122
QY 409 ----- 409
Db 4123 ATGCTGTCTCGGACCACTCCAGACTCCAACCTCAGCGACATCTCCTGGGTGGCAGGC 4182
QY 409 ----- 409
Db 4183 AGGGAGGAGAAGTCTCTGGGAGGCCCTTCTTAACAGCAGCTGATGGCAGACTTGGCCTG 4242
QY 409 ----- 409
Db 4243 CACGCTGTCTGCTGTCTCTTTGCCCACTTGTGAGCTGCATGCTGACCGTGGCTTCC 4302
QY 409 ----- 409
Db 4303 CTGGTCTCAGTTTGTAGCTCTGCCATCTGCCCTGCCACCTCCGAAATGCAGCAACTCAACTC 4362
QY 409 ----- 409
Db 4363 TTCTGGCATGGGACAAATTTGGATAAGACCTGGGCTTGTCTTAAATAGGAGGCTCTGG 4422

QY 409 ----- 409
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QY 409 ----- 409
Db 4483 CAGCAGGAAGAGTAGAAGCCTTCAACATTAGCACAGCTGGGGCTGGGGAGGTGGGA 4542
QY 409 ----- 409
Db 4543 AGAGGGACATTCTCTCTGCTTGGGTCTACTGATTTCTCCCTGCCCAAGGCTGGGGACA 4602
QY 409 ----- 409
Db 4603 AGGAGCTCATGCAGGCGAGCTAGCCTAGTGCATCTGGGACCTCCAGAGAGAGCT 4662
QY 409 ----- 409
Db 4663 TCCTGTCACCGGCAATGAGGATTTCCAGATGTGAGTGGAGGCGAGCAGGAAGAAG 4722
QY 409 ----- 409
Db 4723 GTTAGGAGACCTGCGTGGGTGGGCCATCAGGGGCCCTGCCTTGGCTTTTGTTCCTC 4782
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Db 4783 TGTCTGTGCTCTCTTACCACCGTCTTCATTCGCCCTGTGCTTTTCTTACCTTGGAG 4842
QY 409 ----- 409
Db 4843 CTCTGTCTCTGTGATCTGTGATTTAGTTTGTCTGCCTCTTACCTGTCTTAAGAGGT 4902
QY 409 ----- 409
Db 4903 AGAGGAGACCTAGACTTCTGGGTTTACATTTGTCCCGGCCCTACCCCGTTACCTTCTCC 4962
QY 409 ----- 409
Db 4963 CACTCTGAGGAAGGTCCTGTTAGACTTGGACCAAGTAGGCTCTCCATCTTCTCTCCT 5022
QY 409 ----- 409
Db 5023 GCTCTGATTTCTCATGAGTCCCATTTGCCCTGGGATGGAGGCAAGGCTGTGTTCTACA 5082
QY 409 ----- 409
Db 5083 GCTGGGTGCTCCAGTCTGGGTACACACTGCTCTTCTCCCTTTTCTTCCACCTCT 5142
QY 410 -----PheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAspSe 426
|||||
5143 GCCTTAGGTGTTCTCTGCCAAATACCGAGGGGACACTGGAGGTGTAGCAGTGAGGACAG 5202
QY 426 rLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisVa 446
|||||
5203 CCTGATGACCACTTCTCTCCAGGCCCTAAGCTGGAGCTCCCTTCCCTTAATGGACACT 5262
QY 446 lGlyAlaGlySerGlyLeuLeuProProProLaLeuCysGlyAlaSerAlaCy 466
|||||
5263 GGTGCTGGAGCAGTGGCTCTCCACCTCCACCGGCTCTGGGGGCCCTCTGCTG 5322
QY 466 sAspValSerValArgValValValGlyGluProThrGluAlaArgValValProGlyAr 486
|||||
5323 TCATGCTCCGTACGTGTGGTGGTGAGCCACCGAGGCGCAGGCTGGTTCGCGGCGG 5382
QY 486 gGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaPr 506
5383 GGGCATCTGCTTGAGCTCCCATCTGGATAGTGCCTTCTCTCTCCAGGTGGCCCC 5442
QY 506 oSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSe 526
|||||
5443 ATCCCTGTTTATGGGCTCCATTTGTCAGCTCAGCCAGTCTGTCTACCTATATGCTGTC 5502
QY 526 rAlaAlaGlyLeuGlyLeuValAlaIleIleThrPheAlaThrGlnValValPheAspLysSe 546

|||||
Db 5503 TGCCGAGCGCTGGGTCCTGGTCCCATTTACTTTGTCTACACAGGTAGTATTGACAAGAG 5562
QY 546 rAspleuAlaLysTyrSerAla 553
Db 5563 CGACTTGGCCAAATACTACGCG 5584
RESULT 25
ABL95412
ID ABL95412 standard; cDNA; 6976 BP.
XX AC ABL95412;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human P553S splice variant SEQ ID NO 705.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002022248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 98US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 98US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
PI Xu J, Dillon DC, Harlocker JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS,
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX

DR WPI; 2002-255649/30.
XX
PT New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer -
XX
XX Claim 1; SEQ ID NO 705; 87pp; English.
XX
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
SQ Sequence 6976 BP; 1312 A; 1996 C; 1961 G; 1706 T; 1 other;
Alignment Scores:
Pred. No.: 6,81e-161 Length: 6976
Score: 2144.00 Matches: 551
Percent Similarity: 30.48% Conservative: 0
Best Local Similarity: 30.48% Mismatches: 2
Query Match: 74.94% Indels: 1257
DB: 24 Gaps: 3
US-09-593-793A-113 (1-553) x ABL95412 (1-6976)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 165 ATGGTCCAGAGGCTGTGGGTGAGCCGCTGCTGCCGACCGGAAACCCAGCTCTTGCTG 224
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyValPro 40
Db 225 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCGAGGCATCACCTATGTGCCG 284
QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeu----- 57
Db 285 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGTGTGCT-GGGTGAGTC 343
QY 57 ----- 57
Db 344 ACTACATCCTCCTTCTCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA 403
QY 57 ----- 57
Db 404 CCTCTGCCCTGGAGCTGCTTGGAGGAGAGGTGGTCTGCTGGGAAGGCATTGCTGGGCA 463
QY 57 ----- 57
Db 464 GGAGGTGACCTTGGGCTGAGGGGGCACACCAAGAGAAAGAGAATAACCAAGGACATA 523
QY 57 ----- 57
Db 524 CCCCAGTCACCTCTGGATCCCTGGTCTGTCACAGAGCCCTGGCTCATAGGAGACACTGGAG 583
QY 57 ----- 57
Db 584 AAATGCTCCTAACTTTGGCTAGCCCTTTTATAATTATAGCGATTATCTCATTTAATGC 643
QY 57 ----- 57
Db 644 TTACAACCACTTTGAGGTGATCCATTTTACAGAGAAGGAAGAGAGGCTTTTAAGAGG 703
QY 57 ----- 57
Db 704 TTAGGTAAGTCTTAGCCAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 763
QY 57 ----- 57
Db 764 GGTCCTCCAGCGAGCTTGTCTTACCCTTAGGACAAAGGGGTGGACTCCTGACTCTGCA 823
QY 57 ----- 57
Db 824 GATAAATCTACAAAAGCCACAGAGGGAAGTAGTAACCATTTGTGTGACAACCCCTCAC 883

Db 3043 CTGGCAAGCAACTTTGGAGAAATGCTTCTTTGAATCAGAGAAGACTTATCCTAGCCCCA 3102
QY 409 ----- 409
Db 3103 GGGCCAGAGGCTTGGCTGCAGAACAGTGTAGATTCTGGGAATGACTTCCTTGGGG 3162
QY 409 ----- 409
Db 3163 TCAGGACTGTAGCACTTGAATGGATGATTCAGGAAATGCAAAATACGATAGTGGAA 3222
QY 409 ----- 409
Db 3223 TCCCGAAGGTCAGGCCACAGAGCCCTAGGCTTCTAGGCTGGTTGTTCTATGGAGAG 3282
QY 409 ----- 409
Db 3283 CAGGGGCTGAATCAGATCACCCCTGGGCCATTACGCTTCAGCAGACGGAGTGGAAATG 3342
QY 409 ----- 409
Db 3343 GTCCAGCCCTTAGCAACACCTTTCTTCAGGAGCAGCAACCTGACTTAGCCTGTATCCTAC 3402
QY 409 ----- 409
Db 3403 TCTGGTCTGAGATGGGCGAGGCTCCTTCCTACCCCCCTTCTTCTGGCTTATTTTCT 3462
QY 409 ----- 409
Db 3463 TTTCTGTCTAATTCCTTTTCTTCTGCATCCCTCTTTGGCTCCTTCCCTTCTCCT 3522
QY 409 ----- 409
Db 3523 TCCCCCTTCCCTTCCCTGTGGAGATATCTGAGCTTGACACTGACCCACTCACTTTGG 3582
QY 409 ----- 409
Db 3583 CACTGTGTAAAGTTGTGGGACCTCCTTCTTGTGTGGCCCTACACTAACAGCCCTCCAG 3642
QY 409 ----- 409
Db 3643 GGGCCCCCTTCCCTTGGGAAGCCACCTAACCCAGGTAGTGTGTATCCTTTGCCCTCCA 3702
QY 409 ----- 409
Db 3703 CTGACCTCACTGAGCTACAACTTGGTGTCTGGACTCTGCCCTTGAGGGCATGAAGTTGG 3762
QY 409 ----- 409
Db 3763 GGTGTCCCAAGGAGGAGGAGATGCAGGACTGCTCTCATAGAGCTCTCAGACTGTAGGA 3822
QY 409 ----- 409
Db 3823 AGACCTGCCCCCTGCGTCTCGTAGCACTTGAGGAGAGGAGTAGGTAAAGTTGCTAGCTGAGA 3882
QY 409 ----- 409
Db 3883 GGCTGGTTAACTGAGTAGTAGCTGCAGGGGTGAGAGGTATGGAGGGAGGGCTAAAGT 3942
QY 409 ----- 409
Db 3943 TTTGGTTGGGGAGCCTGTGCTCCTGAGACCCCTGTTAGCCCACTGATAACCTTCTTCAGC 4002
QY 409 ----- 409
Db 4003 CTTTCACTCTTCTGCTTGGCTGGGGCAGGGGGCTGGCATCAGCGGCCAGGCCTGA 4062
QY 409 ----- 409
Db 4063 GTATGTGCTGCTGCCAGGAACGTTCTGGGGCTAGCCATCTTCTCCAGATGGAGGACC 4122
QY 409 ----- 409
Db 4123 ATGTCTGTCTCGGACCACTCCAGACTCCAACTCAGCGGACATTCTTGGGGTGGCAGGC 4182

QY 409 ----- 409
Db 4183 AGGGAGGAGAGTCTCTGGGAGGCCCTTCTTAACACAGCTGATGCGACAGCTTGGCACTG 4242
QY 409 ----- 409
Db 4243 CACGCTGTCTGCTGTCTCTTTGCCACCTTTGTAGCTGCATGGTGAGCCGTGGCTTCC 4302
QY 409 ----- 409
Db 4303 CTGGTGTACAGTTTGAGCTCTGCCATGGCTCCACCTTCGAAATGCAGCCAACTCAACTC 4362
QY 409 ----- 409
Db 4363 TTCTGCAATGGGACAATCTTGATAAGACCTGGCCCTTGTCTTAATAGAGGCTCTGG 4422
QY 409 ----- 409
Db 4423 GCCATCAGGGCAGGGGTTTGGGGGATGTTGGTCCGACAGTCACTCTGATCTAAGTCAGA 4482
QY 409 ----- 409
Db 4483 CAGCAGGAAGAGTGAGAAGCCTTCAACATTAGCACAGCTGGGGCTGGGGAGGTGGGA 4542
QY 409 ----- 409
Db 4543 AGAGGGACATTCTCTCTGCTTGGGGTCTACTGGATTCTCCCTGCCCAAGGCTGGGACA 4602
QY 409 ----- 409
Db 4603 AGGGAGCTCATGGCAGGCGAGCTACCTAGTGGCATCTGGACCCAGAGAGCAGAGCT 4662
QY 409 ----- 409
Db 4663 TCTCTGCACCGGCAATGAGGATTTCCAGATGTCCGAGTGGAGGAGGAGCAGGAAG 4722
QY 409 ----- 409
Db 4723 GTTAGGAGAGCCTGCGTGGGGTTTGGGCCATCAGGGGCCCTGCCCTGGGCTTTGTCTC 4782
QY 409 ----- 409
Db 4783 TGTCTGTGCATCTCTTACCACCGTCTTCATTCGCCCTGTCTTTTCTTCCCTTACCTTGGAG 4842
QY 409 ----- 409
Db 4843 CTCTGTTCTCTCTGATCTGTGATATTGAGTTTGTCTGCTCTTACCTGTTCTAAGAGGCT 4902
QY 409 ----- 409
Db 4903 AGAGGAGACCTTAGACTTCTGGGTTTCACATTTGTCCCGGCCCTACCCCTTACCTTCTCC 4962
QY 409 ----- 409
Db 4963 CACTCTGAGGAAGGTCCTGTTAGACTTGGACCAAGTAGGGTCTCCATCTCTCTCCT 5022
QY 409 ----- 409
Db 5023 GCTCCTGATTTCTATGAGTCCCATTTGCCCTGGGATGGAGGCAAGGGTCTGTCTCTACA 5082
QY 409 ----- 409
Db 5083 GCTGGGTGGTCCAGTGTGGGTACACACCTGTCTCTTCCCTTTTCTTCCACCCCTCT 5142
QY 410 ----- PheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAspSe 426
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Db 5143 GCCTTAGGTTCTCTGCCCAATACCGAGGGGACACTGGAGGTGTAGCAGTGAGGACAG 5202
QY 426 rLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisVa 446
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Db 5203 CCTGATGACCACTTCTCTGCCAGGCCCTAAGCTGGAGTCCCTTCCCTTAATGGACAGT 5262

QY 446 lGlyAlaGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCy 466
|||||
Db 5263 GGCTGCTGGAGGAGTGGCTGCTCCACCTCCACCGCGCTCGCGGGCCCTCTGCCCTG 5322

QY 466 sAspValSerValArgValValGlyGluProThrGluAlaArgValValProGlyAr 486
|||||
Db 5323 TGATGTCTCGTACGTGTGTGTGGGTGAGCCACCGAGCGGTGTTCCGGCGCG 5382

QY 486 gGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaPr 506
|||||
Db 5383 GGGCATCTGGCTGGACTGCCATCTGGATAGTGCCTTCTCTGCCAGGTGCCCC 5442

QY 506 oSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSe 526
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Db 5443 ATCCCTGTTTATGGCTCCATTTGCCAGCTCAGCCAGTGTGTCACTGCCTATATGTGTC 5502

QY 526 rAlaAlaGlyLeuGlyLeuValAlaIleIleTyrPheAlaThrGlnValValPheAspLysSe 546
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Db 5503 TGGCGGAGGCGCTGGGTCTGGTCCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAG 5562

QY 546 rAspLeuAlaLysTyrSerAla 553
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Db 5563 CGACTTGGCCAAATACCTACGCG 5584

RESULT 26
AAS64039
ID AAS64039 standard; cDNA; 2904 BP.
XX
AC AAS64039;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA P553S splice variant #2.
XX
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
OS Homo sapiens.
XX
PN WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedwick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2001-639232/73.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Claim 1; Page 482-483; 579pp; English.
XX
CC The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of

CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
SQ Sequence 2904 BP; 542 A; 875 C; 773 G; 714 T; 0 other;

Alignment Scores:
Pred. No.: 1.52e-143 Length: 2904
Score: 1920.50 Matches: 390
Percent Similarity: 77.23% Conservative: 0
Best Local Similarity: 77.23% Mismatches: 1
Query Match: 67.13% Indels: 115
DB: 22 Gaps: 1

US-09-593-793A-113 (1-553) x AAS64039 (1-2904)

QY 163 ValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAsp 182
|||||
Db 1 GTCTATGCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCTGCTGCTGCATTTGAC 60

QY 183 TrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeu 202
|||||
Db 61 TGGGACACCAAGTGGCTGGCCCTTACCTGGGACCCAGGAGGAGTGCCTCTTTGGCCCTG 120

QY 203 LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluAlaAla 222
|||||
Db 121 CTCACCTCATCTTCTCCTACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGAGCG 180

QY 223 LeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCys 242
|||||
Db 181 CTGGGCCCCACCGAGCAGCAGAAAGGCTGTGGGCCCTCTCTTGGCCCCACTGCTGT 240

QY 243 ProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGln 262
|||||
Db 241 CCATGCGCGCGCGCTTGGCTTTCGGAACCTGGGCGCCCTGCTTCCCGGGCTGCACAG 300

QY 263 LeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrp 282
|||||
Db 301 CTGTGCTGCGCATGCCCGCACCTCTGCGCGGCTCTTGGTGGCTGAGCTGTGCAGCTGG 360

QY 283 MetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlyLeuTyrGln 302
|||||
Db 361 ATGGCACTCATGACCTTCACGCTGTGTTTACAGGGATTCGTGGGCGAGGGGCTGTACCAG 420

QY 303 GlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGlyVal --- 321
|||||
Db 421 GCGTGGCCAGAGCTGAGCGCGGACCGAGGCGCCGAGACACTATGATGAGGAAG-GCC 479

QY 321 ----- 321
Db 480 TCTGGCTGCTAGGAGTCTGATCAGAGTCTGTGCCCTTTCAGAGAAGAAAGCGCG 539

QY 321 ----- 321
Db 540 AGCTTATTCAAAGTCTAGAGGAGTGGAGGAGTTAAGGCTGGATTTTCAGATCTGCTGGT 599

QY 321 ----- 321
Db 600 TCCAGCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCCAAATATCTCACCAGCGCCT 659

QY 321 ----- 321
Db 660 TCCAGCTCAGCGCTCTAGAAAGCGCTTGAAGCCTATGGCAGCTGCTCTTGTGTCCCT 719

QY 321 ----- 321
Db 720 CTCACCGCGCTGTCTCTACAGTGTAGACTCCAGGAAACCTTCAGACTACCTTCCTCTGC 779

Db 421 GCGGTGCCAGAGCTCAGCGGGCCAGCCAGAGCGCCGAGACACTATGATGAAGAAAG-GCC 479
QY 321 ----- 321
Db 480 TCTGTGCTGCTAGGAGTCTGATCAGAGTCTGTGCCCCAGTTTGACAGAAGGAAGCGG 539
QY 321 ----- 321
Db 540 AGCTTATCAAGTCTAGAGGAGTGGAGAGTTAAGGCTGGATTTTCAGATCTGCCTGT 599
QY 321 ----- 321
Db 600 TCCAGCGGAGTGTGCCCTCTGCTCCCAACAGACTTTCCAAATAATCTCACAGGCGCT 659
QY 321 ----- 321
Db 660 TCCAGCTCAGCGCTCCTAGAGGCTCTTGAAGCCTATGCCACCTGCTCTTGTGTCCCT 719
QY 321 ----- 321
Db 720 CTCACCCGCTGTCTCTCACAGCTGAGACTCCAGAGAAACCTTCAGACTACCTTCCTCTGC 779
QY 322 -----ArgMetGlySerLeuGlyLeu 328
Db 780 CTTTCAAGAGGGCGGTGGCCCAATCTCTGAGGGCGTTTCGATGGCGACCTGGGGCTG 839
QY 329 PheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArg 348
Db 840 TTCTCTCAGTGGCCATCTCCCTGGCTCTCTCTGCTCATGGACCGGCTGGTGACGCA 899
QY 349 PheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAla 368
Db 900 TTGGGCACTCGAGCAGCTATTGTCAGCTGTGGCAGCTTTCCTCTGGCTGGCGGTGC 959
QY 369 ThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThr 388
Db 960 ACATGCTCTGCCACAGTGTGGCGGTGGACAGCTTCAGCGCCCTCACCGGGTTTCACC 1019
QY 389 PheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGlnGlyGln 408
Db 1020 TTCTCAGCCCTGCAGATCTGCCCTACACACTGGCTCTCTACCCCGGGGAGAGCAG 1079
QY 409 ValPheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMet 428
Db 1080 GTGTTCTGCCCAATACCGAGGGACACTGGAGGTGTAGCAGTGAGGACAGCCTGATG 1139
QY 429 ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAla 448
Db 1140 ACCAGCTTCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTTAATGGACACGTGGGTGT 1199
QY 449 GlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspVal 468
Db 1200 GGAGGAGTGGCTGCTCCCACTCCACCGCGCTCTGGCGGCTCTGCGCTGTGATGTC 1259
QY 469 SerValArgValValValGlyGluProThrGluAlaArgValValProGlyArgGlyIle 488
Db 1260 TCCGTACGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1319
QY 489 CysLeuAspLeuAlaIleLeuAspSerAlaPheLeuSerGlnValAlaProSerLeu 508
Db 1320 TCCCTGGACCTGCCATCTGGATAGTGGCTTCCCTGCTGCCAGGTGGCCCGCCATCCCTG 1379
QY 509 PheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAla 528
Db 1380 TTTATGGGCTCCATGTCTCAGCTCAGCCAGTCTGTACACTGCTATATGTTGTCGCCGA 1439
QY 529 GlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeu 548
Db 1440 GGCCTGGGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1499
QY 549 AlaLysTyrSerAla 553
Db 1500 GCCAAATACCTCAGCG 1514

RESULT 28

ABL95410

ID ABL95410 standard; cDNA; 2904 BP.

XX ABL95410;

AC ABL95410;

XX 19-JUL-2002 (first entry)

XX Human p53S splice variant SEQ ID NO 703.

XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;

KW gene therapy; gene; ss.

XX Homo sapiens.

OS US2002022248-A1.

PN 21-FEB-2002.

XX 12-JAN-2001; 2001US-0759143.

XX 25-FEB-1997; 97US-0806099.

PR 01-AUG-1997; 97US-0904804.

PR 09-FEB-1998; 98US-0020956.

PR 25-FEB-1998; 98US-0030607.

PR 14-JUL-1998; 98US-0115453.

PR 23-SEP-1998; 98US-0159812.

PR 15-JAN-1999; 99US-0232149.

PR 09-APR-1999; 99US-0288946.

PR 13-JUL-1999; 99US-0352616.

PR 12-NOV-1999; 99US-0439313.

PR 18-NOV-1999; 99US-0443686.

PR 14-JAN-2000; 2000US-0483672.

PR 27-MAR-2000; 2000US-0536857.

PR 09-MAY-2000; 2000US-0568100.

PR 12-MAY-2000; 2000US-0570737.

PR 13-JUN-2000; 2000US-0593793.

PR 27-JUN-2000; 2000US-0605783.

PR 10-AUG-2000; 2000US-0636215.

PR 29-AUG-2000; 2000US-0651236.

PR 06-SEP-2000; 2000US-0657279.

PR 02-OCT-2000; 2000US-0679426.

PR 10-OCT-2000; 2000US-0685166.

XX (XUJJ/) XU J.

PA (DILL/) DILLON D C.

PA (MITC/) MITCHAM J L.

PA (HARL/) HARLOCKER S L.

PA (JIAN/) JIANG Y.

PA (KALO/) KALOS M D.

PA (FANG/) FANGER G R.

PA (RETT/) RETTER M W.

PA (STOL/) STOLK J A.

PA (DAYC/) DAY C H.

PA (VEDV/) VEDVICK T S.

PA (CART/) CARTER D.

PA (LISX/) LI S X.

PA (WANG/) WANG A.

PA (SKEI/) SKEIKY Y A W.

PA (HEPL/) HEPLER W T.

PA (HEND/) HENDERSON R A.

XX

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

PI Fanger GR, Retter MW, Stoik JA, Day CH, Vedvick TS, Carter D;

PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;

XX WPI; 2002-255649/30.

XX

PT New prostate-specific polynucleotides for diagnosing and treating

PT diseases, in particular prostate cancer, and as markers for the

PT progression of cancer

XX

PS Claim 1; SEQ ID NO 703; 87pp; English.
 XX The present invention provides prostate-specific coding sequences and
 CC their encoded proteins. These can be used in the diagnosis and treatment
 CC of cancers, particularly prostate cancer. The present sequence is a cDNA
 CC described in the invention.
 XX

SQ Sequence 2904 BP; 542 A; 875 C; 773 G; 714 T; 0 other;

Alignment Scores:

Pred. No.: 1.52e-143 Length: 2904
 Score: 1920.50 Matches: 390
 Percent Similarity: 77.23% Conservative: 0
 Best Local Similarity: 77.23% Mismatches: 1
 Query Match: 67.13% Indels: 115
 DB: 24 Gaps: 1

US-09-593-793a-113 (1-553) x ABL95410 (1-2904)

Qy	163	ValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAsp	182
Db	1	GTCTATGCTTCATGATCAGTCTTGGGGCTGCTGGGCTACCTCTGCTGCCATTGAC	60
Qy	183	TrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPheGlyLeu	202
Db	61	TGGGACACAGTGCCCTGGCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTG	120
Qy	203	LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluAlaAla	222
Db	121	CTACCCCTCATCTTCTCACCCTGCTAGCAGCACACACTGCTGGTGGCTGAGGAGCAGC	180
Qy	223	LeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCys	242
Db	181	CTGGGCCCCACGACGACGAGAGGGCTGTGGGCCCTCTCTTCTGCCCCACTGCTGT	240
Qy	243	ProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGln	262
Db	241	CCATGCCGGGCGCGCTTGGCTTCCGGAACCTGGGCGCCCTGCTTCCCGCGGTGCCACG	300
Qy	263	LeuCysCysArgMetProArgThrLeuArgLeuGluPheValAlaGluLeuCysSerTrp	282
Db	301	CTGTGCTGCCGATGCCCGCACCTGGCGCGGCTCTTCGTGGCTGAGCTGTGACGCTGG	360
Qy	283	MetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGln	302
Db	361	ATGGCACTCATGACCTTACCGCTGTTTACACGGATTTCGTGGGCGAGGGCTGTACCAG	420
Qy	303	GlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal---	321
Db	421	GCGGTGCCACAGCTGAGCCGGGCACCGAGGCCGAGACACATATGATGAAGGAAG-GCC	479
Qy	321	-----	321
Db	480	TCTGCTGCTTAGAGTCTGATCAGAGTCTGTTGCCCGAGTTTGACAGAAAGCGG	539
Qy	321	-----	321
Db	540	ACCTTATTCAAAGTCTAGAGGAGTGGAGGAGTTAAGCTGGATTTCAGATCTGCTGGT	599
Qy	321	-----	321
Db	600	TCCAGCCGAGTGTGCCCTCTGCTCCCGCACGACTTTCCAAATAATCTCACCAGCGCT	659
Qy	321	-----	321
Db	660	TCCAGCTCAGCGCTCTAGAGCGTCTTGAAGCCCTATGGCCAGCTGTCTTGTGTTCCCT	719
Qy	321	-----	321
Db	720	CTCACCCTGCTCTCTCAGCTGAGACTCCCGAGAAACCTTCAGACTACCTTCTCTGCG	779
Qy	322	-----ArgMetGlySerLeuGlyLeu	328

Db	780	CTTCAGCAAGGGCGTGTGCCACATTCCTCTCAGGCGCTTCGATGGCAGCGCTGGGCTG	839
Qy	329	PheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArg	348
Db	840	TTCTTGCAGTGGCGCATCTCCCTGGTCTCTCTGGTCAATGACCGGCTGGTGGAGGA	899
Qy	349	PheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAla	368
Db	900	TTCCGCACTCGAGCAGTCTATTGGCCAGTGTGGCAGCTTCCCTGTGGTGGCGTCC	959
Qy	369	ThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThr	388
Db	960	ACATGCCCTGTCCACAGTGTGGCGTGTGACAGCTTCAGCGCCCTCAGCGGTTACCC	1019
Qy	389	PheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGln	408
Db	1020	TTCTCAGCCCTGCAGATCTGCCCTACACACTGGCCTCCCTCTACACCGGAGAGCAG	1079
Qy	409	ValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMet	428
Db	1080	GTGTTCTCTGCCAATACCGAGGGCAGCTGGAGGTGTAGCAGTGAGCAGCCTGATG	1139
Qy	429	ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAla	448
Db	1140	ACCAGCTTCTGCCAGGCGCTAAGCTGTGAGCTCCCTTCCCTTAATGGACACGTGGT	1199
Qy	449	GlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspVal	468
Db	1200	GGAGCAGTGGCCTCTCCACCTCCCGCGCTCTGGGGGCTCTGCTGTGATGTG	1259
Qy	469	SerValArgValValGlyGluProThrGluAlaArgValValProGlyArgGlyIle	488
Db	1260	TCCGTACCTGTGGTGGTGGTGAGCCACCGAGGCGAGGTGGTTCGCGCGCGGCGCATC	1319
Qy	489	CysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeu	508
Db	1320	TGCTTGGACCTCGCCATCTGTGATAGTGCCTTCTCTGCTGCCAGGTGCCCATCCCTG	1379
Qy	509	PheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAla	528
Db	1380	TTATGGGCTCATGTCCAGCTCAGCCAGCTGTGCTATATGCTGTCTGCCCA	1439
Qy	529	GlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeu	548
Db	1440	GSCCTGGTCTGGTGGCCATTTACTTTCCTACACAGGTAGTATTTGACAGAGCGACTG	1499
Qy	549	AlaLysTyrSerAla 553	
Db	1500	GCCAAATACACGCG 1514	
RESULT 29			
ABA91284			
ID	ABA91284	standard; DNA; 1593 BP.	
XX			
AC	ABA91284;		
XX			
DT	08-APR-2002	(first entry)	
XX			
DE	Thioredoxin-ubiquitin-P501S(aal-320)His triple gene fusion.		
KW	Thioredoxin; trxA; ubiquitin; P501S; tumour; prostate; antigen;		
KW	cancer; vaccine; therapy; human; gene; ds.		
XX			
OS	Chimeric - Homo sapiens.		
OS	Chimeric - Escherichia coli.		
FH	Key	Location/Qualifiers	
FT	CDS	1..1593	
FT		/*tag=	
FT		/transl_except= (pos:607..609,aa:Xaa)	
FT		/note= "Xaa not given in amino acid sequence of	
FT		Figure 12b (AAM50662), which has a Val	
FT		residue at amino acid position 208 not	

FT not encoded by the present sequence"

PN W0200200892-A1.
XX
PD 03-JAN-2002.
XX
PF 19-JUN-2001; 2001WO-EP06952.
XX
PR 26-JUN-2000; 2000GB-0015619.
PR 30-OCT-2000; 2000GB-0026484.
XX
XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
PA
XX Cabezon Silva TEV, Delisse AEF;
PI
XX WPI: 2002-147888/19.
DR P-PSDB; AAM50662.
XX
XX Novel DNA sequence encoding triple fusion protein comprising ubiquitin
PT fused between thioredoxin and polypeptide of interest, useful for
PT producing recombinant polypeptide of interest suitable for medicinal
PT use -
XX
XX Example 8; Fig 12b; 87pp; English.
XX
XX The present sequence is that of a triple gene fusion comprising,
CC from the 5' end, the trxA thioredoxin gene from Escherichia coli,
CC the human ubiquitin coding sequence, the prostate antigen P501S
CC (amino acids 1-320) coding sequence, and DNA encoding a histidine
CC tail. The triple fusion was constructed in plasmid pRIT15115,
CC under the control of the lambda pL promoter. Triple fusion
CC protein (see AAM50662) was produced in E. coli G1724 transformants.
CC This is an example of the production of triple fusion proteins of
CC the invention comprising ubiquitin fused between thioredoxin and a
CC protein of interest, in this case P501S(aal-320). A claimed method
CC of producing a recombinant protein of interest involves: culturing
CC a host cell (preferably E. coli) under conditions which allow
CC for co-expression of the triple fusion and a ubiquitin-specific
CC endoprotease (especially Upl from Saccharomyces cerevisiae);
CC and recovering the recombinant protein directly from the bacterial
CC cells after it has been subjected to the action of the
CC ubiquitin-specific endoprotease in vivo. In the present case,
CC expression was controlled by addition of tryptophan. The
CC recombinant protein can be used as a vaccine for cancer therapy.
XX
SQ Sequence 1593 BP; 308 A; 472 C; 461 G; 352 T; 0 other;

Alignment Scores:
Pred. No.: 5,84e-126 Length: 1593
Score: 1696.00 Matches: 320
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 59.28% Indels: 0
DB: 24 Gaps: 0

US-09-593-793a-113 (1-553) x ABA91284 (1-1593)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
DB 604 ATGGTCCAGAGGCTGTGGGTGAGCCGCTGCTGGCGCCGGAAGCCAGCTCTGTGCG 663
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaClyleThrTrpValPro 40
DB 664 GTCAACCTGCTAACTTTGGCTGGAGGTGTCTTTGGCGCAGGCATCACCTATGTGCGG 723
QY 41 ProLeuLeuLeuGluValGlyValGluLysPheMetThrMetValLeuGlyLeGly 60
DB 724 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAGTTCATGACCATGTGCTGGGCATTGCT 783
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
DB 784 CCAGTGTGGGCTGGTCTGTCCGCTCTCCAGGCTCAGCCAGTGACCACTGTGGCTGGA 843

QY 81 ArgTyrGlyArgArgProPheHleTrpAlaLeuSerLeuGlyLeuLeuSerLeu 100
DB 844 CGCTATGGCGCGCGCGCCCTTCATCTGGCACTGTCTTGGCATCTCTGTGAGCCTC 903
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
DB 904 TTTTCATATCCCAAGGCGCGCTGGGTAGCAGGCTGTGTGCCCGATCCAGGCCCTTG 963
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
DB 964 GAGCTGGCACTGCTCATCTCTGGCGTGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTC 1023
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheAspProAspHisCysArgGlnAla 160
DB 1024 ACTCCACTGGAGGCCCTGCTCTGACCTCTTCGCGGACCCGACCACTGTCCAGGCC 1083
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrIleLeuProAla 180
DB 1084 TACTCTGTCTATGCCCTTCATGATCAGTCTTGGGGCTGCTGGGTACCTCTGCTGCTGC 1143
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe 200
DB 1144 ATTGACTGGGACACCACTGCTGCCCTTACCTGGGACCCAGGAGGAGTGCCTCTTT 1203
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
DB 1204 GGCTGCTCACCTCATCTTCCTACCTGCTAGCAGCCACACTGCTGTGCTGAGGAG 1263
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
DB 1264 CGAGCGCTGGGCGCCACCGAGCAGCAGAGGCGTGTCCGCCCTCTCTTGTGCGCCAC 1323
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyValAlaLeuLeuProArgLeu 260
DB 1324 TGCTGTCCATGCGGCGCCGCTTGGCTTCCGGAACCTGGGCGCCCTGCTTCCCGGCTG 1383
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
DB 1384 CACCACTGTGCTGCGCATGCCGACCCGCGCGCTCTTGTGGCTGAGCTGTGC 1443
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPheValGlyGlyLeu 300
DB 1444 AGCTGGATGGCACTCATGACCTTTCACGCTGTGTTTACAGGATTTCTGGGCGAGGGCTG 1503
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTrpAspGluGly 320
DB 1504 TACCAGGGGCTGCCAGAGCTGAGCGGGCACCGAGGCCGCGAGACACTATGATGAAGGC 1563
RESULT 30
ABN81320
ID ABN81320 standard; cDNA; 3663 BP.
XX
AC ABN81320;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human mast cell related gene MC14 SEQ ID NO 3.
KW Human; mast cell; MC; antiallergic; antinflammatory; antiasthmatic;
KW vasotrophic; dermatological; allergy; hypersensitivity; rhinitis; asthma;
KW gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 294..746
FT /*tag= a
FT /product= "MC14-1"
FT 1238..2218
FT /*tag= a
FT /product= "MC14-2"
XX
PN W0200246389-A2.

XX	Ral2-P501S-E2 construct cDNA sequence.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
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Qy 105 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeu 124
Db 619 AGGGCGGCTGGCTAGCAGGGGCTGCTGCCGGATCCAGGCCCTCGAGCTGGCACTG 678
Qy 125 LeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGlu 144
Db 679 CTCATCCCTGGGCGTGGGCTGCTGACATCTCTGGCCAGGTGTGCTTCACTCCACTGGAG 738
Qy 145 AlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyr 164
Db 739 GCCCTGCTCTGACACTCTTCGGGAGCCCGGACCACTGTGCCAGGCTACTCTCTCTAT 798
Qy 165 AlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAsp 184
Db 799 GCCTTCATGATCAGCTTTGGGGCTGCTGGCTACCTCCTGCTGCCATTGACGGGAC 858
Qy 185 ThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPheGlyLeuLeuThr 204
Db 859 ACCAGTGCCTGGCCCTTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCTGCTCACC 918
Qy 205 LeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGly 224
Db 919 CTCATCTTCCCTACCTGGCTAGCAGCCACACTGCTGGTGGTAGAGGACGCGTGGGC 978
Qy 225 ProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCys 244
Db 979 CCCACCGAGCAGCAGAGGGCTGCGGCCCTCTCTGTCGCCCACTGCTGTCCATGC 1038
Qy 245 ArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCys 264
Db 1039 CGGGGCCCTTGGCTTCCGGAACCTGGGCGCCCTGCTTCCCGGCTGCACCACTGTGC 1098
Qy 265 CysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAla 284
Db 1099 TGCCCGCATGCCCGCACCTGCGCGGCTCTCTGCTGGCTGAGCTGTGCGATGGCA 1158
Qy 285 LeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlu 298
Db 1159 CTCATGACCTTCACGCTGTTTACACGGATTTCGTGGTGGCGAG 1200
RESULT 33
ABL95524
ID ABL95524 standard; cDNA; 1203 BP.
AC ABL95524;
DT 19-JUL-2002 (first entry)
XX
DE Ra12-P501S-E2 construct cDNA sequence SEQ ID NO 851.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
OS Chimeric - Mycobacterium tuberculosis.
OS Chimeric - Homo sapiens.
XX
PN US2002022248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
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PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
(XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
WPI; 2002-255649/30.
XX
New prostate-specific polynucleotides for diagnosing and treating
diseases, in particular prostate cancer, and as markers for the
progression of cancer -
PT
PT
XX
XX
Example 17; SEQ ID NO 851; 87pp; English.
XX
The present invention provides prostate-specific coding sequences and
their encoded proteins. These can be used in the diagnosis and treatment
of cancers, particularly prostate cancer. The present sequence is a cDNA
described in the invention.
XX
SQ Sequence 1203 BP; 175 A; 415 C; 368 G; 245 T; 0 other;
Alignment Scores:
Pred. No.: 9,07e-103 Length: 1203
Score: 1403.50 Matches: 267
Percent Similarity: 97.45% Conservative: 0
Best Local Similarity: 97.45% Mismatches: 2
Query Match: 49.06% Indels: 5
DB: 24 Gaps: 1
US-09-593-793A-113 (1-553) x ABL95524 (1-1203)
Qy 30 ValCysLeuAlaAlaGly-----IleThrTyrValProLeuLeuLeu 44
Db 379 GTGACATTGGCGGAGGAGCCCGCCCGCAATTCACTACCTATGTGCCGCTCTGCTGTG 438
Qy 45 GluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGly 64
Db 439 GAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGGTGGCATGGTCCAGTGTGGGC 498
Qy 65 LeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGlyArg 84
Db 499 CTGGTCTGTGCCGCTCCTAGGCTCAGCCAGTACCAGTGGCGTGGAGCTATGCGCGC 558
Qy 85 ArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIlePro 104
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Db 559 GCGCGGCCCTTCACTGGGCACTGCTTGGGCACTCCCTGGGCACTCTTCTCATCCCA 618
Qy 105 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeu 124
Db 619 AGGCGCGCTGGCTAGCAGGCTGCTGTGCCGGATCCAGGCCCTGGAGCTGGCACTG 678
Qy 125 LeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGlu 144
Db 679 CTCATCTCTGGCGCTGGGCTGCTGGACTCTGTGTGCCAGGTGTGCTTCACTCCACTGGAG 738
Qy 145 AlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyr 164
Db 739 GCCCTGCTCTGTGACCTCTCCGGAGCCCGACCACTGTCCAGGCTACTCTGTCTAT 798
Qy 165 AlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAsp 184
Db 799 GCCCTTCATGATCAGTCTTGGGGCTGCTGGGCTACCTCTCTGCTGCCATTTGACTGGGAC 858
Qy 185 ThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPheGlyLeuLeuThr 204
Db 859 ACCAGTGCCTGGCCCTACCTGGGCACCCAGGAGGAGTGCTCTTTGGCTGCTCACC 918
Qy 205 LeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluAlaLeuGly 224
Db 919 CTCATCTCTCCTACCTGCTGTAGCAGCCACACTGTGTGTGGTGGAGGAGCGCTGGGC 978
Qy 225 ProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCys 244
Db 979 CCCACCGAGCCAGCAGAGGCTGTGGCCCCCTCTTGTGCCCCACTGTGTGCCATGC 1038
Qy 245 ArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCys 264
Db 1039 CGGCGCGCTGGCTTCCGGAACCTGGCGCCCTGCTTCCCGGCTGCACCACTGTGC 1098
Qy 265 CysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAla 284
Db 1099 TGGCGCATGCCGCCACACCTCGCGCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGCA 1158
Qy 285 LeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlu 298
Db 1159 CTCATGACCTTCACGCTGTTTTACAGGATTCGTGGGCGAG 1200
RESULT 34
AAC64928
ID AAC64928 standard; DNA; 2133 BP.
XX
AC AAC64928;
XX
XX 07-FEB-2001 (first entry)
XX Human prostate-related PS108 partial coding sequence SEQ ID NO: 16.
XX Human: prostate cancer; PS108; antibody; tumour; metastasis; ds.
XX Homo sapiens.
XX US6130043-A.
XX PD 10-OCT-2000.
XX 01-MAY-1998; 98US-00711710.
XX 02-MAY-1997; 97US-0850713.
XX (ABBO ) ABBOTT LAB.
XX Cohen M, Colpitts TL, Friedman PN, Gordon J, Granados EN;
PI Billing-Medel PA, Klass MR, Roberts-Rapp L, Stroupe SD, Yu H;
PI Kratochvil JD, Russell JC, Hodges SC;
XX WPI; 2000-655655/63.
XX
PT Methods for detecting target prostate-specific polynucleotides or
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PT diseases of the prostate (e.g. prostate cancer), comprising detecting
PT the presence of any of PS108 nucleic acid sequences in a test sample -
XX Claim 1; Column 77-80; 55pp; English.
XX
CC The present invention is related to a number of partial coding and
CC protein sequences for the human prostate tissue protein PS108. These
CC sequences can be used in the diagnosis and prognosis of prostate
CC diseases, particularly prostate cancer. They can also be used to produce
CC antibodies which can be used in treatment. The present sequence is one
CC of the PS108 partial coding sequences.
XX
SQ Sequence 2133 BP; 414 A; 618 C; 561 G; 540 T; 0 other;

Alignment Scores:
Pred. No.: 3,78e-93 Length: 2133
Score: 1287.00 Matches: 255
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.98% Indels: 0
DB: 21 Gaps: 0

US-09-593-793a-113 (1-553) x AAC64928 (1-2133)
Qy 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAsp 318
Db 2 GGGCTGTACCAAGGGCTGCCAGAGCTGAGCGGGCAGGCGCGAGACATATCAT 61
Qy 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGCGCTCGGATGGGCGAGCTGGGGCTGTCTCTGTCAGTGGCCATCTCCCTGGCTCTC 121
Qy 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGGTCAATGGACCGGCTGGTGCAGGATTCGSCATCGAGCAGTCTATTGGCCAGT 181
Qy 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal 378
Db 182 GTGGCAGCTTTCCCTGTGGCTGCCGGTGCACATGCCTGTCCACAGTGTGGCGTGGTG 241
Qy 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 242 ACAGCTTCAGCGCGCCCTCACCGGGTTTCACTTCTCAGCCCTGCAGATCTCCCTTACACA 301
Qy 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 302 CTGGCTCCCTCTACCAACCGGAGAGCAGGTGTCTCTGCCAATACCGAGGGGACACT 361
Qy 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 362 GGAGTGCTAGCAGTAGGACAGCCTGATGACCACTCTCTGCCAGGCCCTTAAGCCTGGA 421
Qy 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 422 GCTCCCTTCCCTTAATGGACACAGTGGTGTGGAGCAGTGGCTGCTCCACCTCCACCC 481
Qy 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr 478
Db 482 GCGCTCTCGGGGGCTCTGCTGCTGTGATGCTCCGCTACGTGTGGTGGTGGGAGCCCAACC 541
Qy 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 542 GAGGCCAGGGTGGTTCGGGGCGGGGCATCTGCTGGAGCTCGCCATCTCGATAGTGCC 601
Qy 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 602 TTCCTGTGTCCAGGTGGCCCATCTCCCTGTTTATGGGCTCCATTTGTCAGCTCAGCCAG 661
Qy 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 662 TCTGTCACTGCCTATATGGTGTCTGCCGAGGCGCTGGGTCTGGTCGCAATTTACTTGT 721
Qy 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
```


CC diseases, particularly prostate cancer. They can also be used to produce
CC antibodies which can be used in treatment. The present sequence is one
CC of the PS108 partial coding sequences.

XX
SQ Sequence 2124 BP; 411 A; 616 C; 558 G; 539 T; 0 other;

Alignment Scores:

Pred. No.: 8.56e-92 Length: 2124
Score: 1270.00 Matches: 252
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.39% Indels: 0
DB: 21 Gaps: 0

US-09-593-793A-113 (1-553) x AAC64927 (1-2124)

QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaAArgHisTyrAspGluGlyVal 321
DB 3 CAGGGCGTCCCGAGAGCTGAGCCGGCAGCCGAGCCGAGACACTATGATGAAGCGTT 62
QY 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
DB 63 CGATGGGAGCTGGGGCTTCTTCGACAGTGGCCATCTCCCTGCTCTCTCTCTGCTC 122
QY 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
DB 123 ATGACCGGCTGGTGCAGCGATTCCGCACTCGAGCAGTCTATTGGCCAGCTGTGGCAGT 182
QY 362 PheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAlaSer 381
DB 183 TTCCTGTGGCTGCCGGTGCCACATCCCTGTCACAGTGTGGCCGTGTGACAGCTTCA 242
QY 382 AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401
DB 243 GCGCCCTCACCGGTTACCTTCTCAGCCCTGCACATCTGCCCTACACACTGGGCTCC 302
QY 402 LeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAla 421
DB 303 CTCTACACCGGAGAAGCAGGTGTCTCTGCCAAATACCGAGGGACACTGGAGGTGCT 362
QY 422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProphe 441
DB 363 AGCAGTGAGGACAGCTGATGACAGCTTCTGTCGACAGCTTCCGAGCTGAGCTCCCTTC 422
QY 442 ProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCys 461
DB 423 CCTAATGGACAGCTGGGTGCTGGAGCAGTGGCTGCTCCACCTCCACCGCGCTCTGC 482
QY 462 GlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAlaArg 481
DB 483 GGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 542
QY 482 ValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501
DB 543 GTGGTTCCGGGGGGGCGCATCTGCTGGACCTGCGCATCTGGATAGTCCCTTCCTGCTG 602
QY 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521
DB 603 TCCAGGTGGCCCATCTCCCTGTTATGGGCTCCATGTCAGCTCAGCCAGCTGTCAC 662
QY 522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 541
DB 663 GCCTATATGGTGTCTGCCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 722
QY 542 ValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 723 GTATTTGACAAGAGCAGCTTGGCCAAATACTCAGCG 758
RESULT 38
ID AAS07601
XX AAS07601 standard; cDNA; 2124 BP.
AC AAS07601;

XX
DT 23-OCT-2001 (first entry)
XX
DE Prostate gene PS108-specific cDNA clone 1711346IH.
XX
KW Prostate; PS108; immunogen; drug screening; image localisation;
KW diagnostic; therapeutic; prostate tissue disease; cancer; metastasis;
KW expressed sequence tag; EST; ss.
XX
OS Homo sapiens.
XX
PN US6252047-B1.
XX
PD 26-JUN-2001.
XX
PF 15-MAR-2000; 2000US-0525397.
XX
PR 01-MAY-1998; 98US-0071710.
PR 02-MAY-1997; 97US-0850713.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
PI Russell JC, Stroupe SD, Yu H;
XX
DR WPI; 2001-424488/45.
XX
PT Novel PS108 polypeptide useful in assays for detecting antibodies to
PT prostate tissue, and as immunogens to produce PS108 antibodies -
XX
PS Example 1; Fig 1; 55pp; English.
XX
CC The sequence represents the coding sequence of prostate gene PS108 -
CC specific expressed sequence tag (EST) cDNA clone 1711346IH. The sequence
CC was used along with other overlapping cDNA clones to produce a full
CC length consensus sequence (see AAS07155). This sequence could then be
CC used to produce PS108 polypeptides which are useful in assays for
CC detecting antibodies to prostate tissue, and as immunogens to produce
CC antibodies. The polypeptide is useful for screening compounds which
CC specifically bind to the polypeptide and for screening for drugs,
CC compounds, or any other agent which can be used to treat diseases
CC associated with PS108. The antibody is useful to detect, or for image
CC localisation of PS108 antigen in a patient, for detecting or diagnosing a
CC disease or condition, as delivery agents for therapeutic agents as well
CC as for diagnostic tests and for screening for diseases or conditions
CC associated with PS108, especially cancer. The antibody is also useful for
CC generating chimeric antibodies for therapeutic use, for inhibiting the
CC biological activity of PS108, in therapy (for e.g. to treat prostate
CC tissue disease including prostate cancer and its metastases), and to
CC detect the presence of any polypeptide in a test sample which shares one
CC or more antigenic determinants with the PS108 polypeptide.
XX
SQ Sequence 2124 BP; 411 A; 616 C; 558 G; 539 T; 0 other;

Alignment Scores:

Pred. No.: 8.56e-92 Length: 2124
Score: 1270.00 Matches: 252
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.39% Indels: 0
DB: 22 Gaps: 0

US-09-593-793A-113 (1-553) x AAS07601 (1-2124)

QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaAArgHisTyrAspGluGlyVal 321
DB 3 CAGGGCGTCCCGAGAGCTGAGCCGGCAGCCGAGACACTATGATGAAGCGTT 62
QY 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
DB 63 CGATGGGCGAGCTGGGGCTGTCTTCGACAGTGGCCATCTCCCTGCTCTCTCTGCTC 122

Oy 342 MetAspArgLeuValGlnAArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
Db 123 ATGGACCGGCTGGTCAGCAGATTCGGCACTCGAGCAGTCTATTTCGCCAGTGTGCAGCT 182
Oy 362 PheProValAlaAlaGlyAlaValThrCysLeuSerHisSerValAlaValThrAlaSer 381
Db 183 TTCCTGTGGCTGGCGGTGGCCACATGCTCTCCACAGATGGCGGTGGTGACAGCTTCA 242
Oy 382 AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401
Db 243 GCCGCCCTCACCGGTTTCACCTTCTCAGCCCTGCAGATCTCCCTACACACTGGCCCTCC 302
Oy 402 LeuTyrHisArgGluGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAla 421
Db 303 CTCTACCAACCGGGAGAGAGCGTGTCTCTGCCAATACCGAGGGGACACTGGAGGTGCT 362
Oy 422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
Db 363 AGCAGTGAGGACAGCTGATGACCACTCTCTCCAGGCGCTTAAGCCTGGAGCTCCCTTC 422
Oy 442 ProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeuCys 461
Db 423 CCTAATGACACAGTGGGTGCTGGAGGAGTGGCTCTCCACCTCCACCGCGCTCTGC 482
Oy 462 GlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAlaArg 481
Db 483 GGGCGCTCTGCTGTATGCTCTCCGTACGTGTGGTGGTGGTGGTGGTGGTGGTGGTGG 542
Oy 482 ValValProGlyArgGlyGlyCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501
Db 543 GTGGTTCGGGCGCGGCGATCTGCTGACCTCGCCATCTCTGGATAGTGGCTTCTGCTG 602
Oy 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521
Db 603 TCCAGGTGGCCCATCCCTGTTATGGCTCCATGTTCCAGCTCAGCAGTCTGCTACT 662
Oy 522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 541
Db 663 GCCTATATGGTGTCTGCGCGCAGGCTGGGTGCTGGTGGTGGTGGTGGTGGTGGTGG 722
Oy 542 ValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 723 GTATTGACAGAGGACTTGGCCAAATACTACGCG 758
RESULT 39
AAV71180
ID AAV71180 standard; cDNA: 2143 BP.
AC AAV71180;
XX 12-FEB-1999 (first entry)
DT
XX
XX
DE Clone 17113461H, the PS108 gene contig full length sequence.
XX
KW PS108 gene; prostate disease; benign prostatic hyperplasia; BPH;
RW prostatitis; prostatic intraepithelial neoplasia; PIN; cancer;
XX drug screening; gene therapy; ss.
XX
OS Homo sapiens.
XX
XX WO9850567-A1.
XX
XX 12-NOV-1998.
XX
XX 01-MAY-1998; 98WO-US08930.
XX
XX 02-MAY-1997; 97US-0850713.
XX
XX (ABBO) ABBOTT LAB.
XX
XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN;
PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;

XX WPI: 1999-034731/03.
DR
XX
PT New isolated prostate-specific polynucleotides - used to develop
PT products for the diagnosis and treatment of prostate diseases, e.g.
PT benign hyperplasia, prostatic or prostate cancer
XX
PS Claim 1; Fig 1A-E; 122pp; English.
XX
CC The present sequence represents the full length contig of the PS108
CC gene, as represented by clone 17113461H. This clone is the contig of
CC overlapping clones AAV71166-79. The clone sequences are PS108
CC gene-specific. They are used in the method of the invention. The
CC specification describes a method for detecting the presence of a
CC target PS108 polynucleotide in a test sample. The method comprises
CC contacting the test sample with at least 11 PS108-specific polynucleotide
CC or complement, and detecting the presence of the target PS108
CC polynucleotide. The products can be used for detecting, diagnosing,
CC staging, monitoring, prognosticating, in vivo imaging, preventing or
CC treating, or determining predisposition to diseases or conditions of
CC the prostate such as benign prostatic hyperplasia (BPH), prostatitis,
CC prostatic intraepithelial neoplasia (PIN) and cancer. In particular the
CC products can be used in drug screening and gene therapy.
XX
SQ Sequence 2143 BP: 418 A; 621 C; 563 G; 541 T; 0 other;
Alignment Scores:
Pred. No.: 8,66e-92 Length: 2143
Score: 1270.00 Matches: 252
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.39% Indels: 0
DB: 20 Gaps: 0
US-09-593-793a-113 (1-553) x AAV71180 (1-2143)
Oy 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGlyVal 321
Db 3 CAGGGCGTGGCCAGAGCTGAGCGGGCACCAGCGGGCCGAGACACTATGATGAAGCGCTT 62
Oy 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
Db 63 CGGATGGGCGAGCTGGGGCTGTCTCTGAGTGGCGCATCTCCCTGGTCTCTCTGTC 122
Oy 342 MetAspArgLeuValGlnAArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
Db 123 ATGGACCGGCTGGTCAGCAGATTCGGCACTCGAGCAGTCTATTTCGCCAGTGTGCAGCT 182
Oy 362 PheProValAlaAlaGlyAlaValThrCysLeuSerHisSerValAlaValThrAlaSer 381
Db 183 TTCCTGTGGCTGGCGGTGGCCACATGCTCTCCACAGATGGCGGTGGTGACAGCTTCA 242
Oy 382 AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401
Db 243 GCCGCCCTCACCGGTTTCACCTTCTCAGCCCTGCAGATCTCCCTACACACTGGCCCTCC 302
Oy 402 LeuTyrHisArgGluGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAla 421
Db 303 CTCTACCAACCGGGAGAGAGCGTGTCTCTGCCAATACCGAGGGGACACTGGAGGTGCT 362
Oy 422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
Db 363 AGCAGTGAGGACAGCTGATGACCACTCTCTCCAGGCGCTTAAGCCTGGAGCTCCCTTC 422
Oy 442 ProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeuCys 461
Db 423 CCTAATGACACAGTGGGTGCTGGAGGAGTGGCTCTCCACCTCCACCGCGCTCTGC 482
Oy 462 GlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAlaArg 481
Db 483 GGGCGCTCTGCTGTATGCTCTCCGTACGTGTGGTGGTGGTGGTGGTGGTGGTGGTGG 542
Oy 482 ValValProGlyArgGlyGlyCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501

|||||
Db 543 GTGGTTCCGGCGGGGCATCTGCCTGGACCTCGCCATCTGGATAGTCCCTTCCTGCTG 602
QY 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521
Db 603 TCCCAAGTGGCCCAATCCCTGTTTATGGGCTCCATGTGCCAGCTCAGCCAGTCTGTCACT 662
QY 522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 541
Db 663 GCGTATATGGTCTGCGCCAGCGCTGGGCTCTGGTGGCCATTACTTTGCTACACAGGTA 722
QY 542 ValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 723 GTATTGTACAAGAGCGACTTGGCCAAATACTCAGCG 758

RESULT 40

AAZ45677

ID AAZ45677 standard; cDNA; 2462 BP.

XX AC AAZ45677;

XX DT 06-APR-2000 (first entry)

XX DE cDNA sequence of a novel prostate cancer-associated gene.

XX KW Prostate cancer-associated gene; Incyte clone 1864683; bone cancer;
XX KW cell proliferation; cancer; adrenal gland cancer; bladder cancer;
XX KW prostate cancer; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 376..1071

XX FT /tag= a

XX FT /product= "prostate cancer-associated protein"

XX FT sig_peptide 376..516

XX FT /tag= b

XX PN W09567384-A2.

XX PD 29-DEC-1999.

XX PF 15-JUN-1999; 99WO-US13524.

XX PR 22-JUN-1998; 98US-0102615.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Walker MG, Volkmut W, Klingler TM, Sprinzak EA;

XX DR WPI; 2000-126631/11.

XX DR P-PSDB; AAY54369.

XX PT Identifying biomolecules for the diagnosis and treatment of diseases
XX PT associated with cell-proliferation -

XX PS Claim 8; Page 47-48; 52pp; English.

XX CC The present sequence is derived from a prostate cancer-associated
XX CC gene, and is represented by Incyte clone number 1864683. The sequence
XX CC is used in the method of the invention. The specification
XX CC describes a method for identifying biomolecules for the diagnosis or
XX CC treatment of diseases associated with cell proliferation. The method
XX CC comprises examining polynucleotides, consisting of prostate cancer-
XX CC specific genes, and genes of unknown function, expressed in cDNA
XX CC libraries. The patterns of both gene sets are compared to identify
XX CC genes of unknown function with similar expression patterns to the
XX CC prostate cancer-specific genes. The biomolecules identified by the
XX CC method form pharmaceutical compositions useful for the diagnosis and
XX CC treatment of diseases associated with cell proliferation. Such diseases
XX CC include cancer of the adrenal gland, bladder and bone, but especially
XX CC prostate cancer. The method may also be applied using other disease-
XX CC specific genes. The prostate cancer-specific genes facilitate the

CC diagnosis and treatment of cell proliferation disorders.

XX SQ Sequence 2462 BP; 483 A; 726 C; 632 G; 621 T; 0 other;
Alignment Scores:

Pred. No.: 9,08e-84 Length: 2462
Score: 1170.50 Matches: 241
Percent Similarity: 88.28% Conservative: 0
Best Local Similarity: 88.28% Mismatches: 9
Query Match: 40.91% Indels: 23
DB: 21 Gaps: 2

US-09-593-793A-113 (1-553) x AAZ45677 (1-2462)

QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAsp 318
Db 265 GGTCTCGTGCAGCAGGTACCTGTGTTCGGCCTTCT- -CATCTCCCT 309
QY 319 Glu- - - - -Gly 320
Db 310 GAGACTGCTCCGACCTTCCCTCCAGGCTCTGTCTGATGGCCCTCTCCCTCTGCAGGC 369
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 370 GTTCGGATGGCGAGCTGGGGCTGTTCTCTGCAGTGGCCATCTCCCTGGTCTTCTCTCTG 429
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 430 GTCATGGAGCCGGCTGGTGCAGGATTTCGGCACTTCGAGCAGTCTATTGGCCAGTGTGGCA 489
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 490 GCTTTCCTCTGTGGTGGCTGCCAGTCCCTGTCCACAGTGTGCCGTGTGCAGCT 549
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 550 TCAGCCGGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 609
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 610 TCCCTCTACCCACCGGGAAGCAGGTGTTCCTGCCCCAATCCGAGGGGACACTGGAGT 669
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 670 GCTACGAGTGGAGACAGCTGATGACACAGTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC 729
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
Db 730 TTCCCTAATGGACACGTGGGTGCTGGAGCAGTGGCCTGCTCCCACTCCACCCCGCTC 789
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 790 TCGGGGGCTCTGCGCTGTGATGCTCCCGTACGTGTGGTGGTGAGCCACCGAGGCC 849
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 850 AGGGTGGTTCGGGGCGGGGCATCTGCCTGGACCTGCCATCTCGATAGTGCCTTCTCTG 909
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 910 CTGTCCCAAGTGGGCCCATCCCTGTTTATGGGCTCCATTTGTCCAGCTCAGCCAGTCTGTC 969
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 970 ACTGCTATATGTTGTTCTGCCCGACCGCTGGGTCTGGTGGCCATTACTTTTCTACACAG 1029

QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553

Db 1030 GTAGTATTGTACAAGAGCGACTTGGCCCAATACTCAGCG 1068
RESULT 41
AAV61144
ID AAV61144 standard; cDNA; 789 BP.


```
US-09-593-793A-113 (1-553) x AA058487 (1-789)
QY 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
DB 3 GTCTATNTGCCAGTGGCAGCTTTCCTGTGGCTGGCGTGGCCACATGCTGCCCCAC 62
QY 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
DB 63 AGTGTGGCGGTGGTACAGCTTCAGCGCCCTCAGCGGCTTCCACCTTCAGCCCTGCGAG 122
QY 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluGlnValPheLeuProLys 413
DB 123 ATCTCTCCCTACACATGCGCTTCTTACCACCGGAGAGCAGGTGTCTGCCCCAAA 182
QY 414 TyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
DB 183 TACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCTGATGACCACTTCCTGCCA 242
QY 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeu 453
DB 243 GGCCTTAAGCTGGAGCTCCCTTCCCTAATGGACAGTGGGTGCTGGAGGACAGTGGCCCTG 302
QY 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
DB 303 CTCCCCACCTCCACCGCGCTCTCGGGGCTCTGCGTGTGATGCTCTCCGTACGTGTGGTG 362
QY 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAla 493
DB 363 GTGGGTGAGCCACACCGAGGGTGTCCGGCGCGGGGACATGCTGACCTGCGCC 422
QY 494 IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
DB 423 ATCTGTGATAGTGC-TTCCTGTGCTCCCAAGTGGCCCATCCCTGTTTATGGGCTCCATT 481
QY 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyVal 533
DB 482 GTCCAGCTCAGCCAGTCTGTCTACATGCTATATGGTGTCTGCGCGAGGCTGGGTCTG 541
QY 534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAlaAlaLysTyrSerAla 553
DB 542 CC-ATTACTTGTCTACACAGGTANTATTGACAGACGANTTGGCCAAATACTCAGCG 600

RESULT 43
AAA06250
ID AAA06250 standard; cDNA; 789 BP.
XX AC AAA06250;
XX XX
DT 13-JUN-2000 (first entry)
XX XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:10.
XX XX
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine; ss.
XX XX
OS Homo sapiens.
XX XX
PN WO200004149-A2.
XX XX
PD 27-JAN-2000.
XX XX
PF 14-JUL-1999; 99WO-US15838.
XX XX
PR 14-JUL-1998; 98US-0115453.
PR 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 23-SEP-1998; 98US-0159822.
PR 15-JAN-1999; 99US-0232149.
PR 15-JAN-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.
XX XX
PA (CORI-) CORIXA CORP.
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XX Dillon DC, Harlocker SL, Yuqiu J, Xu J, Mitcham JL;
PI WPI; 2000-171268/15.
XX
XX New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein -
XX
XX Claim 1; Page 99; 263pp; English.
XX
CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (ptp). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AAA06241 to AAA0691 and
CC AA082000 to AA082020 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;

Alignment Scores:
Pred. No.: 2,49e-64 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 21 Gaps: 0

US-09-593-793A-113 (1-553) x AAA06250 (1-789)
QY 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
DB 3 GTCTATNTGCCAGTGGCAGCTTTCCTGTGGCTGGCGTGGCCACATGCTGCCCCAC 62
QY 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
DB 63 AGTGTGGCGGTGGTACAGCTTCAGCGCCCTCAGCGGCTTCCACCTTCAGCCCTGCGAG 122
QY 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluGlnValPheLeuProLys 413
DB 123 ATCTCTCCCTACACATGCGCTTCTTACCACCGGAGAGCAGGTGTCTGCCCCAAA 182
QY 414 TyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
DB 183 TACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCTGATGACCACTTCCTGCCA 242
QY 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeu 453
DB 243 GGCCTTAAGCTGGAGCTCCCTTCCCTAATGGACAGTGGGTGCTGGAGGACAGTGGCCCTG 302
QY 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
DB 303 CTCCCCACCTCCACCGCGCTCTCGGGGCTCTGCGTGTGATGCTCTCCGTACGTGTGGTG 362
QY 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAla 493
DB 363 GTGGGTGAGCCACACCGAGGGTGTCCGGCGCGGGGACATGCTGACCTGCGCC 422
QY 494 IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
DB 423 ATCTGTGATAGTGC-TTCCTGTGCTCCCAAGTGGCCCATCCCTGTTTATGGGCTCCATT 481
QY 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyVal 533
DB 482 GTCCAGCTCAGCCAGTCTGTCTACATGCTATATGGTGTCTGCGCGAGGCTGGGTCTG 541
QY 534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAlaAlaLysTyrSerAla 553
DB 542 CC-ATTACTTGTCTACACAGGTANTATTGACAGACGANTTGGCCAAATACTCAGCG 600
```

Db 542 CC-ATTACTTGTACACAGGTANTATTGACAGAAGCAGTTGGCCAAATCTACGCG 600
AAS63458

RESULT 44

ID AAS63458 standard; cDNA; 789 BP.

AC AAS63458;

DT 29-JAN-2002 (first entry)

DE Human prostate cDNA sequence #10.

XX Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.

XX Homo sapiens.

XX WO200173032-A2.

XX PD 04-OCT-2001.

XX PF 27-MAR-2001; 2001WO-US09919.

XX PR 27-MAR-2000; 2000US-0536857.

XX PR 09-MAY-2000; 2000US-0568100.

XX PR 13-JUN-2000; 2000US-0570737.

XX PR 13-JUN-2000; 2000US-0593793.

XX PR 27-JUN-2000; 2000US-0605783.

XX PR 10-AUG-2000; 2000US-0636215.

XX PR 29-AUG-2000; 2000US-0651236.

XX PR 06-SEP-2000; 2000US-0657279.

XX PR 02-OCT-2000; 2000US-0679426.

XX PR 10-OCT-2000; 2000US-0685166.

XX PA (CORI-) CORIXA CORP.

XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

XX PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;

XX PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;

XX DR WPI; 2001-639232/73.

XX PT New human prostate-specific polypeptides and polynucleotides useful for
the diagnosis and treatment of cancer, especially prostate cancer -
Claim 1; Page 232-233; 579pp; English.
The invention relates to isolated prostate-specific
polynucleotides, polypeptides, fusion proteins of the polypeptides,
antibodies raised against the polypeptides (or antigenic epitopes
derived from them) and antigen-presenting cells expressing the
polypeptides. The antibodies are useful for detecting the presence of
cancer, especially prostate cancer. The polypeptides, polynucleotides and
the antigen-presenting cells are useful for stimulating and/or expanding
T cells specific for a tumour protein, and for inhibiting the development
of cancer especially prostate cancer. Compositions comprising the
polynucleotide and/or polypeptide are useful for stimulating an immune
response, and for treating cancer. The oligonucleotide is useful for
detecting cancer. The present sequence is a prostate specific
polynucleotide of the invention.

XX SQ Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;

Alignment Scores:

Pred. No.:	2,49e-64	Length:	789
Score:	919.00	Matches:	192
Percent Similarity:	96.50%	Conservative:	1
Best Local Similarity:	96.00%	Mismatches:	7
Query Match:	32.12%	Indels:	2
DB:	22	Gaps:	0

US-09-593-793A-113 (1-553) x AAS63458 (1-789)

QY 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCATNTGGCCAGTGTGGCAGCTTTCCCTCTGGGTGCGGTGCACATGCTGTGCCAC 62
QY 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCCGGTTTCACCTTCTTCAGCCCTGCAG 122
QY 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
Db 123 ATCTGCTCCCTACACACTGGCCCTCTACACCCGGGAGAGCAGGTGTTCTCTGCCCAAA 182
QY 414 TyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
Db 183 TACCGAGGGGACACTGGAGGTGCTAGCAGTGCAGGACAGCCTGATCACCAGCTTCTCTGCCA 242
QY 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeu 453
Db 243 GGCCTTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGAGTGGCCCTG 302
QY 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
Db 303 CTCCACCTCCACCCGCCCTCTCGGGGCCCTCTGCTGTGATGCTCTCGTACGTGTGTGTG 362
QY 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 493
Db 363 GTGGGTGAGCCACCGANGCCAGGTGGTTCGGGCCGGGCATCTGCCTGACCTCGCC 422
QY 494 IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
Db 423 ATCTGTGATAGTGC-TTCCTGCTGTCCANGTGGCCCATCCCTGTTTATGGGTCCATT 481
QY 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyVal 533
Db 482 GTCCAGCTCAGCCAGTCTGTCACCTGCTATATGTTGTTCTGCCGAGGCTGGGTCTGTGTC 541
QY 534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 542 CC-ATTACTTGTGTACACAGGTANTATTGACAAGAAGCAGTATGGCCAAATCTACGCG 600

RESULT 45

AAS10009

ID AAS10009 standard; cDNA; 789 BP.

XX AC AAS10009;

XX DT 24-OCT-2001 (first entry)

XX DE Human prostate tumour cDNA L1-12 #1.

XX KW Human; prostate tumour protein; prostate cancer; ss.

XX OS Homo sapiens.

XX PN US6262245-B1.

XX PD 17-JUL-2001.

XX PF 25-FEB-1998; 98US-0030607.

XX PR 25-FEB-1997; 97US-0806099.

XX PR 01-AUG-1997; 97US-0904804.

XX PR 09-FEB-1998; 98US-0020956.

XX PA (CORI-) CORIXA CORP.

XX PI Xu J, Dillon DC;

XX DR WPI; 2001-440862/47.

XX PT Novel polynucleotide encoding polypeptide comprising a portion of
prostate tumour protein useful for inhibiting development of prostate
cancer or for treating prostate cancer in a patient -

XX Example 1; Column 32-33; 105pp; English.
XX The sequence is a human prostate tumour cDNA which encodes a
CC partial tumour protein. The DNA is useful for inhibiting the development
CC of prostate cancer or for treating prostate cancer in a patient.
XX
SQ Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;

Alignment Scores:
Pred. No.: 2,49e-64 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 22 Gaps: 0

US-09-593-793A-113 (1-553) x AAS10009 (1-789)

QY 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
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Db 3 GTCTATNTGGCCAGTGTGCACGCTTCCCTGTGGCTGCGGGTGCACATGCTGCCCCAC 62

QY 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
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Db 63 AGTGTGGCGGTGGTGACAGCTTCAGCGGCCCTCACCGGGTTCCACCTTCTCAGCCCTGCAG 122

QY 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
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Db 123 ATCCTGCGCCTACACACTGCGCTTCCCTCTACACCGGGAGACAGGTGTCTCTGCCCAA 182

QY 414 TyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
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Db 183 TACCGAGGGGACACTGGAGGTGTAGCAGTAGGAGGACGCTGATCACCAGCTTCTCTGCCA 242

QY 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeu 453
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Db 243 GGCCCTAAGCCTGAGCTGCCCTTCCCTAATGGACACGTGGGTGCTGGAGGACGTGGCCTG 302

QY 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
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Db 303 CTCCACCTCCACCGCGCTCTGCGGGGCTCTGCTGTGATGTCTCCGTAGTGTGGTG 362

QY 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 493
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Db 363 GTGGGTGAGCCACCGANGCCAGGTGTTCCGGGCGGGGCGATCTGCTGGACCTCGCC 422

QY 494 IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
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Db 423 ATCCTGGATAGTGC-TTCTGCTGTCCANGTGGCCCATCCCTGTTTATGGGTCCATT 481

QY 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuVal 533
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Db 482 GTCCAGCTCAGCCAGCTGTCTACTGCCCTATATGGTGTCTGCCGAGGCTGGGTCTGGTC 541

QY 534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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Db 542 CC-ATTTACTTTGCTACAGAGTANTATTGACAGAGAGCAGANTTGGCCCAATACTCAGCG 600

Search completed: February 19, 2003, 03:53:21
Job time : 353 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 03:49:54 ; Search time 53 Seconds

(without alignments)
3199.854 Million cell updates/sec

Title: US-09-593-793A-113

Perfect score: 2861

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents_NA: *
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5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2861	100.0	3410	4	US-09-030-607-110
3	2861	100.0	3410	4	US-09-030-607-110
4	2861	100.0	3410	4	US-09-030-607-110
5	2861	100.0	3410	4	US-09-030-607-110
6	2861	100.0	3410	4	US-09-030-607-110
7	2861	100.0	3410	4	US-09-030-607-110
8	2716.5	94.9	4034	4	US-09-030-607-110
9	2538.5	88.7	4894	4	US-09-030-607-110
10	2144	74.9	6976	4	US-09-030-607-110
11	1920.5	67.1	2904	4	US-09-030-607-110
12	1287	45.0	2152	3	US-09-071-710-16

c 86 113 3.9 4403765 4 US-09-103-840A-2 Sequence 2, Appli
c 87 113 3.9 4411529 4 US-09-103-840A-1 Sequence 1, Appli
c 88 112.5 3.9 3378 4 US-09-513-783A-151 Sequence 151, App
c 89 112.5 3.9 4833 4 US-09-513-783A-21 Sequence 21, Appl
90 111.5 3.9 4391 4 US-09-207-857-1 Sequence 1, Appli
91 110 3.8 2571 4 US-09-336-643A-80 Sequence 80, Appl
c 92 110 3.8 3511 3 US-08-892-747-13 Sequence 13, Appl
c 93 109 3.8 1765 1 US-08-459-586-15 Sequence 15, Appl
c 94 109 3.8 1765 2 US-08-282-696-15 Sequence 15, Appl
c 95 109 3.8 2304 1 US-08-464-266-1 Sequence 1, Appli
c 96 109 3.8 2304 1 US-08-464-273-1 Sequence 1, Appli
c 97 109 3.8 2304 1 US-08-464-514-1 Sequence 1, Appli
c 98 109 3.8 2304 4 US-08-486-403-1 Sequence 1, Appli
c 99 109 3.8 111282 4 US-09-754-250-3 Sequence 3, Appli
c 100 108.5 3.8 35060 3 US-08-814-095-7 Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-020-956-110
; Sequence 110, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; ATTORNEY/AGENT INFORMATION:
; DILLIN, DAVIN C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

US-09-020-956-110
Alignment Scores:
Pred. No.: 9,55e-264 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-020-956-110 (1-3410)
QY 1 MetValGlnArgLeuTrpValSerArgLeuArgHisArgLysAlaGlnLeuLeu 20

Db 284 ATGGTCCAGAGGCTGGGTGAGCGCCCTGCTGCGGCACCGGAAAGCCAGCTCTTGTCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTrpValPro 40
Db 344 GTCAACCTGCTAAACCTTTGGCCCTGGAGGTGTGTTGGCCCGCAGGCATCATGTATGCGCG 403
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGAAAGTGGGGGTAGAGGAGAAATTCATGACCATGCTGGGCATATGCT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
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QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
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QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
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QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
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QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
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QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
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QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPheValGlyGluGlyLeu 300
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QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTrpAspGluGly 320
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QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGATGGGCGAGCTGGGGCTGTTCCTGCGAGTGGCGCATCTCCTGGTCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGGACCGGCTGGTGCAGCGATTTCGCACTCGAGCAGTCTATTTGGCCAGTGTGCA 1363
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Db 1424 TCAGCGCCCTCACCAGGTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1483
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RESULT 2

US-09-030-607-110
; Sequence 110, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030.607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3410 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-607-110
Alignment Scores:
Pred. No.: 9,55e-264 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-593-793A-113 (1-553) x US-09-030-607-110 (1-3410)
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QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
DB 1244 GTTCGGATGGGAGCGCTGGGGGTGTTCCTGCAGTGGCCATCTCCCTGGCTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
DB 1304 GTCATGGACCGGCTGGTGAGCGATTCCGCACCTCGACAGTCTATTGGCCAGTGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
DB 1364 GCTTTCCCTGTGGCTGCCGTGCCACATGCCTGTGCCAGTGTGGCGGTGGACAGCT 1423
QY 381 SerAlaAlaLeuThrClyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
DB 1424 TCAGCGCCCTCACCAGGTTACCTTCTCAGCCCTGCAGATCTCTCCCTTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
DB 1484 TCCCTCTACCCAGCGGAGAGCAGGTGTTCCTGCCAATACCGAGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
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QY 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
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QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
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DB 1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942

RESULT 3
US-09-605-785-110
; Sequence 110, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
```

```
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-605-785-110

Alignment Scores:
Pred. No.: 9,55e-264 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-605-785-110 (1-3410)
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DB 344 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTGGCCGAGGATACCTATGTGGCG 403
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DB 404 CCTCTGCTGCTGAAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGCTGTGGCATTTGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
DB 464 CCAGTGTGGGCTGTGTGTCTCCGCTCTCTAGGCTCAGCCAGTACACACTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTyrAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
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QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
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QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
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QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
DB 764 TACTCTGTCTATGCTTTCATGATAGTCTTGGGGGTGCTGGGTACCTCTCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
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QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
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Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
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Db 1184 TACCAGGCGGTGCCAGAGCTGAGCGGGCCAGCGGCGGAGGCGGAGACACTATGATGAAGGC 1243
Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
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RESULT 4

US-09-439-313-110
; Sequence 110, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: fastseq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-110

Alignment Scores:
Pred. No.: 9.55e-264 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-439-313-110 (1-3410)

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Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
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Db 464 CCAGTGTCTGGGCTGTGTGTCTGCCGCTCTAGGCTCAGCCAGTGTGACCTGTGGCGT 523
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
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Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
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US-09-352-616A-110
; Sequence 110, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuhui
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-110

Alignment Scores:
Pred. No.: 9,55e-264 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-352-616A-110 (1-3410)
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QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCCTGTGCTGCGCGTCCACATGCTCTCCACAGTGTGGCGGTGTGACAGCT 1423

QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProThrThrLeuAla 400
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RESULT 6

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US-09-602-877A-100
; Sequence 100, Application US/09602877A
; Patent No. 6432707
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.446C5
; CURRENT APPLICATION NUMBER: US/09/602,877A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-602-877A-100
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Alignment Scores:
Pred. No.: 9,55e-264 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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US-09-593-793A-113 (1-553) x US-09-602-877A-100 (1-3410)

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QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
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QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
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Db 944 GCACGCGTGGCGCCACCAGCAGCCAGAGGCGCTGTCGGCCCGCTCTGTGCGCCCGCAC 1003
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QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
|||||
Db 1004 TGTGTCCATGCGCGCGCGCTGGCTTTCCGGAACCTGGCGCCCTGCTTCCCGCGCTG 1063
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QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgLeuPheValAlaGluLeuCys 280
|||||
Db 1064 CACACGCTGCTGCGCGATGCCCGCCAGCCCTGCGCGGCTCTCTGCTGCTGAGCTGTGC 1123
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QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrAspPheValGlyGluGlyLeu 300
|||||
Db 1124 AGCTGGATGCACTATGACCTTCACGCTGTTTACACGGATTTCGTGGCGAGGGGCTG 1183
|||||
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
|||||
Db 1184 TACCAGGGCGTGCACAGAGCTGAGCGCGGCACCGAGGCGCGGAGACACTATGATGAAGC 1243
|||||
QY 321 ValArgMetClySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
|||||
Db 1244 GTTCGGATGGCAGCGCTGGGGCTTCTCCAGTGGCCATCTCCCTGGTCTCTCTCTG 1303
|||||
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
|||||
Db 1304 GTCATGACCGCGCTGTGCGCGGATTCGCGACCTCGACAGCTCTATTGGCCAGTGGCA 1363
|||||
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
|||||
Db 1364 GCCTTCCCTGTGCGTGCCTGCGCGACATGCTGTCACAGTGTGCGCGTGTGACAGCT 1423
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QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProThrLeuAla 400
|||||
Db 1424 TCAGCGCCCTACCGGGTTACCTTCTCAGCCCTGCAGATCTGCCCTACACACTGGCC 1483
|||||
QY 401 SerLeuTyrHisArgGluGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
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Db 1484 TCCTCTACACCGGAGAGCAGGTGTTCTGCCCAATACCGAGGGACACTGGAGGT 1543
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QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
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Db 1544 GCTAGCAGTGGAGACAGCTGATGACAGCTTCTGCCAGCGCTTCCGCCAGCGCTAAGCCTGAGCTCC 1603
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QY 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuProProProProAlaLeu 460
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Db 1604 TTCCCTAAATGGACACGTGGGTGCTGGAGGAGTGGCGCTGCTCCACCTCCACCGCGCTC 1663
|||||
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480
|||||
Db 1664 TGGCGGCGCTCTGCCCTGTGATGCTCCGTACGTGTGGTGGTGGTGGCCAGCGGCC 1723
|||||
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
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Db 1724 AGGGTGTTCGGGCGCGGCGCATCTGCCTGGACCTCGCCATCTCGCATAGTGTCTCTG 1783
|||||
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
|||||
Db 1784 CTGTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1843
|||||
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
|||||
Db 1844 ACTGCCATATGCTGTGCCGAGCGCTGGGTCTGGTGGCCATTTACTTGTGTACACAG 1903
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QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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Db 1904 GTAGTATTTGACAAGAGCGCACTTGGCCAAATACTCAGCG 1942
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RESULT 7

US-09-232-149A-110

; Sequence 110, Application US/09232149A

; Patent No. 6465611

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; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-110
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Alignment Scores:
Pred. No.: 9,55e-264 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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US-09-593-793A-113 (1-553) x US-09-232-149A-110 (1-3410)

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QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
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Db 284 ATGGTCCAGAGGCTGGGGTGAGCGCCCTGCGCGCACCGGAAGCCAGCTCTGTGCTG 343
|||||
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||||
Db 344 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCCGAGGCATCACCTATGTGCGG 403
|||||
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
|||||
Db 404 CCTCTGCTCTGCTGGAAGTGGGGTAGAGAGAGTTTCATGACCATGGTGTGGGCATTGT 463
|||||
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
|||||
Db 464 CCAGTGTCTGGGCTGTGCTGTGTCGGCTCCTAGGCTCAGCCAGTACCATGGCGGTGGA 523
|||||
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
|||||
Db 524 CGCTATGGCGCGCGCGCGCTTCATCTGGGCACCTGCTCTGGGCATCTCTGTGAGCCCTC 583
|||||
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
|||||
Db 584 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTGCCCGCATCCAGGCCCTG 643
|||||
QY 121 GluLeuAlaLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
|||||
Db 644 GAGCTGGCACTGCTCATCTGGGCGTGGGCGTCTGGACTTCTGTGGCCAGGTGTGCTTC 703
|||||
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
|||||
Db 704 ACTCCACTGGAGCCCTGCTCTGACCTTCTCCGGGACCCGACCCACACTGTGCCAGGCC 763
|||||
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrIleLeuProAla 180
|||||
Db 764 TACTCTGTCTATGCTTTCATGATCATGCTTGGGGGCTGCTGGCTTACCTCTGCTGCTGC 823
|||||
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
|||||
Db 824 ATTAGCTGGGACACCAAGTGGCCCTGGCCCTCTACCTGGGCGCACCCAGGAGGAGTCTCTT 883
|||||
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
|||||
Db 884 GGCTGTCTACCCCTCATCTTCCTCACCTCGTAGCAGGCACACTGCTGTGTGCTGAGGAG 943
|||||
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
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Db 944 GCAGCGCTGGGCCCCACCAGGACAGCAAGAGGCTGTGCGGCCCTCTCTTGTGCCCCAC 1003

QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260

Db 1004 TGCTGTCCATGCGGGCCGCTTGGCTTTCGGGAACCTGGGGCCCTGTCTCCCGGCTG 1063

QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgAlaPheValAlaGluLeuCys 280

Db 1064 CACCAGCTGTGTCGGCATGCCCCACCCCTGCGCGGCTCTCTCGTGGCTGAGCTGTGC 1123

QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluLeu 300

Db 1124 AGCTGATGGCACTCATGACCTTCACGCTGTATACACGGATTTCGTGGCGAGGGCTG 1183

QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320

Db 1184 TACCAGGGGCTGCCAGAGCTGAGCGGACCGAGGCCCGGAGACACTATGATGAGGC 1243

QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340

Db 1244 GTTCGGATGGCAGCCTGGGGCTGTCTCTGCAGTGCACATCTCCCTGTCTTCTCTCG 1303

QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360

Db 1304 GTCATGGACCGGCTGGTGACGGATTTCGGCACTCGAGCAGTCTATTGGCCAGTGTGCA 1363

QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380

Db 1364 GCTTTCCCTGTGGTGGCGGCCACATGCTTGTCCACAGTGTGGCCGTGGTACAGCT 1423

QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400

Db 1424 TCAGCGCGCCTCACGGGTTCACCTTCTCAGCCCTGCAGATCTGCGCTTACACACTGGCC 1483

QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420

Db 1484 TCCTCTACACCGGGAGAAGCAGGTGTCTGCCCAATACCGAGGGGACACTGGAGGT 1543

QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440

Db 1544 GCTAGCAGTGAGGACAGCCTGATGACCACTTCTTGCACAGCCCTAAGCCTGGAGCTCC 1603

QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProProAlaLeu 460

Db 1604 TTCCCTTAATGGACAGCTGGGTGCTGGAGCAGTGGCCTGCTCCACCTCCACCCGCGTC 1663

QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480

Db 1664 TCGGGGGCTCTGCGCTGTGATGTCCTCGGTACGTGTGGTGGTGGAGCCACCGAGGCC 1723

QY 481 ArgValValProGlyValGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500

Db 1724 AGGGTGGTTCCGGCGGGGCATCTGCTGGACCTGCGCATCTCTGGATAGTCCCTTCTCTG 1783

QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520

Db 1784 CTGTCCCAAGTGGCCCATCCCTGTTTATGGCTCCATTGTCCAGTCCAGCCAGCTCTGC 1843

QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540

Db 1844 ACTGCTTATGGTGTCTGCCCGAGCCCTGGGTCTGGTGGCCATTACTTTGCTACACAG 1903

QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553

Db 1904 GTAGTATTGACAAGCGCACTTGGCCAAATACTCAGCG 1942

RESULT 8

US-09-605-785-704
; Sequence 704, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-605-785-704

Alignment Scores:
Pred. No.: 8.19e-250 Length: 4034
Score: 2716.50 Matches: 553
Percent Similarity: 70.09% Conservative: 0
Best Local Similarity: 70.09% Mismatches: 0
Query Match: 94.95% Indels: 236
DB: 4 Gaps: 1

US-09-593-793a-113 (1-553) x US-09-605-785-704 (1-4034)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20

Db 281 ATGGTCCAGAGGCTGTGGTGAGCCGCTGCTGCCGACCGAAGCCAGCTCTTGTG 340

QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40

Db 341 GTCAACCTGCTAACTTGGCCTGGAGGTGTCTTTGGCGCAGGCATCACCTATGTGCG 400

QY 41 ProLeuLeuLeuGluValGlyValGluLysPheMetThrMetValLeuGlyIleGly 60

Db 401 CCTCTGCTCTGGAGTGGGGTAGAGGAGAGTTTCATGACCATGGTGGCATTTGGT 460

QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80

Db 461 CCAGTGTGGGCTGTGTGTCTCCGCTCTTAGGCTCAGCCAGTACACCTGGCGTGA 520

QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100

Db 521 CGCTATGGCGCGCGCGGCTTCTCTGGCACCTGTCTTGGGCATCTGTGGCATCTG 580

QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120

Db 581 TTTCTCATCCCAAGGCGGCTGGCTAGCAGGGCTGTGTGCCGATGCCAGGCCCTG 640

QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140

Db 641 GAGCTGGCACTGCTCATCTCTGGCGCTGGGCTGTGGAGTCTGTGGCAGGTGTGCTTC 700

QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160

Db 701 ACTCCACTGGAGGCCCTGCTCTCACCTCTTCCGGACCCCGACCACTGTCCGAGGCC 760

QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180

Db 761 TACTCTGTATGCTTCATGATCATGCTTGGGGGCTGCTTGGGCTTACCTCTCGCTGCC 820


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; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSTICS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 702
; LENGTH: 4894
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-605-785-702

Alignment Scores:
Pred. No.: 1,17e-232 Length: 4894
Score: 2538.50 Matches: 551
Percent Similarity: 51.11% Conservative: 0
Best Local Similarity: 51.11% Mismatches: 2
Query Match: 88.73% Indels: 526
DB: 4 Gaps: 2

US-09-593-793A-113 (1-553) x US-09-605-785-702 (1-4894)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
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QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 334 GTCAACCTGCTAACCTTTGGCCGTGAGGTGTGTTTGGCGCGACGATCACCTATGTGCGG 393
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeu----- 57
Db 394 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTCAATGACCATGGTGCT-GGGTGAGT 452
QY 57 ----- 57
Db 453 ACTACATCCTCCTCTCCTTCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA 512
QY 57 ----- 57
Db 513 CCTCTGCCCTGGGAGCTGCTGGAGGGAGAGGTGTCTGCTGGAAGGCATTTGCTGGGCA 572
QY 57 ----- 57
Db 573 GGAGGGTGACCTGGGCTGAGGGGSCACACCAGAGAAGAAGAGAAATACCAAGGACATA 632
QY 57 ----- 57
Db 633 CCCCAGTCACCTCTGGATCCCTGGTCTGCACAGAGCCTGGCTCATAGGAGACACTGGAG 692
QY 57 ----- 57
Db 693 AAATGCTCCTAACCTTTGGCTAGCCCTTTTAATAATTTATAGCGAATATCTCAATTAAT 752
QY 57 ----- 57
Db 753 TTACAACCAACCATTTGAGGTGATCCATTTTACAGAGAAGGAGCAGAGCGCTTTTAAGAG 812
QY 57 ----- 57
Db 813 TTAGGTAAGTCTTAGCCAAAGCCAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 872
QY 57 ----- 57
Db 873 GGTCTCCCGCGGAGCTTGCTCTACCCCTAGGACAAAGGGGTGGACTCCTGACTCTGCA 932
QY 57 ----- 57
Db 933 GATAAATTCTACAAAAGCCACAGAGGAAGCAAGTAGTAACCATTTGTGTGACAACCCCTCAC 992
QY 57 ----- 57
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Db 993 CCCAGGAAGAGGGCCCTGTGAGGATTGACGGCTCTGGAGTCACACACTGCTTGTGTAAC 1052
QY 57 ----- 57
Db 1053 GCTGCTCTTTACCCTCCCTAGTCTGCGCCTTTTGAATAGTATACACTTCTTAGTTGCTCC 1112
QY 57 ----- 57
Db 1113 ATGCCTCAGTTTGTCCATCTGAAATGGGGCATCTGTAATGCCTGTGTATATGAGGAGTA 1172
QY 57 ----- 57
Db 1173 AATTACAGCATCCCTGTGAAGACGTAGCACAGTGTGAGTACGGAATGTTATTTCCATCC 1232
QY 57 ----- 57
Db 1233 TTCTCAGGAGCTTGGTTCCCTTCCCTTGGCCCTTACTTGTCCAGCCATTGACTCAT 1292
QY 58 -----GlyIleGlyProValLeuGlyLeuValCysValProLeuLeu 71
Db 1293 ACTACTTCCCTTCTTTCAGGCATTGGTCCAGTGTGGGCTGGTCTGTGTCGCCGTCTTA 1352
QY 72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAla 91
Db 1353 GGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCGCGCCCTTCATCTGGGCA 1412
QY 92 LeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaAlaGlyTrpLeuAlaGly 111
Db 1413 CTGTCTTTGGGCATCCTCTGTCAGCCTCTTCTCATCCCAAGGGCGGCTGGCTACAGGG 1472
QY 112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu 131
Db 1473 CTGCTGTGCCCGATCCAGGCCCTGGAGCTGGGACTGCTCATCTCTGGCGTGGGGCTG 1532
QY 132 LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151
Db 1533 CTGGACTTCTGTGGCAGGTGTCTCACTCCACTGGAGGCCCTGCTCTGACCTCTTC 1592
QY 152 ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
Db 1593 CGGGACCCGGACCACTGCGCCAGGCCTACTGTCTATGCCCTTCATCATGCTTGGG 1652
QY 172 GlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyr 191
Db 1653 GGCTGCTGGGCTACTCTCTGCTGCCATTGACTGGGACACCACTGGCCTGGCCCTTAC 1712
QY 192 LeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
Db 1713 CTGGCACCCAGGAGGAGTGCTCTTTGGCCTGCTCACCTCATCTTCTCACCTGCGTA 1772
QY 212 AlaAlaThrLeuLeuValAlaGluAlaAlaLeuGlyProThrGluProAlaGluGly 231
Db 1773 GCAGCACACTGCTGGTGGCTGAGGAGCAGCGCTGGGCCCCCACCAGCAGCAGAAAGG 1832
QY 232 LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg 251
Db 1833 CTGTGCGGCCCTCTCTGTGCGCCCACTGTGTCATGCGGGGCCCGCTTGGCTTCCGG 1892
QY 252 AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271
Db 1893 AACCTGGGCGCCCTGCTTCCCGGCTGCACCAGCTGTGCTGCCGATGCCCGCACCCCTG 1952
QY 272 ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291
Db 1953 CGCCGGCTCTTCGTGGCTGAGCTGTGCAGTGGATGGGACTCATGACCTTCACGCTGTT 2012
QY 292 TyrThrAspPheValGlyGluLeuTyrGlnGlyValProArgAlaGluProGlyThr 311
Db 2013 TACAGGATTTTCGTGGCGAGGGGCTGTACCAGGGCGTGGCCAGAGCTGAGCGGGCAC 2072
QY 312 GluAlaArgArgHisTyrAspGlu----- 319
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Db 2073 GAGCCCGGAGACATATGATGAAGGTAAAGGCTTGGCAGCCAGCAGAGCTGTGGG 2132
QY 319 ----- 319
Db 2133 AGCCGCCACCAGAGACACTCGGGGCTGTGTCTGGGCTGTGGCTCTCCATCTCTGGC 2192
QY 319 ----- 319
Db 2193 CCGGACTTCTCTGTCTCAGAAAGTGGGATGGACCCCATCTGCATACACAGGCTTCTCATGG 2252
QY 319 ----- 319
Db 2253 GTCTGGAAACATCTCTGTCTGGCGTTTCAGAAAGGCTCTGGGCTGTCTAGGAGCTGTGATC 2312
QY 319 ----- 319
Db 2313 AGAGTCGTTGCCCCAGTTTCACAGAAGAAAGCGGAGCTTATTCAAAGTCTAGAGGAG 2372
QY 319 ----- 319
Db 2373 TGGAGGAGTTAAGGCTGGATTTTCAGATCTGCCCTGGTTCCAGCGGCAGTGTGCCCTCTGCT 2432
QY 319 ----- 319
Db 2433 CCCCCAACGACTTTCAAATAATCTCACAGCGCCCTTCAGAGCTCAGGCTCTCTAGAACGG 2492
QY 319 ----- 319
Db 2493 TCTTGAAGCCTATGGCAGCTGCTTTGTGTCTCCCTCACCGGCTGTCCCTCACAGCTG 2552
QY 319 ----- 319
Db 2553 AGACTCCAGGAAACCTTCAGACTACCTTCTCTGCTTTCAGCAAGGGGCTTGGCCACA 2612
QY 319 ----- 319
Db 2613 TTCTCTGAGGTCAGTGGAAAGACCTAGACTCCCATTTGCTAGAGGTAGAAAGGGGAAGGG 2672
QY 319 ----- 319
Db 2673 TGCTGGGAGCAGGCTGGTCCACAGCAGGTCTCTGTGCAGCAGGTACCTGTGTTCCGCC 2732
QY 319 ----- 319
Db 2733 TTCTCATCTCCCTGAGACTGCTCCGACCCCTTCCTCCAGGCTCTGTCTGATGGCCCTC 2792
QY 320 ----- GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe 336
Db 2793 TCCTCTGCAGGCTTTCGGATGGCAGCCTGGGGCTGTTCCTGCAGTGGCCATCTCCCT 2852
QY 336 uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe 356
Db 2853 GGCTTCTCTCTGTGTCATGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATT 2912
QY 356 uAlaSerValAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl 376
Db 2913 GGCCAGTGTGGCAGCTTCCCTGTGGCTGCCGTGCCACATGCTCTCCACAGTGTGGC 2972
QY 376 aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 396
Db 2973 CGTGGTACAGCTTTCAGCGCCCTCACCGGTTTCACCTTCTCAGCCCTGCAGATCCGCC 3032
QY 396 oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgG 416
Db 3033 CTACACACTGGCTCCCTCTACACCGGAGAGCAGGTGTTCTTCCCAATACCGAGG 3092
QY 416 yAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLy 436
Db 3093 GGACACTGGAGGTCTAGCAGTGAAGACAGCCTGTATGACCACTTCTCCGCCAGGCCCTAA 3152
QY 436 sProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuProPr 456
Db 3153 GCCTGGAGCTCCCTCCCTTAATGGACACGTGGGTGTGGAGGAGGTGGGCTGCTCCACC 3212

QY 456 oProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyG 476
Db 3213 TCCACCCGCGCTCTGGGGCCCTCTCCCTGTGATGCTCCGTACGTTGGTGGGTGGA 3272
QY 476 uProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAs 496
Db 3273 GCCACCGAGGCGAGGTTGTTCCGGCGGGGCATCTGCCTGGACCTGCCATCCTGGA 3332
... QY 496 pSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLe 516
Db 3333 TAGTGCTTCTGCTGCTGCCAGGTGCCCACTCCCTGTTATGCGGCTCCATGTCAGCT 3392
QY 516 uSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTy 536
Db 3393 CAGCCAGTCTGCTACCTGCCTATATGCTGTCTGCCGAGGCTGGGTCTGGTCCCATTTA 3452
QY 536 rPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 3453 CTTTGTACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 3504

RESULT 10

US-09-605-785-705
; Sequence 705, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John H.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-605-785-705

Alignment Scores:
Pred. No.: 1,09e-194 Length: 6976
Score: 2144.00 Matches: 551
Percent Similarity: 30.48% Conservative: 0
Best Local Similarity: 30.48% Mismatches: 2
Query Match: 74.94% Indels: 1257
DB: 4 Gaps: 3

US-09-593-793A-113 (1-553) x US-09-605-785-705 (1-6976)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgGlyAlaGlnLeuLeu 20
Db 165 ATGGTCCAGAGGCTGTGGGTGAGCCCTGTCTGCGCGACCCGAAAGCCAGCTCTTGTG 224
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaClyIleThrTyrValPro 40
Db 225 GTCAACCTCTAACTTTTGGCCTGGAGGTGTGTTTGGCCGAGGCATACCTATGTGCGG 284

Qy 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeu----- 57
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Db 285 CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAGTTTCATGACCATGGTCT- GGGTGAGTC 343
Qy 57 ----- 57
Db 344 ACTACATCCTCCTCCTCCTCCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA 403
Qy 57 ----- 57
Db 404 CCTCTGCCCTGGGAGCTGCTTGGAGGGAGAGTGCTGTGCTGGGAAGCATTTGTGGGCA 463
Qy 57 ----- 57
Db 464 GGAGGGTGACCTCGGCTGAGGGGACACCAAGAGAGAGAGAAATACCAAGGACATA 523
Qy 57 ----- 57
Db 524 CCCAGTCACCTCTGGATCCCTGCTGCTGCACAGAGCCTGGCTCATAGGACACTGGAG 583
Qy 57 ----- 57
Db 584 AAATGCTCCTTAACCTTTGGCTAGCCCTTTTATAATTATAGCATTTATCTCATTTAATGC 643
Qy 57 ----- 57
Db 644 TTACAAACCACCATTTGAGGTGATCCATTTTACAGAGAAGGAGACAGCGCTTTTAAGAGG 703
Qy 57 ----- 57
Db 704 TTAGGTAAGTCTTTAGCCAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 763
Qy 57 ----- 57
Db 764 GGTCTCCAGCCGGAGCTTGCTTCTACCCCTAGGACAAAGGGGTGACTCTTGACTCTGCA 823
Qy 57 ----- 57
Db 824 GATAAATTCTACAAAGCCACAGAGGCAAGTAGTAGTAAACCATTGTGTGACAACCCCTCACC 883
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Db 884 CCCAGGAAGAGGGGCCCTGTGAGGATTGCAGGCTCTGGAGTGCACACTGCTTGTGTAAC 943
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Db 944 GCTGCCCTTACCCCTCCTAGGTCTGCGCCTTTGAATAAGTATCATCTTMTAGTTGCTCC 1003
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Db 1124 TTCTCAGGAGCTTGGTTTCCCTTCCCTTGGCCCTTTACTTGTCCAGCCATTGACTCAT 1183
Qy 58 -----GlyIleGlyProValLeuGluValCysValProLeuLeu 71
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Db 1184 ACTACTTCCCTTCTTGCAGGCAATGGTCCAGTGTGGGCCCTGGTCTGTGCTCCGCTCCTA 1243
Qy 72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAla 91
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Db 1244 GGCTCAGCCAGTGAACCACTGGCTGGAGCTATGSCGCCGCCCTTCACTCTGGGCA 1303
Qy 92 LeuSerLeuGlyIleLeuLeuSerPheLeuIleProArgAlaGlyTrpLeuAlaGly 111
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Db 1304 CTGCTCTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGCGGCTGCTAGCAGGG 1363

Qy 112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu 131
Db 1364 CTGCTGTGCCGATCCAGGCCCTGGAGCTGGCACTGCTCATCTGGCGTGGGCTG 1423
Qy 132 LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151
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Qy 152 ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
Db 1484 CGGAGCCCGGACCACTGTCCGAGCCCTACTGTCTGTATGCTTCATGATCAGTCTTGGG 1543
Qy 172 GlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyr 191
Db 1544 GGTCCCTGGGTACTCTCTGCTGCCATGACTGGGACACCAAGTGCCTGGCCCTTAC 1603
Qy 192 LeuGlyThrGlnGluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
Db 1604 CTGGCACCCAGGAGGAGTGCCTCTTTGGCCTGTCTCACCCCTCATCTTCTCACCTGCGTA 1663
Qy 212 AlaAlaThrLeuLeuValAlaGluAlaAlaLeuGlyProThrGluProAlaGluGly 231
Db 1664 GCAGCCACACTGCTGCTGGCTGAGGAGGAGCGCTGGGCCCCACCGACGACGAAAGG 1723
Qy 232 LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg 251
Db 1724 CTGTGGGCCCTCTCTTCTGCCCCACTGCTGTCCATGCCGGGCCCTGGCTTTCGGG 1783
Qy 252 AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271
Db 1784 AACCTGGCGGCCCTGCTTCCCGGCTGCACCAAGCTGTCTGCCCATGCCCGCACCTGTG 1843
Qy 272 ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291
Db 1844 CCGCGGCTCTCGTGGCTGAGCTGTGCAGCTGGATGGGACATCATACCTTACCGCTGTT 1903
Qy 292 TyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr 311
Db 1904 TACAGGGATTTCTGGGCGAGGGGCTGTACCAGGSGCTGCCAGAGCTGAGCCGGCAC 1963
Qy 312 GluAlaArgArgHisTyrAspGlu----- 319
Db 1964 GAGGCCCGGAGACACTATGATGAAGTAAAGCCTTTGGCAGCCAGCAGAGGCTGTGTGGG 2023
Qy 319 ----- 319
Db 2024 AGCCGCCCCACAGACAGACACTCGGGGCTGTGTCTGGCTGGTGGCTTCTCCATCCTGGC 2083
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Db 2084 CCCGACTTCTGTTCAGGAAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGG 2143
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Db 2204 AGAGTGTGTTCCCGCAGTTTGACAGAAAGGAGGCGGAGCTTATTCAAAGTCTAGAGGAG 2263
Qy 319 ----- 319
Db 2264 TGGAGGAGTTAAGGCTGGATTTTCAGATCTGCTGTTTCCAGCCGAGTGTGCCCTCTGCT 2323
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Qy 319 ----- 319

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Db	2504	TTCTCTGAGGGTCAGTGGGAAGACCTAGACTCCCATTTGCTAGAGGTAGAAAGGGG	2563
Qy	319	-----	319
Db	2564	TGCTGGGAGCAGGGCTGCTCCACACAGAGTCTGTCGACAGGTACCTTGTTCCGCC	2623
Qy	319	-----	319
Db	2624	TTTCTATCTCCCTGAGACTGCTCCGACCCTTCCTCCAGGCTCTGTCATGGCCCCTC	2683
Qy	320	-----GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe	336
Db	2684	TCCCTCTGCAGGGCTCGGATGGGACAGCTGGGGCTGTTCTTCGAGTGGCCATCTCCCT	2743
Qy	336	uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe	356
Db	2744	GGCTTCTCTCTGGTCATGGACCGCTGTCGACGGATTTCGGCAGCTCGAGCAGCTATTT	2803
Qy	356	uAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl	376
Db	2804	GGCCAGTGTGGCAGCTTTCCTCTGGCTGGCTGCCGGTGCCACATGCTCTCCACAGTGTGC	2863
Qy	376	aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr	396
Db	2864	CGTGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCTGCC	2923
Qy	396	oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnVal	409
Db	2924	CTACACACTGGCTCCCTCTACCACCGGAGAGCAGGT-ACTCATTTGCCAGTGGGTGG	2982
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Db	3043	CTGGCAAGCAACTTTGGAGAAATGCTTCTTTGAATCAGAGAAGAGCTTATCCTAGCCCA	3102
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Db	3103	GGGCCAGAGGCTTGGGCTGCAGAACAGTGTAGATTAGATTCTGGGAATGACTTCTCTGGGG	3162
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Db	3163	TCAGGACTGTGAGCACTTGAATGGATGATTCAGGAAATGCAGAAATACGATAGTGGAA	3222
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Db	3223	TCCCGAAGGTCAGGCCAGCAGGCCCTAGGCTTCTAGGCTGGTTGTTCTATGGAGAGG	3282
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Db	3283	CAGGGCGCTGAATCAGATGACCCCTGGGCCATTTCAGCCTCAGCAGCGGAGTGGGAATG	3342
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Db	3343	GTCCAGCCTTAGCAACACCTTTCTCAGGGAGCAGCAACCTGACTTAGCCTGTATCCTAC	3402
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Db	3403	TCTGGTCTGAGATGGGGCAGGCTCTTCCTACCCCTTTCTTCTGGCTTATTTTCT	3462
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Db	3463	TTTCTGTCTAATTCCCTTTTCTTCTCCTGCATCCCTTTTGCCTTTCCTTCTCCT	3522
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Db	3523	TCCCTTCCCTTCCCTGTGCAGATATCTGAGCTTGACACCTGACCCACTCACTTGGG	3582
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Db	3583	CACTGTGTAAGTTGTGGGACCTCCTTCTTGGTTGGCCCTACACTAACCCAGCCCTCCAG	3642
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Db	3703	CTGACCTCACTGAGCTACAAACCTGGGTGCTGACTCTGCCTTGAGGGGCATGAAGTTGG	3762
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Db	3823	AGACCTGCCCTCGCTCGTAGCACCTTCAGGAGAGGAGTAGTAAGTTTCGTAGCTGAGA	3882
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Db	4063	GTATGTGCTGCTGTCGCCAGGAAACGTTCTGGGGCTAGCCATCTTCTCCAGATGGAGAGC	4122
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Db	4123	ATGCTGTCTCGGACCACCTCCAGACTCCAACCTCAGCGGACATTCCTGGGGTGGCAGGC	4182
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Db	4183	AGGGAGGAGAAGTCTCGGAGGCCCTTCCTAACAGACAGCTGATGCGACACTTTGGCACTG	4242
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Db	4303	CTGGTGTCAAGTTTGAGCTCTGCCATGGCTCCCACCTCGCAATGCAGCCAACCTCAACTC	4362
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Db	4363	TTCTGGCATGGGACAAATGTTGGATAAGACCTGGCCTTCTCTTAAATAGGAGGCTCTGG	4422
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Db	4423	GCCATCAAGGCGAGGGTTGGGGGATGGTGTGCAACCACTGATCTGATCTAAGTTCAGA	4482
Qy	409	-----	409
Db	4483	CAGCAGGAAGGAAGTGAGAAGCCTTCAACATTTAGCACAGCTGGGCTGGGGAGGTGGA	4542
Qy	409	-----	409
Db	4543	AGAGGGACATTCCTCCTGCTGGGTCTACTGGATTCTCCCTGCCCAAGGCTGGGGACA	4602
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Db	4603	AGGGAGCTCATGGCAGGCAGCTACCTAGTGGCATCTGGGACCCAGAGAGCAGCT	4662

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Qy 409 ----- 409
Db 4663 TCTCTGACCGGCAATGAGGATTTCCAGATCTCGAGTGGAGGCGAGGAGAG 4722
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Db 4783 TGTCTGTGCATCTTTACCAACCGCTTCATTTCCCCCTGTGTCTTTTCTTACCTTGGAG 4842
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Db 4843 CTCCTCTCTGATCTGTGATATTGAGTTGTGTGCTCTTACCTGTCTTAAGAGSCT 4902
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Db 4903 AGAGGAGACCTAGACTTCTGGGTTTCCATTTGTCCCGCCTACCCCGTTACCCCTTCTCC 4962
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Db 5083 CCTGGGGTGGTCCAGTCTGGGTACACACCTGTCTCTTCCCTTTTCTTACCCCTCT 5142
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Db 5143 GCCTTAGTGTCTTCCGCCCAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAG 5202
Qy 426 rLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisVa 446
Db 5203 CCTGATGACAGACTTCTTCGCCAGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACAGT 5262
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Qy 506 oSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSe 526
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Qy 526 rAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSe 546
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Qy 546 rAspLeuAlaLysTyrSerAla 553
Db 5563 CGACTTGGCCCAATACTCAGCG 5584
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RESULT 11

US-09-605-785-703
: Sequence 703, Application US/09605785
: Patent No. 6321716
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.

: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yuqui
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darriek
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C16
: CURRENT APPLICATION NUMBER: US/09/605,785
: CURRENT FILING DATE: 2000-06-27
: NUMBER OF SEQ ID NOS: 835
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 703
: LENGTH: 2904
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-605-785-703

Alignment Scores:
Pred. No.: 6,94e-174 Length: 2904
Score: 1920.50 Matches: 390
Percent Similarity: 77.23% Conservative: 0
Best Local Similarity: 77.23% Mismatches: 1
Query Match: 67.13% Indels: 115
DB: 4 Gaps: 1

US-09-593-793A-113 (1-553) x US-09-605-785-703 (1-2904)

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Db 1 GTCATATGCTTCATGATCAGTCTTGGGGGCTGCCCTGGGCTACCTCCTCGCTGCCATTGAC 60
Qy 183 TrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPheGlyLeu 202
Db 61 TGGGACACACAGTGGCTTGGCCCCCTTACCTGGGACCCAGGAGGAGTGCCTCTTTGGCCTG 120
Qy 203 LeuThrLeuIlePheLeuThrCysValAlaIleAlaThrLeuLeuValAlaGluAlaIle 222
Db 121 CTCACCTCTCATCTTCTCCCTCAGCTAGCAGCACACTGCTGGTGGCTGAGGAGCAGCG 180
Qy 223 LeuGlyProThrGluProAlaGluClyLeuSerAlaProSerLeuSerProHisCysCys 242
Db 181 CTGGCCCCCAGGAGCCAGAGAGGGCTGTGGGCCCTCTCTGTGTCGCCCTGCTGTGT 240
Qy 243 ProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGln 262
Db 241 CCATGCCGGGCGGCTTGGCTTTCGGAAACCTGGGGGCCCTGCTTCCCGGCTGCACCG 300
Qy 263 LeuCysCysArgMetProArgThrLeuArgLeuPheValAlaGluLeuCysSerTrp 282
Db 301 CTGTGCTGCCCATGCCCGCCAGCCCTGCGCGGGCTCTTCTGGTGGCTGAGCTGTGAGCTGG 360
Qy 283 MetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGln 302
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Qy 303 GlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal--- 321
Db 421 GCGGTGCCCGCAGAGCTGAGCCGGGACCGGAGGCCCGGAGACACTATGATGAAGGAAG-GCC 479
Qy 321 ----- 321
Db 480 TCTGGCTGCTTAGGAGTCTGATCAGAGTCTGTGGCCCGCTTGTGACAGAGGAAAGCGG 539
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QY 321 ----- 321
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QY 321 ----- 321
Db 660 TCCAGCTCAGGCGTCTCTAGAGCGTCTTGAAGCCTATGCCAGCTCTCTTTGTGTCCCT 719
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Db 720 CTCACCCGCTCTCTCTCACAGCTGAGACTTCCAGGAAACCTTCAGACTACCTCTCTCTGC 779
QY 322 ----- ArgMetGlySerLeuGlyLeu 328
Db 780 CTTTCAGCAAGGGCGGTGGCCCACTTCTCTGAGGGCGTTTCGGATGGCGACCTGGGGCTG 839
QY 329 PheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArg 348
Db 840 TTCTTCGAGTGGCCCATCTCCCTGCTCTCTCTGCTCATGGACCGGCTGTGTGACGCA 899
QY 349 PheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAla 368
Db 900 TTTCGGCAGCTCGAGCAGCTCTATTGTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCC 959
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QY 429 ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAla 448
Db 1140 ACCAGCTCTCTGCCAGGCGCTTAAGGCTGGAGCTCCCTTCCCTTAATGGACACCTGGGTGCT 1199
QY 449 GlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspVal 468
Db 1200 GGAGCAGTGGCTGCTCCCACTCCACCCGCGCTCTGCGGGGCGCTCTGCTGTGTATGTC 1259
QY 469 SerValArgValValGlyGluProThrGluAlaArgValProGlyArgGlyIle 488
Db 1260 TCCGTACGTGTGTGTGGGTGAGCCACCGAGGCCAGGGTGGTTCCGGCGCGGGGCATC 1319
QY 489 CysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeu 508
Db 1320 TCCTGGAGCTCGCATCTCGATGATGCTTCCCTGCTGCTCCAGGTGGCCCACTCCCTG 1379
QY 509 PheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAla 528
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QY 529 GlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeu 548
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QY 549 AlaLysTyrSerAla 553
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RESULT 12

US-09-071-710-16

; Sequence 16, Application US/09071710

; Patent No. 6130043

; GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,710
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,713
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2152 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-710-16
Alignment Scores:
Pred. No.: 1,76e-113 Length: 2152
Score: 1287.00 Matches: 255
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.98% Indels: 0
DB: 3 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-071-710-16 (1-2152)
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Db 2 GGGCTGTACCAAGGCGTGTCCAGAGCTGAGCGGGCCAGGCGCCGAGACACTATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
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Db 62 GAAGGCGTTCGGATGGCAGCGCTGGGGGCTGTTCCTGCGAGTGGCCATCTCCCTGGTCTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
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Db 122 TCTCTGGTCAATGGACCGGCTGGTGGCGGATTCGGCAGCTCGGAGCAGTCTATTTGGCCAGT 181
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378

Db 182 GTGCAGCTTTCCTGCTGGCTGCCGTGCCACATGCTGTCCACAGTGTGGCGTGGTG 241
QY ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 242 ACAGCTTCAGCCCTCCACCGGGTTACCTTCTCAGCCCTGCAGATCTGCCCTACACA 301
QY LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 302 CTGGCTCCCTCTACCAACGGGAGAGAGGTGTCTCTGCCAAATACCGAGGGGACACT 361
QY GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 362 GGAGGTGCTAGCAGTGAAGACACCTGATGACACAGCTTCTGCGAGCCCTAAGCCCTGA 421
QY AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 422 GCTCCCTTCCCTAATGACACGTGGGTGCTGGAGGAGTGGCTGCTCCACCTCCACCC 481
QY AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr 478
Db 482 GCGCTCTCGGGGCTCTGCTGTGATGCTCCGTACGTGTGGTGGGTGAGCCACC 541
QY GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 542 GAGGCCAGGCTGGTTCGGGCGGGGCATCTGCTGGACCTGCCATCTGGATAGTGCC 601
QY PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
Db 602 TTCCCTGCTGCCAGTGGCCCATCCCTGTTATGGGCTCCATTTGCCAGTCCAGCCAG 661
QY SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 662 TCTGTACATGCCTATATGCTGTCTCGCGCAGGCTGGGTCTGGTCCCATTTACTTTGT 721
QY ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 722 ACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTACGCG 766

RESULT 13
US-09-525-397-16
Sequence 16, Application US/09525397
Patent No. 6252047
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAUL A.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: SROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/525.397

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/071,710
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2152 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-525-397-16
Alignment Scores:
Pred. No.: 1.76e-113 Length: 2152
Score: 1287.00 Matches: 255
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.98% Indels: 0
DB: 4 Gaps: 0
US-09-593-793a-113 (1-553) x US-09-525-397-16 (1-2152)
QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAsp 318
Db 2 GGGCTGTACACGGGCGTGCCAGAGCTGAGCCGGGACCGAGGCCGCGGAGACACTATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGCGTTCCGATGGCAGCCTGGGGCTGTCTCTCAGTGGCCATCTCCCTGGTCTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGGTTCATGGACGGCTGGTGGAGCGATTTCGGCAGCTCGAGCAGCTATTTTGGCAGT 181
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 182 GTGGCAGCTTTCCTGTGCTGGCTGGCGGTGCCACATGCCGTGCCACAGTGTGGCGTGGTG 241
QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 242 ACAGCTTCAGCCGCTCACCAGGTTCACCTTCTCAGCCCTGCAGATCTGCCCTACACA 301
QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 302 CTGGCTCCCTCTACCAACGGGAGAGAGGTGTCTCTGCCAAATACCGAGGGGACACT 361
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 362 GGAGGTGCTAGCAGTGAAGACACCTGATCACCAGCTTCTGCCAGGCCCTAAGCCCTGA 421
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 422 GCTCCCTTCCCTAATGACACCTGGGTGCTGGAGGAGTGGCTGCTCCACCTCCACCC 481
QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr 478
Db 482 GCGCTCTCGGGGCTCTGCTGTGATGCTCCGTACGTGTGGTGGGTGAGCCACC 541
QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
Db 542 GAGGCCAGGCTGGTTCGGGCGGGGCATCTGCTGGAGCCTGCCATCTCCCATTTAGTGC 601
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518

Db 602 TTCTGCTGCCAGGTGGCCCATCCCTGTTATGGGCTCCATTGTCCAGCTCAGCCAG 661
QY 519 SerValThrAlaTyrMetValSerAlaAAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Db 662 TCTGTCACTGCCATATATGTTGTCGCGCAGGCTGGGTCTGGTCGCCATTACTTTGCT 721
QY 539 ThrGlnValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 722 ACAGGTAGTATTGTGACAAGAGCGACTTGGCCAAATACTCAGCG 766
RESULT 14
US-09-071-710-15
; Sequence 15, Application US/09071710
; Patent No. 6130043
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/850,713
; FILING DATE: 02-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2143 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-710-15
Alignment Scores:
Pred. No.: 7,38e-112 Length: 2143
Score: 1270.00 Matches: 252
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.39% Indels: 0
Gaps: 0
Db:

US-09-593-793a-113 (1-553) x US-09-071-710-15 (1-2143)
QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGlyVal 321
Db 3 CAGGGGCTGCCAGAGCTGAGCGGGCCAGGAGCCGGAGACACTATGATGAAGCGTT 62
QY 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
Db 63 CGGATGGCAGCGCTGGGGCTGTTCTTCAGTGGCCATCTCCCTGGTCTCTCTCGTGC 122
QY 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaA 361
Db 123 ATGGACCGGCTGGTCAGCGATTCGGCACTCGAGCAGTCTATTGGCCAGTGGGAGCT 182
QY 362 PheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSer 381
Db 183 TTCCCTGTGGCTGCCGCTGCCACATGCTCCACAGTGTGGCCGTGGTGACAGCTTCA 242
QY 382 AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401
Db 243 GCGGCCCTCACCAGGTTCACCTTCTCAGCCCTGCAGATCTGCCCTACACACTGGCCTCC 302
QY 402 LeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyAla 421
Db 303 CTCTACACCGGAGAGAGAGGTGTTCTGCCCAATACCGAGGGACACTGGAGGTGCT 362
QY 422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
Db 363 AGCAGTGAAGACAGCCTGATGACCACTTCTGCCAGGCCCTAAGCTGGAGCTCCCTTC 422
QY 442 ProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeuCys 461
Db 423 CCTAATGGACACGTGGGTGCTGGAGCAGTGGCTGCTCCACCTCCACCGCGCTCTGC 482
QY 462 GlyAlaSerAlaCysAspValSerValArgValValValGlyGluAlaArg 481
Db 483 GGGGCCCTCTGCCTGTGATGCTCCGTACGTGTGGTGGTGAGCCACCGAGGCCAGG 542
QY 482 ValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501
Db 543 GTGGTTCGGGGCGGGGACATCTGCTGGACCTCGCCATCTCGATAGTGCCTTCTCTGCTG 602
QY 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521
Db 603 TCCAGGTGGCCCATCTCCCTGTTATGGCTCCATTGTCCAGCTCAGCCAGCTGTGCACT 662
QY 522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 541
Db 663 GCCTATATGGTGTCTGCCGAGCGCTGGGTCTGGTGGCCATTACTTTGCTACACAGGA 722
QY 542 ValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 723 GTATTGACAAGAGCGACTTGGCCAAATACTCAGCG 758
RESULT 15
US-09-525-397-15
; Sequence 15, Application US/09525397
; Patent No. 6252047
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE


```
US-09-593-793A-113 (1-553) x US-09-020-956-10 (1-789)
;
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ... US-09-030-607-10

Alignment Scores:
Pred. No.: 6,14e-79 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-030-607-10 (1-789)
QY 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
DB 3 GTCTATNTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCACATGCGCTGCCAC 62
QY 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
DB 63 AGTGTGGCCGTGGTACAGCTTCAGCGCCCTCACCGGTTCCACCTTCTCAGCCCTGCAG 122
QY 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
DB 123 ATCCCTGCCCTACACACTGGCCTCCCTCTACACCGGGAGACAGGTGTCTCTGCCCAA 182
QY 414 TyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
DB 183 TACCCAGGGGACACGTGGAGGTGCTAGCAGTGAGACAGCCTGATGACACAGCTTCTGCCA 242
QY 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeu 453
DB 243 GGCCTTAAGCCTGGAGCTCCCTTCCCTAATGACACGTGGGTGCTGGAGGCAGTGGCCTG 302
QY 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
DB 303 CTCCACCTCCACCCCGCTCTCGGGGCTCTCGGGGCTCTGCTGTGTGATGCTCTCCGTG 362
QY 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAla 493
DB 363 GTGGGTGAGCCACCCAGCCAGGGGTGTCCGGCCGGGGCATCTGCCCTGGACCTCGCC 422
QY 494 IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
DB 423 ATCTGGATAGTGC-TTCTCTGCTGCCANGTGCCCATCCCTGTTTATGGCTCCATT 481
QY 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyVal 533
DB 482 GTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCCGCAGGCTGGGTCTG 541
QY 534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
DB 542 CC-ATTACTTTGCTACACAGGTANTATTTGACAAGACGANTTTGGCCAAATACTCAGCG 600

RESULT 17
US-09-030-607-10
; Sequence 10, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
```

APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605.785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 789
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(789)
OTHER INFORMATION: n = A,T,C or G
US-09-605-785-10

Alignment Scores:
Pred. No.: 6.14e-79 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-605-785-10 (1-789)

Qy 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCATATNTGGCCAGCTGGCAGCTTCCCTGTGGCTGGCGTGGCCACATGCTGTCCAC 62
Qy 374 SerValAlaValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGGCCGTGGTGCACAGCTTACGCCGCTTCACCGGGTTCACCTTCTCAGCCCTGCAG 122
Qy 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
Db 123 ATCTGTGCCCTACACACTGGCCCTCTTACCACCGGGAGAGCAGGTGTTCTCTGCCCAA 182
Qy 414 TyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
Db 183 TACCGAGGGACACTGGAGGTGCTAGCAGTGGACACGCTGTGACACAGCTTCTCTGCCA 242
Qy 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeu 453
Db 243 GGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGCTGGGTGTGGAGGAGTGGCTG 302
Qy 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
Db 303 CTCCACCTCCACCGCGCTCTGGGGGCTCTGCTGTGATGCTCTCGTACGTGTGGTG 362
Qy 474 ValGlyGluProGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 493
Db 363 GTGGGTGAGCCACCCAGGAGGAGTGTTCGGGGCGGGGCACTGTGCTGGAGCTCCGC 422
Qy 494 IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
Db 423 ATCTGGGATAGTC-TTCTGCTGTCCANGTGGCCCATCCCTGTTTATGGGTCCATT 481
Qy 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuVal 533
Db 482 GTCCAGCTCAGCCAGCTGTCTCACTGCCTATATGTTGTGTGTCGCCGAGGCGCTGGGTCTGTC 541

Qy 534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 542 CC-ATTACTTGTGTACACAGGTANTATTGACAAAGACGANTTGGCCAAATACTCAGCG 600
RESULT 19
US-09-439-313-10
Sequence 10, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqui
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439.313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 789
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(789)
OTHER INFORMATION: n = A,T,C or G
US-09-439-313-10

Alignment Scores:
Pred. No.: 6.14e-79 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-439-313-10 (1-789)

Qy 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCATATNTGGCCAGCTGGCAGCTTCCCTGTGGCTGGCGTGGCCACATGCTGTCCAC 62
Qy 374 SerValAlaValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGGCCGTGGTGCACAGCTTACGCCGCTTCACCGGGTTCACCTTCTCAGCCCTGCAG 122
Qy 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
Db 123 ATCTGTGCCCTACACACTGGCCCTCTTACCACCGGGAGAGCAGGTGTTCTCTGCCCAA 182
Qy 414 TyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
Db 183 TACCGAGGGACACTGGAGGTGCTAGCAGTGGACACGCTGTGACACAGCTTCTCTGCCA 242
Qy 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeu 453
Db 243 GGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGCTGGGTGTGGAGGAGTGGCTG 302
Qy 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
Db 303 CTCCACCTCCACCGCGCTCTGGGGGCTCTGCTGTGATGCTCTCGTACGTGTGGTG 362
Qy 474 ValGlyGluProGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 493

Db 363 GTGGGTGAGCCACCGAGGCGGTTCGCGGCGCGGCGATCTGCGCTGGACCTCGCC 422
Qy 494 IleLeuAspSerAlaPheLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
Db 423 ATCTGGATAGTGC-TTCTGTCTGTCCCGANGTGGCCCATCTCTTTATGGGCTCCATT 481
Qy 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuVal 533
Db 482 GTCCAGCTCAGCAGTCTGTCTACTGTCTATATGGTGTCTGCGCAGCGCTGGGTCTGGTC 541
Qy 534 AlaIleTyrPheAlaThrGlnValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 542 CC-ATTACTTTGCTACAGGTANTATTGACAAGACGANTTGGCCAAATACTCAGCG 600
RESULT 20
US-09-352-616A-10
; Sequence 10, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-10
Alignment Scores:
Pred. No.: 6.14e-79 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 4 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-352-616A-10 (1-789)
Qy 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCTATNTGGCAGGTGGCAGCTTCCCTGTGGCTGCGCGGTGCCACATGCTGCCAC 62
Qy 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGGCGGTGTGACAGCTTCACCGCCCTCACCAGGTTACCTTCTCAGCCCTGCAG 122
Qy 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
Db 123 ATCTGCCCTACACATGCGCTCTCTACACCGGGAGACAGCTGTCTCTGCCCAA 182
Qy 414 TyrArgGlyAspThrGlyAlaSerGluAspSerLeuMetThrSerPheLeuPro 433
Db 183 TACCGAGGGGACACTGGAGGTCTAGCAGTGAGGACGCTGATACACAGCTTCTCTGCCA 242
Qy 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeu 453
Db 243 GGCCTTAAGCTGGAGCTCCCTTCCCTAATGGACAGCTGGGTGCTGGAGGAGTGGCCTG 302
Qy 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473

Db 303 CTCCACCTCCACCGCGCTCTGCGGGGCGCTCTGCTGTGTGTCTCCGTACGTGTGGTG 362
Qy 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 493
Db 363 GTGGGTGAGCCACCGANGCGAGGTGGTTCGCGGCGCGGGGCGATCTGCTGGACCTCGCC 422
Qy 494 IleLeuAspSerAlaPheLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
Db 423 ATCTGGATAGTGC-TTCTGTCTGTCCCGANGTGGCCCATCTCTTTATGGGCTCCATT 481
Qy 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuVal 533
Db 482 GTCCAGCTCAGCAGTCTGTCTACTGTCTATATGGTGTCTGCGCAGCGCTGGGTCTGGTC 541
Qy 534 AlaIleTyrPheAlaThrGlnValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 542 CC-ATTACTTTGCTACAGGTANTATTGACAAGACGANTTGGCCAAATACTCAGCG 600
RESULT 21
US-09-232-149A-10
; Sequence 10, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-10
Alignment Scores:
Pred. No.: 6.14e-79 Length: 789
Score: 919.00 Matches: 192
Percent Similarity: 96.50% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 7
Query Match: 32.12% Indels: 2
DB: 4 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-232-149A-10 (1-789)
Qy 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCTATNTGGCAGGTGGCAGCTTCCCTGTGGCTGCGCGGTGCCACATGCTGCCAC 62
Qy 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGGCGGTGTGACAGCTTCACCGCCCTCACCAGGTTACCTTCTCAGCCCTGCAG 122
Qy 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
Db 123 ATCTGCCCTACACATGCGCTCTCTACACCGGGAGACAGCTGTCTCTGCCCAA 182
Qy 414 TyrArgGlyAspThrGlyAlaSerGluAspSerLeuMetThrSerPheLeuPro 433
Db 183 TACCGAGGGGACACTGGAGGTCTAGCAGTGAGGACGCTGATACACAGCTTCTCTGCCA 242
Qy 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeu 453
Db 243 GGCCTTAAGCTGGAGCTCCCTTCCCTAATGGACAGCTGGGTGCTGGAGGAGTGGCCTG 302

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Qy 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
Db 303 TTTCCACCTCCACCGCGCTCTCGGGGCTCTGCTGTGATGTCTCGGTACGTGTGGTG 362
Qy 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 493
Db 363 GTGGGTGAGCCACCGAGCCAGGCTGTCTCGGGCCGGGGCAGCTGCTGGACCTCGCC 422
Qy 494 IleLeuAspSerAlaPheLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
Db 423 ATCCGTGGATAGTC-TTCTCTGCTGTCCANGTGGCCCATCCCTGTTATGGCTCCATT 481
Qy 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuVal 533
Db 482 GTCCAGCTCAGCCAGCTGTCTCACTGCCTATATGGTGTCTGCCGAGGCTGGGTCTGTC 541
Qy 534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 542 CC-ATTACTTGTGTACACAGGTANTATTGACAAAGACGANTTGGCCAAATACTACGCG 600

RESULT 22
US-09-071-710-3
; Sequence 3, Application US/09071710
; Patent No. 6130043
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/850,713
; FILING DATE: 02-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083 US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

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; FEATURE:
; NAME/KEY: base_polymorphism
; LOCATION: 215
; OTHER INFORMATION: /note= " N' represents an A or G or
; OTHER INFORMATION: T or C polymorphism at this position"
US-09-071-710-3

Alignment Scores:
Pred. No.: 7.37e-34 Length: 255
Score: 440.00 Matches: 83
Percent Similarity: 98.81% Conservative: 0
Best Local Similarity: 98.81% Mismatches: 1
Query Match: 15.38% Indels: 0
DB: 3 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-071-710-3 (1-255)
Qy 379 ThrAlaSerAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
Db 2 ACAGCTTCAGCGCGCTCACCGGGTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACA 61
Qy 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
Db 62 CTGGCTCTCCCTCTACACCGGCAAGCAGGTGTCTCCCAATACCGAGGGGACACT 121
Qy 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
Db 122 GGAGTGTCTAGCAGTGAGGACAGCTGTATGACACGCTTCTGCCAGGCCCTTAGCCTGGA 181
Qy 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
Db 182 GCTCCCTTCCCTTAATGGACACGTGGTGTCTGGANGCAGTGGCTGCTCCACCTCCACCC 241
Qy 459 AlaLeuCysGly 462
Db 242 CGCTCTCGGG 253

RESULT 23
US-09-525-397-3
; Sequence 3, Application US/09525397
; Patent No. 6252047
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/850,713
; FILING DATE: 02-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083 US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```


;; PRIOR APPLICATION DATA: 09/071,710
;; APPLICATION NUMBER: 09/071,710
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Becker, Cheryl L.
;; REGISTRATION NUMBER: 35,441
;; REFERENCE/DOCKET NUMBER: 6083.US.P1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 847/935-1729
;; TELEFAX: 847/938-2623
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 255 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: base_polymorphism
;; LOCATION: 215
;; OTHER INFORMATION: /note= " N' represents an A or G or
;; OTHER INFORMATION: T or C polymorphism at this position"
US-09-525-397-3

Alignment Scores:
Pred. No.: 7.37e-34 Length: 255
Score: 440.00 Matches: 83
Percent Similarity: 98.81% Conservative: 0
Best Local Similarity: 98.81% Mismatches: 1
Query Match: 15.38% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-525-397-3 (1-255)

QY 379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398
DB 2 ACAGCTTCAGCGCCCTCACCAGGTTACCTTCAGCCCTGCAGATCTGCCCTACACA 61
QY 399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
DB 62 CTGGCTCCTCTACACCGGAGAGACAGGTTCCTGCCCAATACCGAGGGACACT 121
QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
DB 122 GGAGGTGCTAGCAGTACGAGACAGCTGATGACACAGCTTCCTGCCAGGCCCTAAGCCTGA 181
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProPro 458
DB 182 GCTCCCTTCCCTTAATGACACGTGGTGTGGANGCAGTGGCTGCTCCACCTCCACCC 241
QY 459 AlaLeuCysGly 462
DB 242 GCGCTCTGCGGG 253

RESULT 24

US-09-071-710-1
; Sequence 1, Application US/09071710
; Patent No. 6130043
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE

;; NUMBER OF SEQUENCES: 41
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Abbott Laboratories
;; STREET: 100 Abbott Park Road
;; CITY: Abbott Park
;; STATE: IL
;; COUNTRY: USA
;; ZIP: 60064-3500
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FASTSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/071,710
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/850,713
;; FILING DATE: 02-MAY-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Becker, Cheryl L.
;; REGISTRATION NUMBER: 35,441
;; REFERENCE/DOCKET NUMBER: 6083.US.P1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 847/935-1729
;; TELEFAX: 847/938-2623
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 258 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-09-071-710-1
Alignment Scores:
Pred. No.: 3.17e-32 Length: 258
Score: 423.00 Matches: 85
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.79% Indels: 0
DB: 3 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-071-710-1 (1-258)
QY 299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAsp 318
DB 2 GGGCTGTACCGAGGGCTGCCAGAGCTGAGCGGGCAGCGAGCGGAGACTATGAT 61
QY 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
DB 62 GAAGCGTTCGGATGGGAGCGCTGGGGTGTCTTCAGTGGCCCATCTCCCTGGTCTTC 121
QY 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
DB 122 TCTCTGGTCATGGACCGGCTGTGCAGCGATTCGGCAGCTCGAGCAGCTCTATTTGGCCACT 181
QY 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal 378
DB 182 GTGGCAGCTTTCCTGTGGCTGCCCGTGCCACATGCTGCCACAGTGTGGCCCGTGGTG 241
QY 379 ThrAlaSerAlaAla 383
DB 242 ACAGCTTCAGCGGCC 256
RESULT 25
US-09-525-397-1
; Sequence 1, Application US/09525397
; Patent No. 6252047
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE

APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/525,397
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/071,710
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083-US.P1
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-525-397-1

Alignment Scores:
Pred. No.: 3.17e-32 Length: 258
Score: 423.00 Matches: 85
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.79% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-525-397-1 (1-258)

Qy 299 GlyLeuTyrglnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAsp 318
Db 2 GGGGTGTACACAGGGCGTGCACAGCTGAGCGGGACCGAGCGCCGAGACACTATGAT 61
Qy 319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338
Db 62 GAAGCGGTTCGGATGGGAGCGCTGGGCGTGTCTCTGAGTGGCGCATCTCCCTGGTCTTC 121
Qy 339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer 358
Db 122 TCTCTGGTCATGGACCGGCTGGTCAGGAGATTCGGCACTCGCAGAGCTATTGGCCAGT 181
Qy 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378
Db 182 GTGCAGCGTTTCCCTGTGGCTGGCGGTGCCACATGCCTGTCCACAGTGTGCCCGTGTGTG 241

Oy 379 ThrAlaSerAlaAla 383
Db 242 ACAGCTTCAGCGCC 256

RESULT 26

US-09-071-710-4
Sequence 4, Application US/09071710
Patent No. 6130043
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,710
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,713
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083-US.P1
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-710-4

Alignment Scores:
Pred. No.: 8.93e-32 Length: 247
Score: 418.00 Matches: 82
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.61% Indels: 0
DB: 3 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-071-710-4 (1-247)

Qy 439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProPro 458
Db 1 GCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCACCTCCACCC 60

QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr 478
|||||
Db 61 GCGCTCTCGGGGCGCTCTCGCTGTGATGTCCTCGTACGTGTGGTGGTGAGCCACC 120
QY 479 GluAlaArgValValProGlyArgGlyLeCysLeuAspLeuAlaIleLeuAspSerAla 498
|||||
Db 121 GAGGCCAGGGTGGTTCCGGCGCGGGGCATCTGCCTGGACCTCGCCATCTGGATAGTGCC 180
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
|||||
Db 181 TTCTCTGTCTCCAGGTGGCCCATCTCCCTGTTATGGGCTCCATGTCCAGCTCAGCCAG 240
QY 519 SerVal 520
|||||
Db 241 TCTGTC 246
RESULT 27
US-09-525-397-4
; Sequence 4, Application US/09525397
; Patent No. 6252047
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/525,397
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/071,710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-525-397-4

Alignment Scores:

Pred. No.: 8.93e-32 Length: 247
Score: 418.00 Matches: 82
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.61% Indels: 0
DB: 4 Gaps: 0
US-09-593-793a-113 (1-553) x US-09-525-397-4 (1-247)
QY 439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProPro 458
|||||
Db 1 GCTCCCTTCCCTTAATGGACACGCTGGGTGCTGGAGGAGTGGCTGCTCCCACTCCACCC 60
QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr 478
|||||
Db 61 GCGCTCTCGGGGCGCTCTCGCTGTGATGTCCTCGTACGTGTGGTGGTGAGCCACC 120
QY 479 GluAlaArgValValProGlyArgGlyLeCysLeuAspLeuAlaIleLeuAspSerAla 498
|||||
Db 121 GAGGCCAGGGTGGTTCCGGCGCGGGGCATCTGCCTGGACCTCGCCATCTGGATAGTGCC 180
QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
|||||
Db 181 TTCTCTGTCTCCAGGTGGCCCATCTCCCTGTTATGGGCTCCATGTCCAGCTCAGCCAG 240
QY 519 SerVal 520
|||||
Db 241 TCTGTC 246
RESULT 28
US-09-071-710-2
; Sequence 2, Application US/09071710
; Patent No. 6130043
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/850,713
; FILING DATE: 02-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-525-397-4

; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 217 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-710-2

Alignment Scores:
Pred. No.: 5.02e-26 Length: 217
Score: 357.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.48% Indels: 0
DB: 3 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-071-710-2 (1-217)

QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGlyVal 321
Db 3 CAGGGCGTGGCCAGAGCTGAGCGGCGCCGAGGCGCCGAGACACTATGATGAAGCGGTT 62
QY 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
Db 63 CGGATGGCGAGCGCTGGGCGTGTCTCGCAGTGCAGCCATCTCCCTGGTCTCTCTGTC 122
QY 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
Db 123 ATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTGGCCAGTGTGGCAGCT 182
QY 362 PheProValAlaAlaGlyAlaThrCysLeuSer 372
Db 183 TTCCCTGTGGTGGCGGTGCCACATGCCTGTGCC 215

RESULT 29

US-09-525-397-2
; Sequence 2, Application US/09525397
; Patent No. 6252047

GENERAL INFORMATION:

; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/525,397
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/071,710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 217 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-525-397-2

Alignment Scores:
Pred. No.: 5.02e-26 Length: 217
Score: 357.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.48% Indels: 0
DB: 4 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-525-397-2 (1-217)

QY 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGlyVal 321
Db 3 CAGGGCGTGGCCAGAGCTGAGCGGCGCCGAGGCGCCGAGACACTATGATGAAGCGGTT 62
QY 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
Db 63 CGGATGGCGAGCGCTGGGCGTGTCTCGCAGTGCAGCCATCTCCCTGGTCTCTCTGTC 122
QY 342 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 361
Db 123 ATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTGGCCAGTGTGGCAGCT 182
QY 362 PheProValAlaAlaGlyAlaThrCysLeuSer 372
Db 183 TTCCCTGTGGTGGCGGTGCCACATGCCTGTGCC 215

RESULT 30

US-08-356-340-3
; Sequence 3, Application US/08356340
; Patent No. 5608146

GENERAL INFORMATION:

; APPLICANT: FROMMER, WOLF-BERND
; APPLICANT: RIESMEIER, JORG
; TITLE OF INVENTION: DNA SEQUENCES WITH OLIGOSACCHARIDE
; TITLE OF INVENTION: TRANSPORTER, PLASMIDS, BACTERIA AND PLANTS CONTAINING A
; TITLE OF INVENTION: TRANSPORTER AS WELL AS A PROCESS FOR THE PREPARATION AND
; TITLE OF INVENTION: TRANSFORMATION OF YEAST STRAINS FOR THE IDENTIFI...
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10036-8403

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,340
; FILING DATE: 21-DEC-1994
; CLASSIFICATION: 800

530	AGGATGAGACACAAATGCTTTTCTCATCTCTATGCGCGTGGAAAAATATCTG	176	TyrLeuLeuProAlaIleAspTrp-----	379	-----ThrAlaSerAlaLeuThrGlyPheThr-----	462	GlyAlaSerAla 465
			:	
590	TACGCGCGGTTTCATATTCTCACCTCTTTTAAAGTATTCCCCTTCTCAAAAACCAAGCC	590	TACGCGCGGTTTCATATTCTCACCTCTTTTAAAGTATTCCCCTTCTCAAAAACCAAGCC	590	TACGCGCGGTTTCATATTCTCACCTCTTTTAAAGTATTCCCCTTCTCAAAAACCAAGCC	590	TACGCGCGGTTTCATATTCTCACCTCTTTTAAAGTATTCCCCTTCTCAAAAACCAAGCC
188	LeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe---GlyLeuLeuThrLeuIle 206	188	LeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe---GlyLeuLeuThrLeuIle 206	188	LeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe---GlyLeuLeuThrLeuIle 206	188	LeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe---GlyLeuLeuThrLeuIle 206
650	TGGACATGTACTACGCAATCTGAAGAGTGTCTTTCATCGTCAATATTCCTTTACTC 709	650	TGGACATGTACTACGCAATCTGAAGAGTGTCTTTCATCGTCAATATTCCTTTACTC 709	650	TGGACATGTACTACGCAATCTGAAGAGTGTCTTTCATCGTCAATATTCCTTTACTC 709	650	TGGACATGTACTACGCAATCTGAAGAGTGTCTTTCATCGTCAATATTCCTTTACTC 709
207	PheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu---AlaAlaLeuGlyPro 225	207	PheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu---AlaAlaLeuGlyPro 225	207	PheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu---AlaAlaLeuGlyPro 225	207	PheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu---AlaAlaLeuGlyPro 225
710	AGCTTAACACCAATACGCTTAACCTTAGTCCGGGAAACAGACTCCCGGAAAGACGAG 769	710	AGCTTAACACCAATACGCTTAACCTTAGTCCGGGAAACAGACTCCCGGAAAGACGAG 769	710	AGCTTAACACCAATACGCTTAACCTTAGTCCGGGAAACAGACTCCCGGAAAGACGAG 769	710	AGCTTAACACCAATACGCTTAACCTTAGTCCGGGAAACAGACTCCCGGAAAGACGAG 769
226	ThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCysArg 245	226	ThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCysArg 245	226	ThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCysArg 245	226	ThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCysArg 245
770	CAAGAAATCAGCAGAAATATAGCCGCGCCGGA-----AAA 805	770	CAAGAAATCAGCAGAAATATAGCCGCGCCGGA-----AAA 805	770	CAAGAAATCAGCAGAAATATAGCCGCGCCGGA-----AAA 805	770	CAAGAAATCAGCAGAAATATAGCCGCGCCGGA-----AAA 805
246	AlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCys 265	246	AlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCys 265	246	AlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCys 265	246	AlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCys 265
806	TCGAAAGTACCGTTT-----TTCGGTGAATTTTGGGCGTTTGAAAGAAATTA----- 853	806	TCGAAAGTACCGTTT-----TTCGGTGAATTTTGGGCGTTTGAAAGAAATTA----- 853	806	TCGAAAGTACCGTTT-----TTCGGTGAATTTTGGGCGTTTGAAAGAAATTA----- 853	806	TCGAAAGTACCGTTT-----TTCGGTGAATTTTGGGCGTTTGAAAGAAATTA----- 853
266	ArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeu 285	266	ArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeu 285	266	ArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeu 285	266	ArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeu 285
854	-----CCTCGACCGATGCGATTCTTCTATTAGTAACTCTGTTCACTGGATCGCGTGG 907	854	-----CCTCGACCGATGCGATTCTTCTATTAGTAACTCTGTTCACTGGATCGCGTGG 907	854	-----CCTCGACCGATGCGATTCTTCTATTAGTAACTCTGTTCACTGGATCGCGTGG 907	854	-----CCTCGACCGATGCGATTCTTCTATTAGTAACTCTGTTCACTGGATCGCGTGG 907
286	MetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValPro 305	286	MetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValPro 305	286	MetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValPro 305	286	MetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValPro 305
908	TTTCCCTTTTCTATACGATACAGATTGGATGGCTAAGGAGTGTTCGGTGA----- 961	908	TTTCCCTTTTCTATACGATACAGATTGGATGGCTAAGGAGTGTTCGGTGA----- 961	908	TTTCCCTTTTCTATACGATACAGATTGGATGGCTAAGGAGTGTTCGGTGA----- 961	908	TTTCCCTTTTCTATACGATACAGATTGGATGGCTAAGGAGTGTTCGGTGA----- 961
306	ArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyValArgMetGlySer 325	306	ArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyValArgMetGlySer 325	306	ArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyValArgMetGlySer 325	306	ArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyValArgMetGlySer 325
962	-----CAAGTCGGTGAT-----GCGAGGTGTACGATTGGGGTGCACGCGCTGGTGCA 1009	962	-----CAAGTCGGTGAT-----GCGAGGTGTACGATTGGGGTGCACGCGCTGGTGCA 1009	962	-----CAAGTCGGTGAT-----GCGAGGTGTACGATTGGGGTGCACGCGCTGGTGCA 1009	962	-----CAAGTCGGTGAT-----GCGAGGTGTACGATTGGGGTGCACGCGCTGGTGCA 1009
326	LeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeu 345	326	LeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeu 345	326	LeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeu 345	326	LeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeu 345
1010	ATGGGATTACTGTGCAATCTGGTCTAGGGTTTATCTCACTTGGGGTGAATCTCTTA 1069	1010	ATGGGATTACTGTGCAATCTGGTCTAGGGTTTATCTCACTTGGGGTGAATCTCTTA 1069	1010	ATGGGATTACTGTGCAATCTGGTCTAGGGTTTATCTCACTTGGGGTGAATCTCTTA 1069	1010	ATGGGATTACTGTGCAATCTGGTCTAGGGTTTATCTCACTTGGGGTGAATCTCTTA 1069
346	ValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAla 365	346	ValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAla 365	346	ValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAla 365	346	ValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAla 365
1070	GGAAAGAAGATTGGT---GGTGTAGAGGTTATGGGGAATTTTGAACCTTTGTTTG--- 1123	1070	GGAAAGAAGATTGGT---GGTGTAGAGGTTATGGGGAATTTTGAACCTTTGTTTG--- 1123	1070	GGAAAGAAGATTGGT---GGTGTAGAGGTTATGGGGAATTTTGAACCTTTGTTTG--- 1123	1070	GGAAAGAAGATTGGT---GGTGTAGAGGTTATGGGGAATTTTGAACCTTTGTTTG--- 1123
366	AlaGlyAlaThrCysLeuSerHisSerValAlaValVal----- 378	366	AlaGlyAlaThrCysLeuSerHisSerValAlaValVal----- 378	366	AlaGlyAlaThrCysLeuSerHisSerValAlaValVal----- 378	366	AlaGlyAlaThrCysLeuSerHisSerValAlaValVal----- 378
1124	-----GCTATTGCTTGCTAT						


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Db 1195 ATTGCAATATTATCTT-----GCTGTTTGTAGCTATGAGGTG 1236
Qy 376 AlaValValThrAlaSerAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeu 395
Db 1237 ---TTAGTTACTAAGTCCCGCAA-----1257
Qy 396 ProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArg 415
Db 1258 ---CACCCTCGTGATGACCCACCATATTATG-----1284
Qy 416 GlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyPro 435
Db 1284 -----1284
Qy 436 LysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuPro 455
Db 1285 -----GGCTCCGCGTCCCTCG 1302
Qy 456 ProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGly 475
Db 1303 CGCGCGCTGCT-----GGTGTAAAGGTGGCGCTTTGGCTATCTTTGCCGCTTCTTGT 1356
Qy 476 GluProThrGluAlaArgVal---ValPro-----484
Db 1357 ATCCCTCTTGGCATCCTTTCAGTATCTTGGCTTGGCGTGGCGTCAATCTTTTCAGCATCT 1416
Qy 485 ---GlyArgGlyLeuCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGln 503
Db 1417 TCCGGTTCAGGACAGGTCTTCTCTAGGAGTCTCAACCTCGCCATCGTGTGACCCAG 1476
Qy 504 Val-----AlaPro 506
Db 1477 ATGTTGTGTCGTAAAGTGGCCATGGGATGCAATGTTTGGTGGAGAAATTTGCCA 1536
Qy 507 SerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyr 523
Db 1537 GCATTCGTGGTGGGAGCTGTAGCAGCAGCAGGAGTTCCTTTTCATTT 1587

RESULT 34
US-09-071-710-5
; Sequence 5, Application US/09071710
; Patent No. 6130043
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,710
; FILING DATE:
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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/850,713
; FILING DATE: 02-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6083-US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-710-5
Alignment Scores:
Pred. No.: 1,84e-15 Length: 231
Score: 247.00 Matches: 57
Percent Similarity: 98.28% Conservative: 0
Best Local Similarity: 98.28% Mismatches: 1
Query Match: 8.63% Indels: 1
DB: 3 Gaps: 0
US-09-593-793a-113 (1-553) x US-09-071-710-5 (1-231)
Qy 496 AspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGln 515
Db 3 GATAGTGCCTTCCTGCTGCCAGGTGCCCATCCCTGTTTATGGCTCCATTGTCCAG 62
Qy 516 LeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIle 535
Db 63 CTCAGCCAGTCTGTCACCTGCTATATGTTGTCGCCGAGGCTGCGGCGCCATT 121
Qy 536 TyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 122 TACTTTGCTACAGGTAGTATTTCACAGAGCGACTTGGCCAAATATCTACGCG 175
RESULT 35
US-09-525-397-5
; Sequence 5, Application US/09525397
; Patent No. 6252047
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
```


Db 6055 GGTGTCGACAGATCTTGTCTCGGGATTTGTCTCGCGCACCTGGGAATCTTCCAACTGCCGA 5996
Qy 143 ---LeuGluAlaLeu-----LeuSerAspLeuPhe 151
Db 5995 ACTGTTTCATCTCTCTGCGCTTTGCAGTAACCTTGTATATACGAAGCTGATTTCTTTT 5936
Qy 152 ArgAspPro-----AspHisCysArgGlnAlaTyrSerValTyrAlaPheMet 167
Db 5935 CTGTTTCCCACTGCCATTCAGATCACTGCGCTGATCTCCCGGTATCGCT----- 5882
Qy 168 IleSerLeuGlyCysLeuGly-TyrLeuLeuProAlaIleAspTrpAspThrSerAl 187
Db 5881 GTTCTTTTCTGCGGCTGAAGCTCTCTCTCCCGATATTGCGTCTCCAGCTCTCGC 5822
Qy 187 a-----LeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLe 205
Db 5821 GCCTTCTCTCTCCCGTTCCTC-----TCTCAGCAGCTGCTCTTCCCTCTCTGCTG 5768
Qy 205 uIlePheLeuThrCysValAlaAlaThrLeuLeu-----ValAl 218
Db 5767 CCTCTTCTCCCGACATTCCTCTCCCGCTCTCGCGCTTCTCTCTCCGGTTCCTCTC 5708
Qy 218 aGluGluAlaAlaLeuGlyPro-----ThrGluProAl 229
Db 5707 TCAGCA-GCTGCTCTTCTCTCTCTCTCCGCTCTCCGATATTCGCTCTCCAGC 5649
Qy 229 aGluGly-----LeuSerAlaProSerLeuSerProHisCysC 242
Db 5648 TCTTGGCGCTTCTCGTCTCCCGTTCCTCTCCAGCAGCTGCTCTCTCTCTCTCTGCTG 5589
Qy 242 sProcysArgAlaArgLeuAlaPheArgAsnLeuGly----- 254
Db 5588 TCCTCTTCTCTCCGATATTCGCTCTCCCGCTCTCGAGCTCTCTCTCTCTCTCTCTCT 5529
Qy 255 -----AlaLeuLeuProArgLeuHisGlnLeuCysCysArg-MetProArgThrL 271
Db 5528 CTCAGCAGCTGCT 5469
Qy 271 eu-----ArgArgLeuPheValAlaGluLeu 280
Db 5468 TCTTGGCGCTTCT 5416
Qy 280 ysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyL 300
Db 5415 -----CTGCAACT 5364
Qy 300 eutyGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluG 320
Db 5363 TTTCTCGGTTCT 5305
Qy 320 lyValArgMetGlySerLeuGlyLeuPhe-----L 330
Db 5304 ATATTGCTTTCT 5245
Qy 330 euGlnCysAlaIleSerLeuLeuPheSerLeuValMetAspArgLeuValGlnArgPheG 350
Db 5244 TTTCT 5185
Qy 350 lyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrC 370
Db 5184 CTCTCGCGCT 5141
Qy 370 ysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPhe- 389
Db 5140 -----CGAGCTGCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5095
Qy 390 -----SerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeu 403
Db 5094 GTACAGCGTGTGGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5041
Qy 403 yHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerS 423
Db 5040 TTGGT-----CGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5011

Qy 423 erGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProA 443
Db 5010 CTCCTGATCCT-----CCTGGAGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4969
Qy 443 snGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCysGlyA 463
Db 4968 TTGGCAGCGTCTCCCGCTGGAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4924
Qy 463 laSerAlaCysAspValSerValArgValValValGlyGlu-----p 477
Db 4923 CTGACGCTCTTTCT 4867
Qy 477 roThrGluAlaArgValValProGlyArgGly 487
Db 4866 CTCGGGAGAAACCGTGTCTCCGCTGCTGGC 4835
RESULT 37
US-08-800-644-93/c
; Sequence 93, Application US/08800644
; Patent No. 5958752
; GENERAL INFORMATION:
; APPLICANT: Steinert, Peter M.
; APPLICANT: Lee, Seung-Chul
; APPLICANT: Kim, In-Gyu
; APPLICANT: Chung, Soo-Il
; APPLICANT: Park, Sang-Chul
; TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
; TITLE OF INVENTION: Methods of Using Same
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800.644
; FILING DATE: 14-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/056,200
; FILING DATE: 30-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fedrick, Michael F.
; REGISTRATION NUMBER: 36,799
; REFERENCE/DOCKET NUMBER: NIH054.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 760-0404
; TELEFAX: (714) 760-9502
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9551 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1507..1644
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1645..2511
; FEATURE:
; NAME/KEY: CDS

LOCATION: 2512...8070
US-08-800-644-93

Alignment Scores:
Pred. No.: 0.000289 Length: 9551
Score: 155.50 Matches: 157
Percent Similarity: 35.78% Conservativity: 62
Best Local Similarity: 25.65% Mismatches: 198
Query Match: 5.44% Indels: 198
DB: 2 Gaps: 31

US-09-593-793A-113 (1-553) x US-08-800-644-93 (1-9551)

Qy	7	ValSerArgLeuLeuArgHisArgGlyAlaGlnLeuLeuValAsnLeuLeuThrPhe	26
Db	6471	CTGACGAGTGTCTCGCGCTCTCCAGCGCAGCTGCTGCTCCCTC---CTTAAGGAATTT	6415
Qy	27	GlyLeuGluValCysLeuAlaAlaGlyIleThrValProProLeuLeuGluVal	46
Db	6414	TCTCTCCGGTTC-----CTCGCGCAGCGCTGCTTCCTC-----	6382
Qy	47	GlyValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal	66
Db	6381	--CTCAGGAATT-TTCTCCCTGTTCCTCATGAGCAGTTCCTCTTCGCGGAATTTTC	6326
Qy	67	CysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTrpArgArgArg	86
Db	6325	TGTCACGCTCTTGCGCAGCAGCGCT-----GTTCCCT	6293
Qy	87	Prophe-----IleTrpAlaLeuSerLeuGlyIleLeu	97
Db	6292	CCCTTTCTCCAGCAGCTGTTCCTCTCGGGAATTTTCTGCTCTCTTTGACGGCGTC	6233
Qy	98	LeuSerLeuPheLeuIlePro-----Arg	105
Db	6232	TCCTCTCTT---CTCTTCTCTCTCAGCACTGCTTTCTCTCTGGACTTCCTGTGCG	6176
Qy	106	AlaGlyTrpLeuAla---GlyLeuLeuCysProAspProArgProLeu-----	120
Db	6175	GCCTTTTGCTCTCTTTTGTCTCTCTGCTCCAGCTGTCTCTCTGGGAAATGCCTGT	6116
Qy	121	-----GluLeuAlaLeuLeuIleLeuGlyVal	129
Db	6115	TGGCGCTGCTGCCAGCGCTCTCTCTTGTGCTACAGATCTCTCTGCTGTTTACCCACGA	6056
Qy	130	GlyLeuLeuAspPheCysGlyGlnValCysPheThrPro-----	142
Db	6055	GGTGCTCAGATCTGTGCTGGATGTCTGTGCGGCACCTGGGAATCTTCCAACTGCCGA	5996
Qy	143	-----LeuGluAlaLeu-----LeuSerAspLeuPhe	151
Db	5995	ACTGTTCTATCTCTGCTTGTGAGTAACTTGTATATACGAACCTGCAATTTCTTTT	5936
Qy	152	ArgAspPro-----AspHisCysArgGlnAlaThrSerValTrpAlaPheMet	167
Db	5935	CTGCTCCCACTGCCATTTTCAGATCACTGCGCTGATCTCTACCCGGTATCGCT-----	5892
Qy	168	IleSerLeuGlyGlyCysLeuGly-TyrLeuLeuProAlaIleAspTrpAspThrSerAl	187
Db	5881	GTTTCTTTTCTGGCGCTGAAGCTCTTCTCTCTCCCGATATGCTCTCCAGCTCTCTGGC	5822
Qy	187	A-----LeuAlaProThrLeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLe	205
Db	5821	GCCTTCTCTTCCCGTCTCTC-----TCTCAGCAGCTGCTCTCTCTCTCCGCTCGACCT	5768
Qy	205	uilePheLeuThrCysValAlaAlaThrLeuLeu-----ValAl	218
Db	5767	CTCTTCTCCCGACATTTGCTCTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	5708
Qy	218	aGluAlaAlaLeuGlyPro-----ThrGluProAl	229
Db	5707	TCAGCA-GCTGCT	5649

RESULT 38
US-09-199-737-3
; Sequence 3, Application US/09199737A
; Patent No. 6287788
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Borowsky, Beth
; APPLICANT: Smith, Kelli E.
; APPLICANT: Branchek, Theresa A.

```

; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; TITLE OF INVENTION: DNA Encoding Galanin GALR3 Receptors And Uses Thereof
; FILE REFERENCE: 52241-D-PCT-US
; CURRENT APPLICATION NUMBER: US/09/199,737A
; CURRENT FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin Ver. 2.0 - beta
; SEQ ID NO 3
; LENGTH: 1417
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-199-737-3

Alignment Scores:
Pred. No.: 0.00618 Length: 1417
Score: 128.50 Matches: 115
Percent Similarity: 29.53% Conservative: 43
Best Local Similarity: 21.50% Mismatches: 178
Query Match: 4.49% Indels: 199
DB: 4 Gaps: 21

US-09-593-793A-113 (1-553) x US-09-199-737-3 (1-1417)

QY 66 ValCysValProLeuLeu-----GlySerAlaSerAspHisTrp---ArgGly 80
DB 20 CTCTGCTCTCCCGCTCCATCTCCACAGAGCTTCAGCCCAACACACCTGGCCAGACCC 79
QY 81 ArgTyrGlyArg-----ArgArgProPheIleTrpAlaLeuSerLeuGly 95
DB 80 AGGTGGGGGAGTTAGTCCCGGGTCAAGCAACAGAACTGGGGCTCTTCCTGTAGGA 139
QY 96 Ile-----LeuLeuSerLeuPheLeuIleProArgAla--- 106
DB 140 TTCCAGCTTCTCTCCAGGTGCGCTCTGTATGGGAGATGCTGTATGCCCAACAATTT 199
QY 106 ----- 106
DB 200 CACTGGACAGCCAGGAGTGTGGGGCGGTGGCAGTGCCTGTGTCTTGGCCCTAAATCT 259
QY 107 -----GlyTrp---LeuAlaGlyLeuLeuCysProAspProA 118
DB 260 TCCTGCTGGGCACAGTGGCAATGGGTGCTGCTGAGTGTCTCTGAGCCTGGCCCGA 319
QY 118 rgProLeuGlu-----LeuAlaLeuLeuIleLeuGlyValGlyLeuLeuA 133
DB 320 GTGCTGGCAGGAGCTGGCAGCACACAGGACCTGTTCATCTCAACCTGGCGGTGGCTG 379
QY 133 spPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgA 153
DB 380 ACCTCTGCTTCATCTGTGCTGCTGCTGCTGCTTCCAGGCCACCATC----- 423
QY 153 spProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyC 173
DB 423 ----- 423
QY 173 ysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuG 193
DB 424 -----TACACGTGGATGCC-----TGG----- 441
QY 193 lyThrGlnGluCysLeuPheGlyLeuLeuThr-----LeuIleP 207
DB 442 -----CTCTTTGGGGCCCTGCTGCAAGCCCGTGCACCTGCTCATCT 484
QY 207 heLeuThrCysValAlaAlaThrLeuValAlaGluAlaLeuGlyProThrG 227
DB 485 ACCTCACCATGTACGCCACGACCTTTACG----- 513
QY 227 luProAlaGluGlyLeuSerAlaProSerProHisCysCysProCysArgAlaA 247
DB 514 -----CTGGCTGCTGCTCCGTGGACAGGTAC----- 540
QY 247 rgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgM 267
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```

DB 541 --CTGGCGGTGGG----- 111 111 111 111 111 111 111 111 111 111
QY 267 etProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetT 287
DB 572 CCTGGGCACGGCGGTACGCGCGGCGAGTGGGGCTGGTGGCTGGCTGGCGGGCCG 631
QY 287 hrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgA 307
DB 632 TCTTCTGGCGGCGCTTACCTACCTACGTACGCGACCGTGGCTACGCGGCGCTGGAGCTCT 691
QY 307 laGluProGlyThrGluAlaArgArgHisTyrAspGluGlyValArgMetGlySerLeuG 327
DB 692 GCGTCCCGCGCTGGGAGGACGCGCGCGCGCGCTGGACGTGGCCACCTTCGTGGCGG 751
QY 327 lyLeuPheLeuGlnCysAla---IleSerLeuValPheSerLeuValMetAspArgLeuV 346
DB 752 GCTACTGCTGCGCGTGGCTGTGGTGGAGCTGGCTGGCGGCGGAGGCTGGCTTCTCTGT 811
QY 346 alGlnArgPheGly-----ThrArgAlaValTyrL 356
DB 812 GGGCGCGCGTGGTCCCGCGGCGCGGCGGCGGAGCGCGGCGGAGGCGGCGACGCGGC 871
QY 356 euAlaSerValAlaAlaPheProValAlaAla----- 366
DB 872 GCGCGGGCGCGCCATGCTGGCGGTGGCGCGCTCTACGCGCTCTGCTGGGGTCCGCACC 931
QY 367 -----GlyAlaThrCysLeuSerHisSerValAlaValV 378
DB 932 AGCGCTCATCTCTGCTTCTGGTACGGCGGCTTCGCCTTCAGCCCGGCGCACCTAGCGCT 991
QY 378 alThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrT 398
DB 992 GCGCGCTGGCGCTCACACTGCCTGGCGCTAGCGCAACTCCTGCTCAACCGCGCTCGTACG 1051
QY 398 hrLeuAlaSerLeuTyr----- 403
DB 1052 CGCTCGCTCGCGCCACTTCCGCGCGCGCTTCCGCGCGCTGTGGCGGTGGCGCGCGCGAC 1111
QY 404 -----HisArgGlnLysGlnValPheLeuProLysTyrArg----- 415
DB 1112 GCGCGCACCGTCCCGCGCGCGCGC---TTGCGTGGCGTGGCGCGCGCTCTCGGGCCAC 1168
QY 416 --GlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyP 435
DB 1169 CGCGTCCCGGAGAGCGCGCGCTAGCGGAGGTGTGCTGTGGTGGCGGCGCGCGCC 1228
QY 435 roLysPro---GlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuL 454
DB 1229 CGAGGCCCGAGGAGGACCCCTCCACGCGGAGAGGCTGCCCGAGGACCGGAATAACCC 1288
QY 454 euProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValV 474
DB 1289 TGCCCGCTGGACTCCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1335
QY 474 alGlyGluProThrGluAlaArgValValProGlyArgGly 487
DB 1336 -----GAAGCGGGGACGCCACCGCGGCGGAGG 1362

RESULT 39
US-09-058-333A-3
; Sequence 3, Application US/09058333A
; Patent No. 6368812
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A
; APPLICANT: Borowsky, Beth
; TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
```

CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058.333A

Alignment Scores:	
Pred. No.:	0.00618
Score:	128.50
Percent Similarity:	29.53%
Best Local Similarity:	21.50%
Query Match:	4.49%
DB:	4
Length:	1417
Matches:	115
Conservative:	43
Mismatches:	178
Indels:	199
Gaps:	21

US-09-593-793A-113 (1-553) x US-09-058-333A-3 (1-1417)

QY	66	ValCysValProLeuLeu	-----GlySerAlaSerAspHisTrp----	ArgGly 80
		:::		:::
Db	20	CTCTGTCTCCCTCCTCCATCTCCACGAGCTTCAGCCGACCAACACCTGGCCAGACC	79	
QY	81	ArgTyrGlyArg	-----ArgArgProPheIleTrpAlaLeuSerLeuGly 95	
			:::	:::
Db	80	AGTCGGGGAGTTAGATCCCGGGGTCAGCAACCAAGACTGGGGGCTCTTGCTCAGGA	139	
QY	96	Ile	-----LeuLeuSerLeuPheLeuIleProArgAla----	106
		:::		:::
Db	140	TTCCAGCTTCTTCCAGGTGCCCTCTGATGGGAGATGGCTGATGCCAGAACATTT	199	
QY	106	-----	-----	-----106
Db	200	CACGTGACAGCCAGGAGTGTGGGGGCGGTGGCACTGGCTGTGGTCTTTGGCCCTAATCT	259	
QY	107	-----	-----GlyTrp--LeuAlaGlyLeuLeuCysProAspProA	118
Db	260	TCCTGTGGGCACAGTGGGCAATGGGCTGTGTGTGGCAGTGTCTCTGCAGCCTGGCCCGA	319	
QY	118	rgProLeuGlu	-----LeuAlaLeuLeuIleLeuGlyValGlyLeuLeuA	133
		:::		:::
Db	320	GTCCCTGGCAGGAGCCTGGCAGCACACGACACCTGTTTCATCCTCAACCTGGCGGTGGCTG	379	
QY	133	spPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgA	153	
Db	380	ACCTCTGCTTCATCCTGTGCTGCTGCCCTTCCAGGCCACCATC	-----	423
QY	153	spProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyC	173	
Db	423	-----	-----	-----423

QY 474 aIGlyGluProThrGluAlaArgValValProGlyArgGly 487
Db 1336 -----GAAGCGGACGCCACCGCGGCGGGA 1362

RESULT 40

US-09-453-702B-197
; Sequence 197, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Nicole T.
; Plunkett, Guy
; Welch, Rod

; TITLE OF INVENTION: No. 6365723e1 Sequences of E. coli 0157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-Dec-1998

; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 197:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4021
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 197:

US-09-453-702B-197

Alignment Scores:
Pred. No.: 0.0464 Length: 4021
Score: 126.50 Matches: 102
Percent Similarity: 33.00% Conservative: 61
Best Local Similarity: 20.65% Mismatches: 153
Query Match: 4.42% Indels: 178
DB: 4 Gaps: 26

US-09-593-793a-113 (1-553) x US-09-453-702B-197 (1-4021)

QY 19 LeuLeuValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGlyIleThrTyr 38
Db 1057 CTGATCATGAATTTCTACCTTT----- 1080
QY 39 ValProProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGly 58
Db 1081 -----TTCTACACCGACGTTTTTGA 1101
QY 59 IleGlyPro-----ValLeuGlyLeuValCys 67
Db 1102 TTAACCTCCGCGCTGGTTGGCACGCTGTTATTGCACTCGCGCTGTTGATGCCATCTCC 1161

QY 68 ValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgPro 87
Db 1162 GACCCGGTGATGGCGTCATTGCCGACCGAGCAAAAGCCGATGGGGCGCTTCCTCGTCG 1221
QY 88 Phe-----IleTrp---AlaLeuSerLeuGlyIleLeu---LeuSerLeuPheLeuLeuPro 104
Db 1222 TGGCAGCTATGGATTGCCATTCCTCCATTCGCGATATCGCATTCACGCTTCAACCGTGC 1281
QY 105 ArgAla-----GlyTrpLeuAlaGlyLeuLeuCysProAspProArg 118
Db 1282 GATCCAGCATGGGAGTAAATCGCTGGCGTTCGGT----- 1320
QY 119 ProLeuGluLeuAlaLeuLeuLeuGlyValGlyLeu-----LeuAspPhe 134
Db 1321 -----ACTTACCTGCTCTTTCAGTCGCTTATACCGCCATCAACGATACGCTAC 1368
QY 135 CysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspPro 154
Db 1369 TCGCGCGGATC-----AACACCATGACCCACCGCCACCAATGAAGTG 1410
QY 155 AspHisCysArgGln-----AlaTyrSerValTyrAlaPheMetIleSerLeu 170
Db 1411 ATCTCTGCCAGTCTCGCGGATTCGTTCTCTCGGGGTAGCGGGATTCTGGTTTCGGTA 1470
QY 171 GlyGlyCysLeuGlyTyrTrpLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaPro 190
Db 1471 GGC-----TTACCGTGGATGGTCTCTTCGGTCAGGCAACGCTGCACGCGCTAT 1524
QY 191 TyrLeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuLeuPheLeuThrCys 210
Db 1525 CAACCTGGCGTCGGGTATTTGTC-----GCCATTGCGCTGGTGTATGTTCTGTCTGT 1578
QY 211 ValAlaAlaThrLeuLeuValAlaGluAlaLeuGlyProThrGluProAlaGlu 230
Db 1579 TTC-----TTCGTGGGTTCTGTAACGGGTG-----CCGCTCTCC 1611
QY 231 GlyLeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPhe 250
Db 1612 ACAATGGGGAATTTACCTCGCGCAACATCTTGC-----GGCGTG 1653
QY 251 ArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThr 270
Db 1654 CGGAACAACGACCACTGCTG----- 1674
QY 271 LeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeu 290
Db 1675 -----CTGATGCTGCTCATGTCTTCTCTGCTG 1701
QY 291 PheTyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGly 310
Db 1702 ATTAACGCTCTTTAACATTCGCGCGGTGGGTATATG----- 1737
QY 311 ThrGluAlaArgArgHisTyrAspGluGlyValArgMetGlySerLeuGly----- 327
Db 1738 -----TACTTCAATACCTACGCTCTTACAGAGCAGCAGCGGTACACGTCG 1782
QY 328 LeuPheLeuGlnCysAla-----IleSerLeuValPheSerLeuValMetAspArgLeu 345
Db 1783 CTGTCTTTCACCATGGTTCACCTTCGCTCCATTCGCTCGGTGATGTCAGCCCGTTA 1842
QY 346 ValGlnArgPheGlyThrArgAlaValTyr-----LeuAlaSerVal 359
Db 1843 ACGCGCGGTTTCGATACCGTCAAAATTTATTACTACCAACCACTGCTCTCTCGCTCACG 1902
QY 360 AlaAlaPhePro-----ValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal 377
Db 1903 GCGGTGTTGATGGTTCCTGCCCTCCGCGCGGTATTAACAACGCTGTGGTGGCGGTG 1962
QY 378 ValThrAlaSerAlaAlaLeuThrGlyPheThrPheSer-----AlaLeuGlnIle 394
Db 1963 ATCTCTGGTAAATGGCGTGATTTCTGGCTTCACATTCGCCACTGCACCTTCTCAITGATG 2022

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Qy 395 -LeuProTyThrLeuAlaSerLeuTyrrHisArgGluLysGlnValPheLeuProLysTy 414
      ||||| ||| |||||
Db 2023 TTTCGGCATGACTACGCGGAGT----- 2044
Qy 414 rArgGlyAspThrGlyClyAlaSerSerGluAspSerLeuMetThrSerPheLeuProG1 434
      ||||| ||| |||||
Db 2045 -----GGAAACCACGATGTTCTTCGCGC 2070
Qy 434 y---ProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLe 453
      ||| ||| :|||
Db 2071 ATGAACATCGCCCTCAATCGTTTTCATCATCAGCTGGCTGGG----- 2113
Qy 453 uLeuProProProAlaLeuCysGlyAlaSerAlaCys 466
      ||||| ||| |||:|||||||
Db 2114 ----CCTCCAGCGCG-----GGATCATCAGCCTGC 2140

RESULT 41
US-08-494-907-13/c
; Sequence 13, Application US/08494907
; Patent No. 5955298
; GENERAL INFORMATION:
; APPLICANT: Thomasow, Linda S
; APPLICANT: Bangera, Mahalaxmi
; APPLICANT: Weller, David M
; APPLICANT: Cook, R. James
; TITLE OF INVENTION: Sequences for Production of
; 2,4-Diacetylphloroglucinol and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Margaret A. Connor, USDA-ARS
; STREET: 800 Buchanan Street
; CITY: Albany
; STATE: CA
; COUNTRY: USA
; ZIP: 94710
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,907
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Connor, Margaret A
; REGISTRATION NUMBER: 30043
; REFERENCE/DOCKET NUMBER: 0009.95
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 559-6067
; TELEFAX: (510) 559-5777
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1269 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Pseudomonas fluorescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (1..1269)
; OTHER INFORMATION: /note= "pHLe DNA sequence. SEQ ID
; OTHER INFORMATION: NO:14 is translation (protein) of SEQ ID NO:13."
US-08-494-907-13

Alignment Scores:
Pred. No.: 0.0176 Length: 1259
Score: 123.00 Matches: 84
Percent Similarity: 41.33% Conservative: 40

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5076 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Pseudomonas fluorescens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: complement (4285..5076)
; OTHER INFORMATION: /note= "phlA, transcribed from
; OTHER INFORMATION: right to left"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: complement (2606..3313)
; OTHER INFORMATION: /note= "phlB, transcribed from
; OTHER INFORMATION: right to left"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: complement (3085..4251)
; OTHER INFORMATION: /note= "phlC, transcribed from
; OTHER INFORMATION: right to left"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: complement (1398..2444)
; OTHER INFORMATION: /note= "phlD, transcribed from
; OTHER INFORMATION: right to left"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3514..4767
; OTHER INFORMATION: /note= "phlR, transcribed from left
; OTHER INFORMATION: to right"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: complement (2..1270)
; OTHER INFORMATION: /note= "phlE, transcribed from
; OTHER INFORMATION: right to left"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..5076
; OTHER INFORMATION: /note= "SEQ ID NO:2 contains genes
; OTHER INFORMATION: involved in synthesis, activity, and/or export of
; OTHER INFORMATION: Phl."
US-08-494-907-2
Alignment Scores:
Pred. No.: 0.143 Length: 5076
Score: 123.00 Matches: 84
Percent Similarity: 41.33% Conservative: 40
Best Local Similarity: 28.00% Mismatches: 124
Query Match: 4.30% Indels: 52
DB: 2 Gaps: 12
US-09-593-793A-113 (1-553) x US-08-494-907-2 (1-5076)
QY 269 ArgThrLeuArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPhe 288
:::||||| ||| ||||| ||||| ||||| |||||
Db 1226 AAGACCGATGGTCTTTGTTCGCTGAGCTT-----CGGGCTGTAGGACTTGA 1176
QY 289 ThrLeuPheThrAspPheVal---GlyGluGlyLeuTyrglnGlyValProArgAla 307
::::: ||| ||| ||||| ||||| ||||| |||||
Db 1175 TCAATCATATCATGCCGTGTTCGCCGGTGATCATGCATGACCTGGCCCTGGACTATFCA 1116
QY 308 GluProGlyThrGluAlaArgArghisTyraSpGlyValArgMetGlyserLeuGly 327
||||| ||||| ||||| ||||| ||||| |||||
Db 1115 GGACCTGGCCCTGTTATCGC-----GATCCTGGCATTTGCCCTGGGAGGCTCGGC 1065
QY 328 -LeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGl 347
||||| ||||| ||||| ||||| ||||| |||||

```

TELECOMMUNICATION INFORMATION:

TELEPHONE: (813) 289-2966

TELEFAX: (813) 289-2967

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 5076 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Pseudomonas fluorescens

FEATURE:

NAME/KEY: misc_feature

LOCATION: complement (4285..5076)

OTHER INFORMATION: /note="phlA, transcribed from

OTHER INFORMATION: right to left"

FEATURE:

NAME/KEY: misc_feature

LOCATION: complement (2606..3313)

OTHER INFORMATION: /note="phlB, transcribed from

OTHER INFORMATION: right to left"

FEATURE:

NAME/KEY: misc_feature

LOCATION: complement (3085..4251)

OTHER INFORMATION: /note="phlC, transcribed from

OTHER INFORMATION: right to left"

FEATURE:

NAME/KEY: misc_feature

LOCATION: complement (1398..2444)

OTHER INFORMATION: /note="phlD, transcribed from

OTHER INFORMATION: right to left"

FEATURE:

NAME/KEY: misc_feature

LOCATION: 3514..4767

OTHER INFORMATION: /note="phlR, transcribed from left

OTHER INFORMATION: to right"

FEATURE:

NAME/KEY: misc_feature

LOCATION: complement (2..1270)

OTHER INFORMATION: /note="phlE, transcribed from

OTHER INFORMATION: right to left"

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..5076

OTHER INFORMATION: /note="SEQ ID NO:2 contains genes

OTHER INFORMATION: Involved in synthesis, activity, and/or export of

OTHER INFORMATION: Phl"

PCT-US96-10986-2

Alignment Scores:

Pred. No.:	0.143	Length:	5076
Score:	123.00	Matches:	84
Percent Similarity:	41.3%	Conservative:	40
Best Local Similarity:	28.00%	Mismatches:	124
Query Match:	4.30%	Indels:	52
DB:	5	Gaps:	12

US-09-593-793A-113 (1-553) x PCT-US96-10986-2 (1-5076)

QY	269	ArgThrLeuArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPhe	288
Db	1226	AAGACCCATGGTCGTTCTTTTCGCTGAGCTT-----CGGCTGCTAGGACTTCA	1176
QY	289	ThrLeuPheTyrThrAspPheVal---GlyGluGlyLeuTyrGlnGlyValProArgAla	307
Db	1175	TGGATTATTATCATGCCCGTTGTTCCCGGTGATCATGACCTGGCCCTGGACTATCA	1116
QY	308	GluProGlyThrGluAlaArgHisTyrAspGluGlyValArgMetGlySerLeuGly	327
Db	1115	GGACCTGGGCGCTGTTATCGGC-----GATCCTGGCATTTGCTGGGGAGGCTCGGC	1065

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,907
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connor, Margaret A
REGISTRATION NUMBER: 30043
REFERENCE/DOCKET NUMBER: 0009.95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 559-6067
TELEFAX: (510) 559-5777
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6170 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Pseudomonas fluorescens
FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (4285..5076)
OTHER INFORMATION: /note= "pHIA, transcribed from
OTHER INFORMATION: right to left"
FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (2606..3313)
OTHER INFORMATION: /note= "pHIB, transcribed from
OTHER INFORMATION: right to left"
FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (3085..4251)
OTHER INFORMATION: /note= "pHIC, transcribed from
OTHER INFORMATION: right to left"
FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (1398..2444)
OTHER INFORMATION: /note= "pHID, transcribed from
OTHER INFORMATION: right to left"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3514..4767
OTHER INFORMATION: /note= "pHIE, transcribed from
OTHER INFORMATION: left to right"
FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (2..1270)
OTHER INFORMATION: /note= "pHIF, transcribed from
OTHER INFORMATION: right to left"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 5781..6170
OTHER INFORMATION: /note= "pHIF, truncated,
OTHER INFORMATION: transcribed from left to right"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..6170
OTHER INFORMATION: /note= "SEQ ID NO:4 contains genes
OTHER INFORMATION: involved in synthesis, and modulation of synthesis
of PhI."
US-08-494-907-4

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Alignment Scores:
Pred. No.: 0.192 Length: 6170
Score: 123.00 Matches: 84
Percent Similarity: 41.33% Conservative: 40
Best Local Similarity: 28.00% Mismatches: 124
Query Match: 4.30% Indels: 52
DB: 2 Gaps: 12

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US-09-593-793A-113 (1-553) x US-08-494-907-4 (1-6170)
QY 269 ArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPhe 288
Db 1226 AAGACGCATGTCGTTCTTTTGTCTGCTGAGCTT-----CGGCTGGTAGGACTGCA 1176
QY 289 ThrLeuPheTyrThrAspPheVal---GlyGluGlyLeuTyrGlnGlyValProArgala 307
Db 1175 TCGATTTCATTATATCGCGCTTGTCCCGGTGATCATGTACCTGGTATCGCTCTCGCATCA 1116
QY 308 GluProGlyThrGluAlaArgHisTyrAspGluGlyValArgMetClySerLeuGly 327
Db 1115 GGACCTGGGCGCTGTTATCGGC-----GATCTGGCATTTGCTGGGAGGCTCGGC 1065
QY 328 -LeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGl 347
Db 11064 CCTCTTCATGGCGCTTGCTATC-----AG 1041
QY 347 nArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaPheProValAlaAlaGl 367
Db 1040 GCGATTGGGCACCAAGCAACTGCTGCTTTCGATTACCTTGGTATCGCTCTCGCCGG 981
QY 367 yAlaThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPh 387
Db 980 CGCATCTGCTGTTGATCTCAAGCCTTATGGGCGCTGCTCTCGCGCGCTTGTGGGAT 921
QY 387 eThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLy 407
Db 920 CTGCGAAGCGCC-----FTCACCCCGGTCACGATCATGTGCCGAT--- 878
QY 407 sGlnValPheLeuProLysTyrArg-GlyAspThrGlyGlyAlaSerSerGluAspSerL 427
Db 877 -GAAGTTTCGCGAGCGTGCAGCGCGGCTCAACC--TGGGCATCCAGCAGCAGCTGTT 822
QY 427 eumethThrSerPhe-LeuProGlyProLysProGly----- 438
Db 821 TCCCATCATCGCGCTGCTGCTGGGCGCGCTGCTGGGCGCGCTGTTGTTGAAATGTTCCG 762
QY 439 -----AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGly----- 452
Db 761 ATCGTGGCGCGCGCTGTTGCGCATCATCTCTGTTGCGGCGCTGCTGGTGGCTGTATCT 702
QY 453 -----LeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerVal 470
Db 701 GTATCGAACTTACCAACCGAGCGCGCCCATCCAGGCGCTCGTAGAACCTCCCG 642
QY 471 ArgValValValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeu 490
Db 641 CAGCCAATGGCGAACAGCCCTGTCCAGCGGCAACGTGGCGCTCAACAT-----TGCCTT 588
QY 491 Asp-LeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMe 510
Db 587 GATGCTATGCATPACTGACGTGCCAATTCCTCTGTGCGCCCTGCTCCCGAGC---TACTT 531
QY 510 tGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLe 530
Db 530 GACAGCGCTGTGCACCTGAGCAATTTCTCCATGCCCATGATCATCTCCGCGATCGGCT 471
QY 530 uGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAsp 547
Db 470 GGGT-----GGTTTTTTCGGCCAGCTGCTCATTCGCGGTTTGTCTGAC 428

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Search completed: February 19, 2003, 05:11:16
Job time : 147 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 03:53:29 ; Search time 232 seconds
(without alignments)
1214.034 Million cell updates/sec

Title: US-09-593-793A-113

Perfect score: 2861

Sequence: 1 MVQRLWVSRLLHRKAQLL.....AIYFATQVVFDSKLAKYSA 553

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 424239 seqs, 254661826 residues

Total number of hits satisfying chosen parameters: 848478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

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-O=/cgn2_1/USPRO_pool/US09593793/runat_13022003_161309_21611/app_query.fasta_1.711
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPLC=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=45 -MODE=LOCAL -OUTFMT=PL0 -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09593793 @CGN1.1.30 @runat_13022003_161309_21611
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications_NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2861	100.0	3320	10	US-09-838-785-1
2	2861	100.0	3410	9	US-09-232-880-110
3	2861	100.0	3410	9	US-10-012-896-110
4	2861	100.0	3410	9	US-09-895-793-110

5	2861	100.0	3410	9	US-09-895-814-110	Sequence 110, App
6	2861	100.0	3410	10	US-09-745-288-100	Sequence 100, App
7	2861	100.0	3410	10	US-09-759-143-110	Sequence 110, App
8	2861	100.0	3410	10	US-09-780-669-110	Sequence 110, App
9	2861	100.0	3410	10	US-09-030-606-110	Sequence 110, App
10	2861	100.0	3410	10	US-09-822-827-110	Sequence 110, App
11	2861	100.0	3410	10	US-09-115-453-110	Sequence 110, App
12	2716.5	94.9	4034	9	US-10-012-896-704	Sequence 704, App
13	2716.5	94.9	4034	9	US-09-895-793-704	Sequence 704, App
14	2716.5	94.9	4034	9	US-09-895-814-704	Sequence 704, App
15	2716.5	94.9	4034	10	US-09-759-143-704	Sequence 704, App
16	2716.5	94.9	4034	10	US-09-780-669-704	Sequence 704, App
17	2716.5	94.9	4034	10	US-09-822-827-704	Sequence 704, App
18	2538.5	88.7	4894	9	US-10-012-896-702	Sequence 702, App
19	2538.5	88.7	4894	9	US-09-895-793-702	Sequence 702, App
20	2538.5	88.7	4894	9	US-09-895-814-702	Sequence 702, App
21	2538.5	88.7	4894	10	US-09-759-143-702	Sequence 702, App
22	2538.5	88.7	4894	10	US-09-780-669-702	Sequence 702, App
23	2538.5	88.7	4894	10	US-09-822-827-702	Sequence 702, App
24	2144	74.9	6976	9	US-10-012-896-705	Sequence 705, App
25	2144	74.9	6976	9	US-09-895-793-705	Sequence 705, App
26	2144	74.9	6976	9	US-09-895-814-705	Sequence 705, App
27	2144	74.9	6976	10	US-09-759-143-705	Sequence 705, App
28	2144	74.9	6976	10	US-09-780-669-705	Sequence 705, App
29	2144	74.9	6976	10	US-09-822-827-705	Sequence 705, App
30	1920.5	67.1	2904	9	US-10-012-896-703	Sequence 703, App
31	1920.5	67.1	2904	9	US-09-895-793-703	Sequence 703, App
32	1920.5	67.1	2904	9	US-09-895-814-703	Sequence 703, App
33	1920.5	67.1	2904	10	US-09-759-143-703	Sequence 703, App
34	1920.5	67.1	2904	10	US-09-780-669-703	Sequence 703, App
35	1920.5	67.1	2904	10	US-09-822-827-703	Sequence 703, App
36	1403.5	49.1	1203	9	US-10-012-896-851	Sequence 851, App
37	1403.5	49.1	1203	9	US-09-895-793-851	Sequence 851, App
38	1403.5	49.1	1203	9	US-09-895-814-851	Sequence 851, App
39	1403.5	49.1	1203	10	US-09-759-143-851	Sequence 851, App
40	1403.5	49.1	1203	10	US-09-780-669-851	Sequence 851, App
41	1403.5	49.1	1203	10	US-09-822-827-851	Sequence 851, App
42	947	33.1	1065	9	US-10-012-896-1010	Sequence 1010, App
43	919	32.1	789	9	US-09-232-880-10	Sequence 10, Appl
44	919	32.1	789	9	US-09-895-814-10	Sequence 10, Appl
45	919	32.1	789	9	US-10-012-896-10	Sequence 10, Appl
46	919	32.1	789	9	US-09-895-793-10	Sequence 10, Appl
47	919	32.1	789	10	US-09-759-143-10	Sequence 10, Appl
48	919	32.1	789	10	US-09-780-669-10	Sequence 10, Appl
49	919	32.1	789	10	US-09-030-606-10	Sequence 10, Appl
50	919	32.1	789	10	US-09-822-827-10	Sequence 10, Appl
51	919	32.1	789	10	US-09-115-453-10	Sequence 10, Appl
52	328.5	11.5	1785	9	US-09-938-842A-1709	Sequence 1709, App
53	323.5	11.3	1539	9	US-09-938-842A-1316	Sequence 1316, App
54	279.5	9.8	1542	9	US-09-938-842A-1624	Sequence 1624, App
55	153.5	5.4	540	10	US-09-864-761-7951	Sequence 7951, App
56	144.5	5.1	1715	10	US-09-919-781-3	Sequence 3, Appli
57	144.5	5.1	1917	10	US-09-919-781-1	Sequence 1, Appli
58	138	4.8	15231	10	US-09-917-800A-1505	Sequence 1505, App
59	132	4.6	16433	10	US-09-995-542-1	Sequence 1, Appli
60	128.5	4.5	1417	9	US-10-007-132-3	Sequence 3, Appli
61	127.5	4.5	1857	10	US-09-970-516-3	Sequence 3, Appli
62	127.5	4.5	2380	10	US-09-817-676A-13	Sequence 13, Appl
63	126.5	4.4	4021	9	US-10-114-170-197	Sequence 197, App
64	125.5	4.4	11575	10	US-09-938-956-5	Sequence 5, Appli
65	125	4.4	469	10	US-09-770-444-232	Sequence 232, App
66	121	4.2	1176	10	US-09-815-242-7814	Sequence 7814, App
67	120.5	4.2	1758	10	US-09-880-107-2157	Sequence 2157, App
68	120	4.2	7563	10	US-09-776-167A-5	Sequence 5, Appli
69	120	4.2	8750	10	US-09-776-167A-8	Sequence 8, Appli
70	119.5	4.2	53522	9	US-09-904-968A-1	Sequence 1, Appli
71	119	4.2	7469	10	US-09-776-167A-6	Sequence 6, Appli
72	119	4.2	7771	9	US-09-832-292-38	Sequence 38, Appl
73	119	4.2	14800	10	US-09-954-456-1601	Sequence 1601, App
74	118.5	4.1	4030	9	US-09-930-046-1	Sequence 1, Appli
75	118	4.1	1830	9	US-09-978-295A-419	Sequence 419, App
76	118	4.1	1830	9	US-09-978-697-419	Sequence 110, App
77	118	4.1	1830	9	US-09-978-192A-419	Sequence 419, App


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QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
|||||
Db 1482 TCCTCTACCCAGGAGAGAGAGGTGTTCTTCCCTGCCCAATACCGAGGGACACTGGAGT 1541
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
|||||
Db 1542 GCTAGCAGTGGAGACAGCTGTATGACAGCTTCCCTGCCAGGCCCTAAGCCTGGAGCTCC 1601
QY 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
|||||
Db 1602 TTCCTTAATGGACAGTGGGTGCTGGAGCAGTGGCTGCTCCACCTCCACCCGGGCHC 1661
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValValValValValValVal 480
|||||
Db 1662 TCGGGGGCTGCTGCTGTATGCTCCGTACGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1721
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
|||||
Db 1722 AGGGTGGTTCCGGGGCGGGGACATCTGCCTGGACCTCGCCATCTGGATAGTGCCTTCCTG 1781
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
|||||
Db 1782 CTGTCCCAAGTGGCCCCATCCCTGTTATGGGCTCCATGTTCCAGTCCAGCTCAGCCAGTGTGC 1841
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
|||||
Db 1842 ACTGCCATATATGTTGTCGCCGAGCCCTGGGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 1901
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||
Db 1902 GTAGTATTGTACAAGAGCAGTGTGCCCAATATCTCAGCG 1940

RESULT 2
US-09-232-880-110
; Sequence 110, Application US/09232880
; Publication No. US20020182596A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianqichun
; APPLICANT: Dillon, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C6
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-880-110

Alignment Scores:
Pred. No.: 1.44e-259 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-232-880-110 (1-3410)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
|||||
Db 284 ATGGTCCAGAGCTGTGGGTGAGCCGCTGCTGGCGCACCGGAAAGCCAGCTCTTGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGlyIleThrTyrValPro 40
|||||
Db 344 GTCACACTGTCTAACCTTTGGGCTGGAGGTGTGTTGGCGCGAGGCATCACCTATGTGGCG 403
QY 41 ProLeuLeuLeuGluValClyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
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Db 404 CCTCTGCTCTGGAGTGGGGGTAGAGGAGAAGTTTCATGACCATGCTGCTGGCGATTGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
|||||
Db 464 CCAGTGTCTGGGCTGTGTGTCTCCGCTCTCCTAGGCTCAGCCAGTACACACTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
|||||
Db 524 CGCTATGGCCGCCGCCCTTCATCTGGGCACTGCTCTTGGGCATCCTGCTGAGCCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
|||||
Db 584 TTTCTCATCCCAAGGCCCGGCTGGTGTAGCAGGCTCTGTGCTGCCGATCCAGGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
|||||
Db 644 GAGCTGGGCACTGCTCATCTGGGCTGGGCTGCTGGACCTTCTGTGGCCAGGTGTGCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
|||||
Db 704 ACTCCACTGGAGGCCCTGCTCTCATCCTCTTCCGGGACCCGACCACTGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
|||||
Db 764 TACTCTGTCTATGCTCATGATCATGCTTGGGGCTGCTGGGCTACCTCTCTGCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
|||||
Db 824 ATTGACTGGACACAGTGCCTTGCCCTTACCTGGGACCCAGGAGAGTGTCTCTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
|||||
Db 884 GGCCTGCTCACCTCATCTTCTCACCTGGGTAGCAGCCACACTGCTGGTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
|||||
Db 944 GCAGCGCTGGGCCCCACCGCAGCAGAGAGGCTGTGGGCCCTTCTGGCGGCTGCTGCTG 1003
QY 241 CysCysProCysArgAlaAlaLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArg 260
|||||
Db 1004 TGCTGTCCATGCGGGGCGGCTTGGCTTTCCGGAACCTTGGGGCGGCTGCTTCCCCGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
|||||
Db 1064 CACCACTGTGCTGCGCATGCCCGCAGCCCTGCGCGGCTCTTCTGGTGGCTGAGTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
|||||
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACAGGGATTTCTGGGGGAGGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
|||||
Db 1184 TACCAGGGCGTGGCCAGAGCTGAGCCGGGACCCGAGGGCCGAGAGACATATGATGAAGGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
|||||
Db 1244 GTTGGATGGGAGCGCTGGGCTGTCTCTGAGTGGCGCATCTCCCTGGTCTTCTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
|||||
Db 1304 GTCATGGACCGGCTGGTGCAGCATTCGCACTCTGAGCAGTCTATTGCGCAGTGTGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValIleThrAla 380
|||||
Db 1364 GCTTTCCCTGTGGCTGGCGGTGCCACATGCTGTGCCACAGTGTGGCGCTGGTGCAGACT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
|||||
Db 1424 TCAGCGCGGCTTCACCGGTTTCACTTCTCAGCCCTGAGATCTCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
|||||
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Db 1484 TCCTCTACACCGGAGAGAGGTGGTTCCTCCCAATACCGAGGGGACACTGGAGGT 1543
QY 421 AlaserSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGAGACAGCCTGATGACAGCTTCTGCCAGGCCCTAAGCCTGAGCTCC 1603
QY 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCTTAATGGACACGTGGGTGCTGGAGGCGAGTGGCTGCTCCACCTCCACCGCGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TCGGGGCCCTCTCCCTGTGATGTCTCCGTACGTGTGGTGGGTGAGCCACCGAGGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGGTGTTCGGGGCCGGGCATCTGCCTGGACCTCGCCATCTCGGATAGTGCCTTCCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCCCATCCCTGTATTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCCATATGTGTCTGCCGAGGCCCTGGGTCTGGTCCCATTTACTTTGCTACACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTTGACAGAGCGACTTGGCCAAATACTACAGG 1942

RESULT 3

US-10-012-896-110
; Sequence 110, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-110

Alignment Scores:

Pred. No.: 1.44e-259 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-593-793A-113 (1-553) x US-10-012-896-110 (1-3410)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 284 ATGGTCCAGAGGCTGGGGTGAGCCCTGCTGGGCACCCGGAAGCCAGCTCTTGTGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTCTTAACCTTTGGCCTGGAGGTGTGTTGGCCGAGGCATCACCTATGTGCGG 403
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGAAAGTGGGGGTAGAGAGAAAGTTTCATGACCATGCTGTGGGCATP 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CAGAGTCTGGGCTGTGTCTGCTCCGCTCTAGGCTCAGCCAGTACACCTGGCGTGA 523
QY 81 ArgTyrGlyArgArgArgProPheIleThrPheAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCGGCTTCATCTGGGCACCTGCTCCTGGGCATCTGCTGAGGCC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGTGTGCCCGGATCCAGGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTGGCGGTGGGCTGTGGACTTCTGTGGCCAGGTGTGCTTT 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCAGTGGAGGCCCTGCTCTGACCTTTCGGGGACCCGACACCTGTGCCAGGCC 763
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTCTATGCTTTCATGATCAGTCTTGGGGGTGCTGGGTACCTCCTGCTGCC 823
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 824 ATTGACTGGGACACCACTGCCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTTT 883
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGCCTGCTCACCTCATCTTCCTCACCCTGAGCAGCCACACTGCTGGTGGCTGAGGAG 943
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGGCTGGGCCCCACCGAGCCAGCAGAGGCGTGTGCCGCCCTCCTGTGTGCCCCAC 1003
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuProArgLeu 260
Db 1004 TGCTGTCCATGCGCGCGCGCTTGGCTTTCGGAACTTGGCGGCCCTGCTTCCCGGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACAGCTGTGCTGCCGATGCCCGACCTGCGCGGCTCTTGTGGCTGAGTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluLeu 300
Db 1124 AGCTGGATGGCACCTCATGACCTTCACGCTGTTTTTACAGGATTTCTGTGGCGAGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCGTGGCCAGAGCTGAGCGGGCACCCGAGGCCGAGGAGACTATGATGAAGC 1243

QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
 Db 1244 GTTCGATGGCAGCCTGGGCTGTTCTCGCAGTGGCCATCTCCCTGGTCTCTCTG 1303
 QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
 Db 1304 GTCATGACCGGCTGGTGCAGGATTCGGCAGCTCGAGCAGTCTATTGGCCAGTGGCA 1363
 QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
 Db 1364 GCTTTCCCTGGCTGCCGGTGCACATGCTTGTCCACAGTGTGCCCTGGTGACAGT 1423
 QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
 Db 1424 TCAGCGCCCTCACCGGTTACCTTCTCAGCCCTGCATCTCGCCCTACACATGGCC 1483
 QY 401 SerLeuTyrHisArgGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
 Db 1484 TCCCTCTACACCGGAGAGCAGGTGTTCTGCCCCAAATACGAGGGGACACTGGAGT 1543
 QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
 Db 1544 GCTAGCAGTGCAGACAGCTGATGACAGCTTCTGCCAGGCCCTAAGCCTGGAGCTCCC 1603
 QY 441 PheProAsnGlyHisValGlyAlaGlySerGlySerGlyLeuLeuProProAlaLeu 460
 Db 1604 TTCCCTAATGGACACGCTGGGTGCTGGAGCAGTGGCTGCTCCACCTCCACCGCGCTC 1663
 QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
 Db 1664 TCGGGGCTCTGCTGCTGATGCTCGTACGTGTGGTGGTGGTGGTGGTGGTGGTGGT 1723
 QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
 Db 1724 AGGTGGTTCGGGGCGGGGACATGCTGCTGGACCTGCCATCTGGATAGTGGCTTCTG 1783
 QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
 Db 1784 CTGTCACAGTGGCCCATCCCTGTTATGGCTCCATGTCAGCTCAGCAGTCTGTC 1843
 QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
 Db 1844 ACTGCTATATGTTGTTCTCCGAGGCTGGGTGCTGGTGGTGGTGGTGGTGGTGGTGG 1903
 QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
 Db 1904 GTAGTATTGACAAGCAGCTTGGCCAAATACTCAGCG 1942

RESULT 4

US-09-895-793-110
 ; Sequence 110, Application US/09895793
 ; Publication No. US20020192763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Devin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yudi
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedwick, Thomas S.
 ; APPLICANT: Carter, Darriek
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aljun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Bassols, Carlota

APPLICANT: Foy, Teresa
 APPLICANT: Fanger, Gary R.
 TITLE OF INVENTION: DIAGNOSIS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121.534C2
 CURRENT APPLICATION NUMBER: US/09/895,793
 CURRENT FILING DATE: 2001-06-29
 NUMBER OF SEQ ID NOS: 982
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 110
 LENGTH: 3410
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-895-793-110

Alignment Scores:
 Pred. No.: 1,44e-259 Length: 3410
 Score: 2861.00 Matches: 553
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-895-793-110 (1-3410)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
 Db 284 ATGGTCCAGAGCTGGGTGAGCCCTGCTGGCGCACCGGAAAGCCAGCTCTTGGCTG 343
 QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
 Db 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCGCAGGCATACCTATGTGCG 403
 QY 41 ProLeuLeuLeuValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
 Db 404 CCTCTGCTCTGGAAGTGGGGTAGAGGAGAGTTCATGACCATGCTGGGTCATGTGT 463
 QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTyrArgGly 80
 Db 464 CCAGTGTCTGGGCTGGTGTGTCGCCCTCCTAGGCTCAGCCAGTACACCTAGCCGTGA 523
 QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
 Db 524 CGCTATGGCGCGCGCGCCCTTCATCTGGGCATCTGCTTGGGCATCTCTGTAGCCCTC 583
 QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
 Db 584 TTTCTCATCCCAAGGGCGGCTGGCTAGCAGGGCTGCTGTGCCGGATCCAGGCCCTG 643
 QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
 Db 644 GAGCTGGCAGCTGCTCATCTGGCGTGGGGCTGCTGGAGCTTCTGTGGCCAGGCTGCTTC 703
 QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
 Db 704 ACTCCACTGGAGCGCTCTCTGTGACCTCTTCCGGGACCCGACCACTGTGCCAGGCC 763
 QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
 Db 764 TACTCTGTCTATGCGCTTCATGATCATGCTGTGGGGCTGCTGGGTACCTCTGCTGCT 823
 QY 181 IleAspTyrAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
 Db 824 ATTGACTGGGACCCAGTGGCTTGGCCCCCTACCTGGGCGGTGCTGGGTACCTCTCTTT 883
 QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
 Db 884 GGCTGCTCACCTCTCATCTTCTCAGCTCGGTAGCAGCCACACTGCTGGTGGCTGAGGAG 943
 QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
 Db 944 GCAGGCTGGGCCCCACCGAGCGCAGAGAAGGGCTGTGCGGCCCTCTCTTGTGCGCCAC 1003

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QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGTGTTCATGCCGGCCCGCTTGGCTTTCCGAAACCTGGCGCCCTGCTTCCCGCTG 1063
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGlnLeuCys 280
Db 1064 CACCAGCTGTGTCGCGCATGCCCGACCTCGCGCGCTCTTCGTGGCTGAGCTGTGC 1123
QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheThrThrAspPheValGlyGlnGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGCGAGGGCTG 1183
QY 301 TyrGlnGlyValProArgAlaGlnProGlyThrGlnAlaArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCTGCCAGAGCTGACGGCGGCACCGAGGCGCGGAGGAGACTATGATGAAGC 1243
QY 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGCAGCTGGGGCTGTTCCCTGACGTGGCCATCTCCCTGGTCTTCTCTG 1303
QY 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGGACCGGCTGGTGACGCACTTCGGCACTCGAGCACTCTATTGGCCAGTGGCA 1363
QY 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCTCTGCTGCGGTGCCATGCTCTCCACAGTGTGGCGGTGACAGCT 1423
QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCTGCCCTACACACTGGCC 1483
QY 401 SerLeuTyrHisArgGlnGlyGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCTCTACCCCGGAGAGCAGGTGTTCTGCCCAATACCGAGGGACACTGGAGGT 1543
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGAGGACAGCTGATGACAGCTTCTGCCAGGCCCTAAGCCTGGAGCTCC 1603
QY 441 PheProAsnGlnHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCCTTAATGGACAGCTGGGTGCTGGAGGAGTGGCTGCTCCCACTCCACCCCGGCTC 1663
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGlnProThrGlnAla 480
Db 1664 TGGCGGCTCTGCCTGTGATGTCCTCGTACGTGTGGTGGGTGAGCCAGGAGCC 1723
QY 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGGTGTTCCGGCGCGGGCATCTGCCCTGGACCTGCCATCTGGATAGTGCCTTCCTG 1783
QY 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATGTCTCCAGCTCAGCCAGTCTGC 1843
QY 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCCATATGGTGTCTGCCGAGGCTGGGTCTGGTCTGGTCCCATTTACTTGTGTACAG 1903
QY 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTTGACAAGAGCAGCTTGGCCAAATACTCAGCG 1942
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RESULT 5

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US-09-895-814-110
; Sequence 110, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
```

```
; APPLICANT: Jiang, Yuguu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-895-814-110
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Alignment Scores:

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Pred. No.: 1,44e-259 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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US-09-593-793A-113 (1-553) x US-09-895-814-110 (1-3410)

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QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db 284 ATGGTCAGAGGCTGGGTGAGCCGCTGCTGCGCACCGGAAAGCCAGCTCTTGGCTG 343
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGlyIleThrTyrValPro 40
Db 344 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTTGGCCGAGGATACCTATGTGCCG 403
QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGGAAGTGGGGGTAGAGAGAGTTCATGACCATGTGCTGGGCATTGGT 463
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTCTCGGGCTGTGCTGTGTCGCTCCTAGGCTCAGCCAGTACCACTGGCGTGA 523
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCGCCCTTCATCTGGGCACTGCTCTTGGGCATCTGCTGACGCTC 583
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGCGGCTGGCTAGCAGGGCTGCTGTGCCCGCATCCAGGCGCCCTG 643
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTCGGCGCTGGGCTGCTGGACTTCTGTGCCAGGCTGCTTC 703
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGCCCTGCTCTGTGACCTTCTCCGGGACCCGAGCCACTGTGCCAGGCC 763
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Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
|||||
Db 824 ATTGACTGGACACCACTGCTGGCCCTACCTGGGACCCAGGAGAGTGCCTCTT 883

Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValaGluGlu 220
|||||
Db 884 GGCCTGCTCACCCTCATCTTCCTACCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAG 943

Qy 221 AlaAlaLeuGlyProThrGlnProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
|||||
Db 944 GCAGCCTGGGCCCCACCAGGACGAGAAAGGCTGTCGGCCCCCTCTCTGTGCCCCAC 1003

Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
|||||
Db 1004 TGCTGTCCATGCGGGCCGCTGGCTTTCGCGAACCTGGCGCCCTGCTCCCGGGCTG 1063

Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValaGluLeuCys 280
|||||
Db 1064 CACCAGCTGTGTCGCGCATGCCCGCACCCCTGCGCGGCTCTTGTGGCTGAGCTGTGC 1123

Qy 281 SerTyrMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValaGlyGluGlyLeu 300
|||||
Db 1124 ACCTGGATGGCACTCATGACCTTCACGCTGCTTACCGGATTTCTGGCGGAGGGGCTG 1183

Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
|||||
Db 1184 TACCAGGGCGTCCCGAGAGCTGAGCGGGCACCGAGGCCGCGAGACACTATGATGAAGC 1243

Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
|||||
Db 1244 GTTCGGATGGCAGGCTGGGGCTGTTCTGTCAGTGGCGCATCTCCCTGCTCTCTCTG 1303

Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
|||||
Db 1304 GTCATGGACCGCTGGTCAGCGATTCGGCACTCGAGCAGTCTATTGGCCAGTGTGGCA 1363

Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
|||||
Db 1364 GCTTTCCTGTCGCTGCGGTGCCACATGCTGTCCTCCACAGTGTGGCGTGTGACAGCT 1423

Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
|||||
Db 1424 TCAGCGCGCTCACCAGGTTACCTTCTCAGCCCTGCAGCTCTCCCTACACACTGGCC 1483

Qy 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
|||||
Db 1484 TCCTCTACCCACCGGAGAGGAGGTGTCCTGCCCAATACCGAGGGGACACTGGAGT 1543

Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
|||||
Db 1544 GCTAGCAGTGAGACAGCTGATGACCACTTCTCTGCCAGGCCCTAAGCCTGGAGCTCCC 1603

Qy 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProProAlaLeu 460
|||||
Db 1604 TTCCCTAAATGGACAGCTGGTGTCTGGAGCAGTGGCCCTGCCACCTCCACCCCGCTC 1663

Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
|||||
Db 1664 TCGGGGGCTCTGCTGTGATGCTCCCGTACGTGTGGTGGGTGAGCCACCGAGGCC 1723

Qy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
|||||
Db 1724 AGGGTGGTTCGGGGCGGCACTGCTGCGTGGACCTCGCATCTCGATATGCTCTCTG 1783

Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
|||||
Db 1784 CTGTCCCAAGTGGGCCCATCTCCCTGTTATGGGCTCCATTTGTCAGCTCAGCCAGTCTGTC 1843

Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
|||||
Db 1844 ACTGCTATATGGTGTCTGCCCGCAGGCTGGGTCTGTGGCTGCTGCTTCTTGTACACAG 1903

Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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Db 1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942

RESULT 7

US-09-759-143-110
; Sequence 110, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-110

Alignment Scores:
Pred. No.: 1,44e-259 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-593-793A-113 (1-553) x US-09-759-143-110 (1-3410)

Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
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Db 284 ATGGTCCAGAGGCTGTGGGTGAGCCGCTGCTGCGCACCGGAAAGCCAGCTCTTGCTG 343

Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||||
Db 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCGCAGGATCACCTATGTGCCG 403

Qy 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
|||||
Db 404 CCTCTGCTGCTGGAAGTGGGGGTAGAGAGATTCATGACCATGCTGTGGCATGTGT 463

Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
|||||
Db 464 CCAAGTGTGGGCTGTGTGTGTCCTGCTAGGCTCAGCCAGTGACCACTGGCGTGA 523

Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
|||||
Db 524 CGCTATGGCGCGCGCGGCTTCATCTGGGCACTGTCTTGGGCACTCTGCTGAGCCCTC 583

Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
|||||
Db 584 TTCTCATCTCCCAAGGCGCGCTGGCTAGCAGGCTGTGTGCTGCCGATCCCCAGGCCCTC 643

Qy	121	GlueuAlaLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyInValCysPhe	140
Db	644	GAGCTGGACATGCTCATCTCGGCGTGGGGCTGCTGGAGATCTTGTGGCCAGGTGCTGCTTC	703
Qy	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160
Db	704	ACTGCACCTGGAGGCGCTGCTCTGTGACCTCTTCCGGGACCGGACCACTGTGCGCAGGCC	763
Qy	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180
Db	764	TACTCTGCTATGCCTTTCATGATCAGTCTTGGGGCTGCCCTGGGCTACCTCTCGCTGCC	823
Qy	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPhe	200
Db	824	ATTGACTGGGACACCACTAGTGCCTGGCCCTTACCTGGCAGCCACAGAGAGTGCCTCTTT	883
Qy	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
Db	884	GGCTGCTCACCTCATCTTCTCACCCTGCTAGCAGCCACACTGCTGGTGGCTTGAGAG	943
Qy	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
Db	944	GCAGCGCTGGGCCCCACCGAGCCAGCAGAAAGGCTGTGGGCCCTCTCTGTGCCCCCAC	1003
Qy	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260
Db	1004	TGCTGTCCATGCGGGCGCGCTGGCTTTCGGGAACCTGGGCGCCTCTTCCCGCGCTG	1063
Qy	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280
Db	1064	CACCAGCTGTGCTGCGCGCATGCCCGCACCCCTGCGCCCGGCTCTTGTGGGCTGAGCTGTGC	1123
Qy	281	SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu	300
Db	1124	AGCTGGATGCACATCATGACCTTCACGCTGTTTTACACGGATTTTCGTGGGCGAGGGCTG	1183
Qy	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly	320
Db	1184	TACCAGGCGCTGCCAGAGCTAGCGGGCACCGAGGGCCCGAGACACTATGATGAAGGC	1243
Qy	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340
Db	1244	GTTGCGATGGCAGCTGGGGCTGTTCCTGCASTGCGGCATCTCCCTGGTCTCTCTCTCTG	1303
Qy	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla	360
Db	1304	GTATGGACCGGCTGGTGACGGATTCGGCACTCAGGACAGTCTATTGGCCACAGTGGCA	1363
Qy	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla	380
Db	1364	GCTTTCCTGTGGCTCGCGTGCCACATGCCCTGTCCCACAGTGTGGCGTGGTGCACAGCT	1423
Qy	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400
Db	1424	TCAGCGCCCTTCACCGGGTTCACCTTCTCAGCCCTGCAAGATCCTGCCCTACACACTGCC	1483
Qy	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	420
Db	1484	TCCCTCTACCACCGGAGAGCAGGTGTTCCTGCCCAATACCCGNGGGGACACTGGAGGT	1543
Qy	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	440
Db	1544	GCTAGCAGTGCAGACACGCTGATGACCAGCTTCCTGCCAGCCCTTAAGCCTGGAGCTCC	1603
Qy	441	PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeu	460
Db	1604	TTCCCTAATGGACACCTGGGTGCTGGAGCAGTGGCTTCCCTCCACCTCCACCCGCGCTC	1663
Qy	461	CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla	480
Db	1664	TGCGGGGCTCTGCCCTGTATGTCCTCGTACGTGTGTGGTGGGTGGAGCCACCGAGGCC	1723
Qy	481	ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500

Db	1724	AGSGTGGTTCCGGCCGGGCAFCCTGCCCTGGACCTCGGCATCCTGGATAGTGCCTTCTG	1783
Qy	501	LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
Db	1784	CTGTCCCAAGGTGGCCCACTCCCTGTATTATGGGCTCCATTTGCAGCTCAGCCAGTCTGTC	1843
Qy	521	ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	540
Db	1844	ACTGCCCTATATGGTGTCTGCCGAGCCCTGGGTCTGGTGCCTATTACTTTGCTACACAG	1903
Qy	541	ValValPheAspLysSerAspLeuAlaLysTyrSerAla	553
Db	1904	GTAGTATTTGACAAGACGGACTTTGGCCAAATACTCAGCG	1942
RESULT 8			
US-09-780-669-110			
; Sequence 110, Application US/09780669			
; Patent No. US20020051977A1			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Dillon, Davin C.			
; APPLICANT: Mitcham, Jennifer L.			
; APPLICANT: Harlocker, Susan L.			
; APPLICANT: Jiang, Yuqul			
; APPLICANT: Henderson, Robert A.			
; APPLICANT: Kalos, Michael D.			
; APPLICANT: Fanger, Gary R.			
; APPLICANT: Retter, Marc W.			
; APPLICANT: Stolk, John A.			
; APPLICANT: Day, Craig H.			
; APPLICANT: Vedvick, Thomas S.			
; APPLICANT: Carter, Darrick			
; APPLICANT: Li, Samuel			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skelky, Yasir A.W.			
; APPLICANT: Hepler, William			
; APPLICANT: Hural, John			
; APPLICANT: McNeill, Patricia D.			
; APPLICANT: Houghton, Raymond L.			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
; FILE REFERENCE: 210121.427C24			
; CURRENT APPLICATION NUMBER: US/09/780,669			
; CURRENT FILING DATE: 2001-02-09			
; NUMBER OF SEQ ID NOS: 943			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 110			
; LENGTH: 3410			
; TYPE: DNA			
; ORGANISM: Homo sapien			
US-09-780-669-110			
Alignment Scores:			
Pred. No.: 1.44e-259 Length: 3410			
Score: 2861.00 Matches: 553			
Percent Similarity: 100.00% Conservative: 0			
Best Local Similarity: 100.00% Mismatches: 0			
Query Match: 100.00% Indels: 0			
DB: 10 Gaps: 0			
US-09-593-793A-113 (1-553) x US-09-780-669-110 (1-3410)			
Qy	1	MetValGlnArgLeuTrpValSerArgLeuAlaArgHisArgLysAlaGlnLeuLeuLeu	20
Db	284	ATGGTCCAGAGGTGTGGGTGAGCGCCCTGTCGGCACCCGGAAGCCAGCTCTTGCTG	343
Qy	21	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro	40
Db	344	GTCACCTGCTACCTTTGGCCTGGAGGTGTGTTGGCCGCGCAGGCATCACCTATGTGCCG	403
Qy	41	ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly	60

Db 404 CCTCTGCTGCTGAAGTGGGGTAGAGAGAGTTTCATGACCATGCTGCTGGGCATTGCT 463
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTCTGGCGCTGCTGTGTCCCGCTCCTAGGCTCAGCCAGTACCCACTGGCGTGA 523
Qy 81 ArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCGCGCTTCATCTGGCAGCTGCTCTGGCATCTGCTGAGCCCTC 583
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTCTCATCCCAAGGCGCGCTGGCTAGCAGGCTGCTGTGCCCGATCCACAGGCGCCCTG 643
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGCACTGCTCATCTGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGCTTC 703
Qy 141 ThrProGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGCGCGCTGCTCTGACCTCTTCGCGGACCGGACCACTGTGCCAGGCC 763
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrIleLeuProAla 180
Db 764 TACTCTGTCTATGCCCTTCATGATCAGCTTGGGGGCTGCTGGGCTACCTCTGCTGCC 823
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 824 ATTGACTGGGACACCACTGCCCTGGCGCCCTACCTGGGACCCAGGAGGAGTGCCTCTT 883
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 884 GGCGCTGCTCACCTCATCTCTCCTACCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAG 943
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGCGCTGGCGCCCAACCGAGCGAGAGGCTGCTGGCGCCCTCTCTGTGCGCCAC 1003
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATGCCGCGCGCTGGCTTTCGCGAACCTGGCGCCCTGCTCCCGCGCTG 1063
Qy 261 HisGlnLeuCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCAGCTGTGTCGCGCATGCCCGCACCTCGCGCGCTCTCTGCTGCTGAGCTGTGC 1123
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTCACCGATTTCTGTGGCGAGGGGCTG 1183
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGly 320
Db 1184 TACCAGGGCTGCCAGACTGAGCGGGCACCGAGGCGCGGACACTATGATGAAGGC 1243
Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGCAGCGCTGGCGGTGTCTCTGTCAGTGGCCATCTCCCTGCTCTCTCTG 1303
Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db 1304 GTCATGGACCGCTGGTGAGCGGATTCGGCACTCGAGCAGTCTATTGGCCAGTTGGCA 1363
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Db 1364 GCTTTCCCTGTGGCTGCCGCTGCCACATGCTGTCCACAGTGTGGCGGTGGTACAGCT 1423
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCTCTGCGCTTACACTGGCC 1483
Qy 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCCTCTACCAACCGGAGAGAGGTGTCTCTGCGCAATAACCGAGGAGGAGACTGGAGT 1543

Alignment Scores:

Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTGAGACAGCCTGATGACCACTTCTGCCAGGCCCTAAAGCTGGAGCTCC 1603
Qy 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
Db 1604 TTCCCTAATGAGACAGTGGGTGCTGGAGCAGTGGGCTCTCCACCTCCACCGCGCTC 1663
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TCGGGGCGCTCTGCTGTGATGCTCCGACGCTGTGGTGGTGGGAGGCCACCGAGGCC 1723
Qy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGTGGTTCCGGCGCGCGGCGCATCTGCCCTGGACCTCGCCATCTGATAGTGCCTTC 1783
Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTCTCCAGGTGCCCATCTCCCTGTTTATGGGTCCATTTGCCAGCTCAGCCAGTCTGC 1843
Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGTTCTCTCCGAGCGCTGGGTCTGGTCTGCCATTTACTTTGCTACACAG 1903
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTTGACAAGAGCGACTTGCCAAATACTCAGCG 1942

RESULT 9

US-09-030-606-110
; Sequence 110, Application US/09030606
; Patent No. US20020081580A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHOD
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,606
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.428C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-606-110

Pred. No.:	1.44e-259	Length:	3410
Score:	2861.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0
US-09-593-793A-113 (1-553) x US-09-030-606-110 (1-3410)			
Qy	1	MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu	20
Db	284	ATGTCACAGAGCGTGGGTGAGCGGCTGCTGGCGCACCGAAGCCACAGCTCTTGCTG	343
Qy	21	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro	40
Db	344	GTCAACCTGCTAACCTTTGGGCTGGAGGTGTTTGGCGCAGGCATCACCTATGTGCG	403
Qy	41	ProLeuLeuLeuGluValGlyValGluLysPheMetThrMetValLeuGlyIleGly	60
Db	404	CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAGTTTCATGACATGTTGGCATTTGGT	463
Qy	61	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly	80
Db	464	CCAGTGTGGGCGCTGGTCTGCTCCGCTCCTAGGCTCAGCCAGTGCACCTGGCGTGA	523
Qy	81	ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu	100
Db	524	CGCTATGGCGCGCGGCCCTTCATCTGGGCACTGCTCTGGGCATCTCTGCTGAGCCT	583
Qy	101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu	120
Db	584	TTTCTCATCCCAAGGGCGGCTGCTAGCAGGGCTGCTGTGCCGGATCCCGAGGCCCTG	643
Qy	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe	140
Db	644	GAGCTGGCAGTGCATCTCTGGGCGTGGGCTGCTGGACTTCTTGGCGCAGGTGCTTC	703
Qy	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160
Db	704	ACTCCACTGGAGGCCCTCTCTGACCTCTCCGGGACCCGACCACTGTGCGCAGGCC	763
Qy	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla	180
Db	764	TACTCTGTCTATGCTTTCATGATCAGTCTTGGGGCTGCCCTGGGCTACCTCTGCTGCC	823
Qy	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe	200
Db	824	ATTGACTGGGACACAGTGCCTGGCCCTACCTTGGGCACCCAGGAGGAGTGCTCTTT	883
Qy	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	220
Db	884	GGCCTGTCACCTTCATCTTCTCACCTGCTAGCAGCCACACTGCTGGTGGCTGAGGAG	943
Qy	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
Db	944	GCAGCGTGGGCCCCACCGAGCAGCAGAGGCTGTGCGGCCCTCTCTGTCGCCCCAC	1003
Qy	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260
Db	1004	TGCTGTCCATGCCGGGCGGCTTGGCTTTCGGAACTTGGCGGCCCTGCTTCCCGCGGTG	1063
Qy	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280
Db	1064	CACCAGCTGTGCTCGCGCATGCCCGCACCTGCGCGCGGCTCTTCTGGGCTGAGCTGTC	1123
Qy	281	SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu	300
Db	1124	AGCTGGATGGCCTCATGACCTTCACGCTGTTTACAGGATTTCTGTTGGCGGAGGGCTG	1183
Qy	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly	320
Db	1184	TACCAGGGCGTGGCCAGAGCTGAGCGCGGACCCAGGCGCGGAGACACTATGATGAAGGC	1243

Qy	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	340
Db	1244	GTTCCGATGGCAGCCTGGGCTGTCTCTGCAGTGGCGCATCTCCCTGCTCTCTCTG	1303
Qy	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla	360
Db	1304	GTCATGGACCGGCTGGTGACGATTCGGCAGCTCGAGCAGTCTATTGGCCAGTGTGCA	1363
Qy	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla	380
Db	1364	GCTTTCCTCTGGCTGGCGTGCACATGCTGTCCACAGCTGGCGGTGGTACAGCT	1423
Qy	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400
Db	1424	TCAGCGCGCCTCACCGGGTTTCACTTCTCAGCCCTGCAGATCTCTGCCCTACACACTG	1483
Qy	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly	420
Db	1484	TCCCTTACCACCGGAGAGCAGGTGTTCTGCCCAATACCGAGGGGACACTGGAGGT	1543
Qy	421	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyValAla	440
Db	1544	GCTAGCAGTAGGACAGCCTGATGACAGCTTCTTCCAGCCCTTAAGCCTGGAGCTCCC	1603
Qy	441	PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu	460
Db	1604	TTCCCTAATGGACAGTGGGTGCTGGAGCAGTGGCTTCCACCTCCACCCGCGCTC	1663
Qy	461	CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla	480
Db	1664	TGCGGGGCTCTGCTGTGTATGCTCTCCGTAGTGTGGTGGTGGTGGTGGTGGTGGT	1723
Qy	481	ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu	500
Db	1724	AGGTGGTTCGGCGCGGGGCTCTGCTGGACCTCGCCATCTCTGGATAGTGGCTTCTG	1783
Qy	501	LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
Db	1784	CTGTCCAGGTGGCGCCATCCTGTTATGGCTTCCATGTCCAGCTCAGCCAGTCTGTC	1843
Qy	521	ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	540
Db	1844	ACTCCCTATATGTTGTTGCTGGCGCAGGCTTGGTCTGGTCTGGCTTCTTCTTCTG	1903
Qy	541	ValValPheAspLysSerAspLeuAlaLysTyrSerAla	553
Db	1904	GTAGTATTTGACAAGAGCAGCTTGGCCAAATACCTACGCG	1942

RESULT 10

US-09-822-827-110
; Sequence 110, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822.827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-822-827-110

Alignment Scores:			
Pred. No.:	1.44e-259	Length:	3410
Score:	2861.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0


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DB: 10 Gaps: 0
US-09-593-793A-113 (1-553) x US-09-822-827-110 (1-3410)
Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgGlyAlaGlnLeuLeuLeu 20
Db 284 ATGGTCCACAGAGCTGTGGGTGAGCGCCCTGCTGCGGCACCGGAAAGCCAGCTCTGTG 343
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIlePheTrpValPro 40
Db 344 GTCAACCTGCTAAACCTTTGGCCCTGAGAGGTGTGTTGGCCGACAGGATCACTATGTGCGG 403
Qy 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 404 CCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 463
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 464 CCAGTGTGGGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 523
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 524 CGCTATGGCGCGCGCGCGCTTCATCTGGGCACACTGCTGCTGGGATCCTGCTGAGCCTC 583
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 584 TTTCTCATCCCAAGGCGCGCTGGCTAGCAGGGCTGCTGTCGCCGATCCACAGGCCCTG 643
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 644 GAGCTGGACACTGCTCATCTGGGCGTGGGCTGCTGGACTTCTGCGCCAGGTGTGCTTC 703
Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 704 ACTCCACTGGAGGCCCTGCTCTGACCTCTTCGCGGACCCGGACCACTGTGCGCAGGCC 763
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 764 TACTCTGTATGCTTCATGATGATGCTTGGGGCTGCCTGGGCTACCTCTGCTGCC 823
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 824 ATTGACTGGGACACAGTGCCTTGGCCCTTACCTTGGGCACCCAGGAGGTGCTCTTT 883
Qy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db 884 GGCTGTCTCACCTCATCTTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 943
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 944 GCAGCGCTGGGCCCCACCGAGCCAGCAGAGGGCTGTGCGGCCCTCTCTTGTGCGCCAC 1003
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1004 TGCTGTCCATGCGCGCGCGCTTGGCTTTCGGAACCTTGGCGCCCTGCTTCCCGGGCTG 1063
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1064 CACCACTGTGTGCGGATGCGCGCACCTTGGCGCCGCTTCTGCTGCTGCTGCTGCTGCTGCT 1123
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlyLeu 300
Db 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTACAGGATTTCTGGCGAGGGGCTG 1183
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db 1184 TACCAGGGGCTGCCAGAGCTGAGCGGGCACCGAGGCGCGGAGACACTATGATGAAGGC 1243
Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db 1244 GTTCGGATGGGAGCGCTGGGGCTGTTCCTGACGTGGCGCATCTCCCTGCTCTCTCTG 1303
Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
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Db 1304 GTCATGGACCGGCTGTGTCAGCGATTTCGCACTCGAGCAGTCTATTTCGCCAGTGTGGCA 1363
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValaValValThrAla 380
Db 1364 GCTTTCCCTGTGCTGCGCGTGCACATGCTGTCCACAGTGTGCCAGTGTGGCGTGTGACAGT 1423
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db 1424 TCAGCGCGCCTCACCGGGTTACCTTCTCAGCGCTGCAGATCCTGCCCTACACACTGGCC 1483
Qy 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db 1484 TCCTCTCTACCAACCGGAGAGCAGGTTCCTCTGCCAAATACCGAGGACACTGGAGGT 1543
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db 1544 GCTAGCAGTAGGACAGCCTGATGACCACTTCTTCCAGGCGCCCTAAGCCTGGAGCTCCC 1603
Qy 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeu 460
Db 1604 TTCCCTAATGACACGTGGTCTTGAGGACGTGGCTGCTCCACCTCCACCCGCGCTC 1663
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
Db 1664 TCGGGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1723
Qy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db 1724 AGGTGGTTCGGGGCGGGGATCTGCTGGACCTGCGCATCTGGATAGTGCCTTCCTG 1783
Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db 1784 CTGTCCTCCAGGTGGCCCATCTCTGTTATGGCTCATTGCTCCAGCTCAGCCAGTCTGTC 1843
Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleIleTyrPheAlaThrGln 540
Db 1844 ACTGCTATATGCTGCTGCGCAGCGCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1903
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 1904 GTAGTATTGACAGAGCGACTTGGCCAAATACTCAGCG 1942

RESULT 11
US-09-115-453-110
; Sequence 110, Application US/09115453B
; Patent No. US20020090372A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE, CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115.453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-115-453-110

Alignment Scores:
Pred. No.: 1,44e-259 Length: 3410
Score: 2861.00 Matches: 553
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x US-09-115-453-110 (1-3410)
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Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db ATGGTCCAGAGGCTGTGGGTAGCGCCCTGCTGCGGCACCGAAAGCCAGCTCTTGCTG 343
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTGGCGCAGGCATCACCTATGTGGCG 403
Qy 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db CCTCTGCTGCTGGAGTGGGGTAGAGGAGAGTTCATGACCATGGTGGTGGGCATTTGGT 463
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db CCAGTGTCTGGGCTGTGTCTGCCGTCTTAGGCTCAGCCAGTGACCACTGGCGTGA 523
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db CCTATGGCGCGCGCGCCCTTCATCTGGGCACCTGTCTTGGGCATCCTGCTGAGCCCTC 583
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db TTCTCATCCCAAGGCGCGCTGGCTAGCAGGCTGTGTGCCGGATCCCAAGGCCCTG 643
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyClnValCysPhe 140
Db GAGCTGGCACTGCTCATCTGGCGCTGGGCTGTCTGGACTTCTGTGGCCAGGTGTCTTC 703
Qy 141 ThrProLeuGluAlaLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db ACTCCACTGGAGGCGCTCTCTGACCTCTTCCGGGACCCGGACCACTGTGCGCAGGCC 763
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db TACTCTGTATGCTTCATGATCACTTGGGGCTGCCTGGGGTACTCTCTGCTGCC 823
Qy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db ATTGACTGGGACACAGTGCCTGCGCCCTACCTGGGCAACCAGGAGGAGTGCCCTTT 883
Qy 201 GlyLeuLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db GGCTGTCTACCCCTCATCTCTACCTGCGTAGCAGCACCACTGCTGCTGGCTGAGGAG 943
Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db GCAGGCTGGGCCCCACGAGCCAGCAGAGGCTGTGCGCCCTCTCTGTGCGCCCAAC 1003
Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db TGCTGTCCATGCGGGCGCGCTTGCTTCCGGAACCTGGGCGCCCTGCTTCCCGGCTG 1063
Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db CACCAGCTGTGCTGGCATGCCCGCACCTGCGCGGCTCTTGGTGGCTGAGCTGTGC 1123
Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCTGGGGCAGGGGCTG 1183
Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Db TACCAGGGCGTGCCAGAGCTGAGCGGGCACCGAGGGCCCGAGACACTATGATGAAGGC 1243
Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340
Db GTTCGATGGGAGCGCTGGGCTGTCTGTCAGTGGCGCATCTCCCTGGTCTCTCTCTG 1303
Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
Db GTCATGGACCGGCTGGTGCACCGATTCGGCACTCAGCAGTCTATTTGGCCAGGTGTGCA 1363
Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380

Db 1364 GCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCACAGTGTGCCGTGGTGCAGCT 1423
Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Db TCAGCGGCGCTACCGGGTTACCTTCTCAGCCCTGCAGATCCTCCCTACACACTGGCC 1483
Qy 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
Db TCCCTCTACCACCGGAGAGCAGGTGTCTTCCGCCAATACCGAGGGGACACTGGAGGT 1543
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Db GCTAGCAGTGAGGACAGCTGATGACCACTCTCTGCGCAGGCGCTAAGCCTGGAGCTCCC 1603
Qy 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460
Db TTCCCTAATGACACAGTGGGTGCTGGAGGAGTGGCTGCCACCTCCACCCCGCGCTC 1663
Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480
Db TCGGGGCGCTCTGCTGTGATGTCTCCGTAGCTGTGGTGGTGGTGGTGGTGGTGGTGG 1723
Qy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500
Db AGGTGTGTCCGGCGCGGCGCATCTGCTGGACCTGCGCATCTCTGATAGTGCCTTCCTG 1783
Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
Db CTGTCCTAGGTGGGCGCCATCTCTTTATGGGCTCCATGTGCCAGCTCAGCAGTCTGTC 1843
Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
Db ACTGCTATATGGTGTCTGCGCAGGCGCTGGTCTGGTCTGGCTGGCTGGCTGGCTGG 1903
Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db GTAGTATTGACAGAGCGACTTGGCCAAATACTCAGCG 1942

RESULT 12

US-10-012-896-704
: Sequence 704, Application US/10012896
: Publication No. US20020183251A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yuqiu
: APPLICANT: Kalos, Michael D.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darlick
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William T.
: APPLICANT: Henderson, Robert A.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Vinals de Bassols, Carlota
: APPLICANT: Foy, Teresa
: APPLICANT: Fanger, Gary R.
: APPLICANT: Wantanabe, Yoshihiro
: APPLICANT: Meagher, Madeleine Joy
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.427C27
: CURRENT APPLICATION NUMBER: US/10/012.896
: CURRENT FILING DATE: 2001-12-10

; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-704

Alignment Scores:
Pred. No.: 7,21e-246 Length: 4034
Score: 2716.50 Matches: 553
Percent Similarity: 70.09% Conservative: 0
Best Local Similarity: 70.09% Mismatches: 0
Query Match: 94.95% Indels: 236
DB: 9 Gaps: 1

US-09-593-793A-113 (1-553) x US-10-012-896-704 (1-4034)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 281 ATGGTCCAGAGGCTGTGGGTGAGCGCCTGCTCGGCGACCGGAAAGCCAGCCTCTGTG 340
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 341 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCCGCGAGGCATCACCTATGTGCGG 400
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 401 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGGTGTGGGCAATTGT 460
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 461 CCAGTGTGGGCTGTGCTGTGTCGCGCTCCTAGGCTCAGCCAGTCACCACTGGCGTGA 520
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 521 CCTATGTGGCGCGCGCGCCCTTCATCTGGGCACCTGTCTTGGGCATCTGCTGAGCCCTC 580
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTTCATCCCAAGGCGCGCTGGCTAGCAGGCTGCTGTGCCCGATCCCAAGGCCCTG 640
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 641 GAGTGGCACTGCTATCTGCGCGCTGGGCTGCTGGACTTGTGTGGCCAGGCTGTCTTC 700
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGGCCCTGCTCTGACCTCTTCGGGACCCCGGACCACTGTGCCAGGCC 760
QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 761 TACTCTGTCTATGCCTTCATGATCAGTCTTGGGGCTGCTGGGTACCTCTGCTGCC 820
QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
Db 821 ATTGACTGGGACACCACTGCTGCGCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTT 880
QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
Db 881 GGCTGTCTCACCCTCATCTCTCCTACCTGCGTAGGACCACTGTGTGGTGTGAGGAG 940
QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 941 GCAGGCTGGGCCCCCAGCCAGCAGAGAGGCTGTGGCCCCCTCTTGTGCGCCCCAC 1000
QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1001 TGCCTGTCCATGCGGCGCGCTGTGGCTTTCCGGAACCTGGGCGCCTGCTTCCCGGGCTG 1060
QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1061 CACCAGCTGTGTGGCGCATGCCCGCACCCCTGCGCGCGCTCTTGTGGCTGAGCTGTGC 1120

QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1121 AGCTGGATGGCACTCATGACCTTCACGCTGTGTTTACACGGATTTCGTGGCGGAGGCGTG 1180
QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGlu--- 319
Db 1181 TACCAGGGCGTCCCGAGAGCTGAGCGGGCACCCGAGGCCCGGAGACACTATGATGAAGT 1240
QY 319 ----- 319
Db 1241 AAGGCTTGGCAGCCAGCAGAGGCTGGTGTGGGAGCCGCCACCAGACAGACACATCGGG 1300
QY 319 ----- 319
Db 1301 GCTGTGTCTGGGCTGTGCTCTCCATCTGCGCCCGACTTCTCTCAGGAAAGTGGGG 1360
QY 319 ----- 319
Db 1361 ATGGACCCCATCTGCATACACGGCTTCTCATGGGTGTGAACATCTCTGCTTTCGGTTTC 1420
QY 319 ----- 319
Db 1421 AGGAAGGCTCTGTGGCTGTCTAGGAGTCTGATCAGAGTCTTGGCCCCAGTTTTCACAGAAG 1480
QY 319 ----- 319
Db 1481 GAAAGCGGAGCTTATTCAAAGTCTAGAGGAGTGGAGGAGTTAAGGCTGGATTTCAGAT 1540
QY 319 ----- 319
Db 1541 CTGCCTGTTCAGCGCCAGTGTGCCCTGTCTCCCCCAACGACTTTCAAAATAATCTCA 1600
QY 319 ----- 319
Db 1601 CCAGCGCTTCCAGCTCAGGCGTCTAGAGGCTTGAAGGCTATGGCCAGCTGTCTTT 1660
QY 319 ----- 319
Db 1661 GTGTTCCCTCTCACCGCGCTGCTCACAGCTGAGACTCCAGGAAACCTTCAGACTACC 1720
QY 319 ----- 319
Db 1721 TTCCTCTGCTTCAGCAAGGGCGTGTGCCACATTTCTGTAGGGTCACTGGAAGAACCCTA 1780
QY 319 ----- 319
Db 1781 GACTCCCATGCTAGAGGTAGAAAGGGAGGAGTGTGGGAGCAGGGCTGTGTCCACAGC 1840
QY 319 ----- 319
Db 1841 AGGTCTCGTGCAGCAGGTACCTGTGTTCCGCTTCTCATCTCCCTGAGACTGCTCCGAC 1900
QY 320 -----GlyValArgMetGlySe 325
Db 1901 CCTTCCCTCCAGGCTGTCTGTGATGGGCCCTCTCCCTCTGCAGGGCTTCGATGGGCGAG 1960
QY 325 rLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLe 345
Db 1961 CTTGGGGCTGTTCCTGACGTGCGCCATCTCCCTGGTCTCTCTGTGTCATGGACCGGCT 2020
QY 345 uValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaPheProValAl 365
Db 2021 GGTGCAGGATTCGGCACTCGAGCAGTCTATTGTGGCAGTGTGGCAGCTTCCCTGTGGC 2080
QY 365 aAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuTh 385
Db 2081 TGCCGGTGCCACATGCTGTCACAGTGTGGCCGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2140
QY 385 rGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisAr 405
Db 2141 CGGGTTACCTTCTCAGCCCTGCAGATCTGCGCCTACACACTGGGCTTCCTCTACACCGG 2200

Qy 405 gLuLySlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAs 425
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Qy 425 pSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHi 445
Db 2261 CAGCCTGATGACCAGCTTCCTGCGAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACA 2320
Qy 445 sValGlyAlaGlySerGlyLeuLeuProProProProAlaLeuCysGlyAlaSerAl 465
Db 2321 CGTGGGTGCTGAGGAGCAGTGCCTGCTCCACCTCCACCGCGCTCTGCGGGGCTCTGC 2380
Qy 465 aCysAspValSerValArgValValValGlyGluProThrGluAlaArgValValProGl 485
Db 2381 CTGTGATGCTCTCCGTACGTGTGGTGGTGGGTGAGCCACCGAGGCCAGGGTGGTTCCGGG 2440
Qy 485 yArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAl 505
Db 2441 CCGGGGATCTGCCTGGACCTCGGCATCCTGGATAGTGCCCTTCCTGTGTCCTCCAGGTGGC 2500
Qy 505 aProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVa 525
Db 2501 CCCATCCCTGTTATGGGCTCCATGTCACGCTCAGCCAGTCTGTCTACTGCTATATGGT 2560
Qy 525 lSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLy 545
Db 2561 GTCTGCGCAGGCCGTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2620
Qy 545 sSerAspLeuAlaLysTyrSerAla 553
Db 2621 GAGCGACTTGGCCAAATACTACGCG 2645

RESULT 13

US-09-895-793-704
; Sequence 704, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-895-793-704

Alignment Scores:

Pred. No.: 7.21e-246 Length: 4034
Score: 2716.50 Matches: 553
Percent Similarity: 70.09% Conservative: 0
Best Local Similarity: 70.09% Mismatches: 0
Query Match: 94.95% Indels: 236
DB: 9 Gaps: 1
US-09-593-793A-113 (1-553) x US-09-895-793-704 (1-4034)
Qy 1 MetValGlnArgLeuTyrValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 281 ATGGTCCAGAGGCTGTGGGTGAGCGCTGTGCGGCACCGGAAGCCACCTCTTGTGTC 340
Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaIleThrTyrValPro 40
Db 341 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCGCGCAGGCATCACCTATGTGCG 400
Qy 41 ProLeuLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeuGlyIleGly 60
Db 401 CCTCTGCTGTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGTCTGGGCATTGGT 460
Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 461 CCAGTGTCTGGGCCCTGGTGTGCTCCGCTCTAGGCTCAGCCAGTGACCATGGCGTGGGA 520
Qy 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 521 CGCTATGGCGCGCGCGCCCTTCATCTGGGCACCTGTCTTGGGCATCTCTGCTGAGCCTC 580
Qy 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTCTCATCCCAAGGCGCGGTGGCTAGCAGGGTGTGTGCCGGGATCCAGGCGCCCTG 640
Qy 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 641 GAGCTGGCACTGCTCATCTCTGGGCTGTGGGCTGTCTGGGCTGTCTGGGCTGTCTGGGCT 700
Qy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCGCGGAGCCGACCATGTCGCGAGGCC 760
Qy 161 TyrSerValTyrAlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAla 180
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Db 821 ATTCACTGGGACACCACTGGCCCTGGCCCCCTTACCTGGGAGGAGGTGCTCTCTTT 880
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; Sequence 704, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-704
Alignment Scores:
Pred. No.: 7, 21e-246 Length: 4034
Score: 2716.50 Matches: 553
Percent Similarity: 70.09% Conservative: 0
Best Local Similarity: 70.09% Mismatches: 0
Query Match: 94.95% Indels: 236
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US-09-593-793A-113 (1-553) x US-09-895-814-704 (1-4034)

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US-09-780-669-704
; Sequence 704, Application US/09780669
; Patent No. US2002005197A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-704

Alignment Scores:
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Score: 2716.50 Matches: 553
Percent Similarity: 70.09% Conservative: 0
Best Local Similarity: 70.09% Mismatches: 0
Query Match: 94.95% Indels: 236
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Db 2021 GGTGCAGCGATTTCGCACTCGAGCAGTCTATTGGCCAGTGTGCAGCTTTCCTCTGTGC 2080
QY 365 aAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuTh 385
Db 2081 TGCCGTTGCCACATGCTCTGCCACAGTGTGCCGTGGTGCACAGCTTCAGCCGCCCTCAC 2140
QY 385 rGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisAr 405
Db 2141 CGGTTTCACCTTCTCAGCCCTGCAGATCTCCCTACACACTGGCCCTCCTCTTACCACCG 2200
QY 405 gGluTyrGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAs 425
Db 2201 GGAGAAGCAGGTTCCTTCCGCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGA 2260
QY 425 pSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHi 445
Db 2261 CAGCCTGTATGACAGCTTCTCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACA 2320
QY 445 sValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAl 465
Db 2321 CGTGGTGTGGAGGAGTGGCTGCTCCACCTCCACCGCGCTCTGGGGCCCTCTGC 2380
QY 465 acYAspValSerValArgValValGlyGluProThrGluAlaArgValValProGl 485
Db 2381 CTGTGATGCTCCGTACGTGTGTGTGGTGGTGAGCCACCAGGCGCAGGCTGTCCGG 2440
QY 485 yArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAl 505
Db 2441 CCGGGCATCTGCTGGAGCTCGCCATCTCTGGATAGTGTCTCTCTGCTGCCAGTGGC 2500
QY 505 aProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVa 525
Db 2501 CCATCCCTGTTATGGGCTCCATTTGCCAGCTCAGCCAGTCTGTCCACTGTCCCTATATGTT 2560
QY 525 lSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLy 545
Db 2561 GNTCGCGCAGGCTGGGTCTGTGCGCCATTACTTTGTACACAGGTAGTATTTGACAA 2620
QY 545 sSerAspLeuAlaLysTyrSerAla 553
Db 2621 GAGCGACTTGGCCAAATACTACGCG 2645
RESULT 17
US-09-822-827-704
; Sequence 704, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28

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; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 704
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-704

Alignment Scores:
Pred. No.: 7,216-246 Length: 4034
Score: 2716.50 Matches: 553
Percent Similarity: 70.09% Conservative: 0
Best Local Similarity: 70.09% Mismatches: 0
Query Match: 94.95% Indels: 236
DB: 10 Gaps: 1

US-09-593-793a-113 (1-553) x US-09-822-827-704 (1-4034)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 281 ATGGTCCAGAGGCTGTGGGTGAGCCGCTGCTGCGGCACCGGAAAGCCAGCTCTTGCTG 340

QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 341 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTGGCCGCGAGCATCACCTATGTGCCG 400

QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 401 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAGTTTCATGACCATGGTGTGGGCATTTGGT 460

QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 461 CCAGTGTGGGCTGTGCTGTGTCGCTGCTAGGCTCAGCCAGTCACCATGTGGCGTGA 520

QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 521 CGCTATGGCGCGCGCGGCGCTTTCATCTGGGCACCTGCTGTTGGGCATCTGCTGAGCCCTC 580

QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 581 TTTCTCATCCCAAGGCGCGGTGGCTAGAGGGCTGCTGTGCCGATCCAGGCCCGCTG 640

QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 641 GAGCTGGCACCTGCTCATCTGGCGCTGGGCTGCTGACTTCTGTGGCCAGGTGTGCTTC 700

QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 701 ACTCCACTGGAGGCGCTGCTCTGTGACCTTCTCCGGGACCGGACCATGTGCGCCAGGCC 760

QY 161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Db 761 TACTGTCTATAGCCTTCATGATCAGCTCTTGGGGCTGCTGGGCTAACCTCTGCTGCC 820

QY 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPhe 200
Db 821 ATTGACTGGGACACCAAGTGCCTGGCCCTACCTGGGCACCCAGGAGGTGCCCTCTT 880

QY 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGlu 220
Db 881 GGCTGCTCACCTCATCTTCTCAGCTGCTAGCAGCCACATGCTGGTGGCTGAGGAG 940

QY 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Db 941 GCAGCGCTGGGCCCCCAGGCGAGGAGGAGGCTGTGGCCCCCTCTCTTGTGCGCCCCAC 1000

QY 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Db 1001 TGGTGTCCATGCGGGCGCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCGGCTG 1060

QY 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Db 1061 CACCAGCTGTGCTGGCGCATGCCCGCACCCCTGCGCGGCTCTTCTGCTGAGCTGTGC 1120
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QY 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Db 1121 AGCTGGATGGCACTCATGACCTTCACGCTCTTTTACAGGATTTCTGCGGCGAGGGCTG 1180

QY 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGlu 319
Db 1181 TACCAGGGGTGCCAGAGCTGAGCGGCGCACCGAGGCGCGGAGACATATGATGAAGT 1240

QY 319 ----- 319
Db 1241 AAGGCCCTTGGACGCCAGCAGAGGCTGGTGTGGAGCGGCCACCAGAGACACTCGGG 1300

QY 319 ----- 319
Db 1301 GCTGTGCTGGGCTGGTGCCTCTCCATCCTGGCCCCGACTTCTCTGTCTCAGAAAGTGGG 1360

QY 319 ----- 319
Db 1361 ATGACCCCATCTGCATACACGCTTCTCATGGGTGTGGAACATCTCTGCTTGGCGTTTC 1420

QY 319 ----- 319
Db 1421 AGGAAGCCCTCTGGCTGCTCTAGGAGTGTGATCAGAGTCTGTTCCCGCAGTTTGCACAGA 1480

QY 319 ----- 319
Db 1481 GAAAGCGGAGCTTATTCAAAGTCTAGAGGAGTGGAGGAGTTAAGCTGGATTTTCAGAT 1540

QY 319 ----- 319
Db 1541 CTGCTGTGTTCCAGCGCAGTGTGCCCTCTGCTCCCGCAACGACTTTCCAAATAATCTCA 1600

QY 319 ----- 319
Db 1601 CCAGCCCTTCCAGCTCAGCGCTCTAGAACGCTCTTGAAGCCTATGGCCAGCTGTCTTT 1660

QY 319 ----- 319
Db 1661 GTGTTCCCTCTCACCGCGCTGTCTCACAGCTGAGACTCCCAGGAAACCTTTCAGACTACC 1720

QY 319 ----- 319
Db 1721 TTCTCTGTGCTTTCAGCAAGGGCGTTGCCACATCTCTGAGGGTCAGTGAAGAACCTA 1780

QY 319 ----- 319
Db 1781 GACTCCCATTTGTAGAGGTAGAAAGGGAGGGTGTGGGAGCAGGGCTGGTCCACAGC 1840

QY 319 ----- 319
Db 1841 AGGTCTCGTGACAGGTACCTGTGTTCCGGCTTCTGATCTCCCTGAGACTGCTCCGAC 1900

QY 320 -----GlyValArgMetGlyse 325
Db 1901 CCTTCCCTCCCGAGCTCTGCTGATGGCCCTCTCCCTCTGCGAGGCTTCGGATGGGCGAG 1960

QY 325 rLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLe 345
Db 1961 CCTGGGGCTGTTCCTCAGTGGCGCATCTCCCTGGGTCTTCTCTGCTCATGGACCGCT 2020

QY 345 uValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAl 365
Db 2021 GGTGACAGCATTCGGGCACTCGAGCATCTATTTGGCCAGTGTGGCAGCTTTCCTGTGGC 2080

QY 365 aAlaGlyAlaThrCysLeuSerHisSerValAlaValAlaValThrAlaSerAlaLeuTh 385
Db 2081 TGGCGGTGCCACATGCTGTCCACAGTGTGGCGGTGTGACAGTTCAGCGCCCTCAC 2140

QY 385 rGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisar 405
Db 2141 CGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCTCCCTCTACACCG 2200
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QY 405 gGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAs 425
Db 2201 GGAGAGCAGGTGTTCTGCCAAAATACCAGGGGACACTGGAGGTGCTAGCAGTGA 2260
QY 425 pSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHi 445
Db 2261 CAGCCTGATGACCAAGTCTCTGCAGGCCCTAAGCCTGAGGCTCCCTTCCCTAATGACA 2320
QY 445 sValGlyAlaGlySerGlyLeuLeuProProProProAlaLeuCysGlyAlaSerAl 465
Db 2321 CGTGGGTGCTGGAGGAGTGGCTGCTCCACCTCCACCGCGCTCTGGGGGCTCTGC 2380
QY 465 acYAspValSerValArgValValValGlyGluProThrGluAlaArgValProGl 485
Db 2381 CTGTGATGTCCTCGTACGTGTGTGGTGAGCCACCGAGGCCAGGCTGTTCCGGG 2440
QY 485 yArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuSerClnValAl 505
Db 2441 CCGGGGCATCTGCTGGACCTCGCCATCTCTGGATAGTGCTTCTGCTGCCAGGTGGC 2500
QY 505 aProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVa 525
Db 2501 CCATCCCTGTTATGGGCTCCATTTGCCAGCTCAGCCAGTCTGTCTACCTATATGGT 2560
QY 525 lSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLy 545
Db 2561 GTCTGCCGAGGCTGGTCTGTGTCGCCATTTACTTTGTGTACACAGGTAGTATTTGACAA 2620
QY 545 sSerAspLeuAlaLysTyrSerAla 553
Db 2621 GAGCGACTTGGCCAAATACTACGCG 2645

RESULT 18

US-10-012-896-702
; Sequence 702, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 702
; LENGTH: 4894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-702

Alignment Scores:
Pred. No.: 5,33e-229 Length: 4894
Score: 2538.50 Matches: 551
Percent Similarity: 51.11% Conservative: 0
Best Local Similarity: 51.11% Mismatches: 2
Query Match: 88.73% Indels: 526
DB: 9 Gaps: 2
US-09-593-793A-113 (1-553) x US-10-012-896-702 (1-4894)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 274 ATGGTCCAGAGGCTGGGTGAGCCCTGCTGCGCACCGGAAAGCCAGCTCTTGGCTG 333
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 334 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTGGCCGCGAGGCATCACCATTATGTC 393
QY 41 ProLeuLeuGluValGlyValGlyValGluGlyLysPheMetThrMetValLeu 57
Db 394 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAGTTCATGACCATGTGCT-GGGTGAGTC 452
QY 57 ----- 57
Db 453 ACTACATCTCCTTCTCTCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA 512
QY 57 ----- 57
Db 513 CCTCTGCCCTGGAGCTGCTTGGAGGAGAGGTGCTCTCTGGGAAGGCATTGCTGGGCA 572
QY 57 ----- 57
Db 573 GGAGGTGACCCCTGGGCTGAGGGGGCACACCAAGAGAGAAGAGATAACCAAGGACATA 632
QY 57 ----- 57
Db 633 CCCCAGTCACCTCTGGATCCCTGGTCTGCACAGAGCCCTGGCTCATAGGAGACACTGGAG 692
QY 57 ----- 57
Db 693 AAATGCTCTAACCTTTGGCTAGCCCTTTTATTAATTATAGCGATTATCTCATTTAATGC 752
QY 57 ----- 57
Db 753 TTACAAACCACCATTTGAGGTGATCCATTTTACAGAGAAGGAAGCAGAGGCTTTTAAGAGG 812
QY 57 ----- 57
Db 813 TTAGGTAAGTCTTAGCCAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 872
QY 57 ----- 57
Db 873 GGTCTCCCAGCCGAGCTTGTCTTACCCTTAGGACAAGGGGTGGACTCCTGACTCTGCA 932
QY 57 ----- 57
Db 933 GATAAATTTACAAAAGCCACAGAGGCAAGTAGTAACCATTTGTGTGACAAACCCCTCAC 992
QY 57 ----- 57
Db 993 CCCAGGAGAGGGGCCCTGTGAGGATTGACGCTCTGGAGTCACACTGCTTTTGAAGAAC 1052
QY 57 ----- 57
Db 1053 GCTGCTCTTTACCCTCCCTAGGTCTGCGGCTTTGAATAAGTATCACTTCTTAGTCTCTCC 1112
QY 57 ----- 57
Db 1113 ATGCCTCAGTTTGTCCATCTGAAATGGGGCATCTGTAATGCTGTGTTATGAGGAGTA 1172
QY 57 ----- 57

Db 1173 AATTACAGCATCCCTGTGAAGAGCTAGCACAGTGTGAGTACGGAATGTTATTTCCATCC 1232
QY 57 ----- 57
Db 1233 TTCTCAGGAGCTTGTTCCTCCCTTCCCTTTACTTGTCCAGCCATTGACTCAT 1292
QY 58 -----GlyIleGlyProValLeuGlyLeuValCysValProLeuLeu 71
Db 1293 ACTACTTCCCTTCTTCCAGGCATTTGGTCCAGTGTGGCTGTGTCTGCTCCGCTCCTA 1352
QY 72 GlySerAlaSerAspHisTrpArgGlyArgTyrglyArgArgProPheIleTrpAla 91
Db 1353 GGCTCAGCAGTAC 1412
QY 92 LeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly 111
Db 1413 CTGTCTTGGGCATCTCTGTAGCCTCTTCTCATCCCAAGGCGCTGGCTAGCAGGG 1472
QY 112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu 131
Db 1473 CTGCTGTGCCCGGATCCCAAGGCGCTGGAGCTGGCAGCTCATCTGCGCGTGGGCTG 1532
QY 132 LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuSerAspLeuPhe 151
Db 1533 CTGGACTTCTGTGGCCAGGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1592
QY 152 ArgAspProAspHisCysArgGlnAlaTyrsrValTyrsrAlaPheMetIleSerLeuGly 171
Db 1593 CGGGACCCCGACCATCTGCCAGGCTACTCTGTCTATGCTTCTATGATCAGTCTTGGG 1652
QY 172 GlyCysLeuGlyTyrsrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrsr 191
Db 1653 GGCTGTCTGGGTACCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1712
QY 192 LeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
Db 1713 CTGGGACCCAGGAGGTGCCTCTTTGGCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1772
QY 212 AlaAlaThrLeuLeuValAlaGluAlaGluAlaLeuGlyProThrGluProAlaGluGly 231
Db 1773 GCAGGCACACTGCTGTGTGCTGAGGAGGAGGCTGGGCCCCACCGAGCCAGAGAGG 1832
QY 232 LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg 251
Db 1833 CTGTGGGCCCCCTCTGTGTGCCACCTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1892
QY 252 AsnLeuGlyAlaLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271
Db 1893 AACCTGGGGCCCCCTGCTTCCCCGGCTGACACAGCTGTGTGTGTGTGTGTGTGTGTGTGT 1952
QY 272 ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291
Db 1953 CCCCCGCTCTTCTGT 2012
QY 292 TyrThrAspPheValGlyGlyLeuTyrglnGlyValProArgAlaGluProGlyThr 311
Db 2013 TACACGGATTTCTGTGGCGAGGGGTGTACAGGGCGTGTGTGTGTGTGTGTGTGTGTGTGT 2072
QY 312 GluAlaArgArgHisTyrsrPheGlu----- 319
Db 2073 GAGGCCCGGAGACATATGATGAAGGTAAAGGCTTGGCAGCCAGCAGAGGCTGTGTGTGTGT 2132
QY 319 ----- 319
Db 2133 AGCCGCCACCAGACGACACTCGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2192
QY 319 ----- 319
Db 2193 CCGGACTTCTCTGT 2252
QY 319 ----- 319
Db 2253 GTGTGGAACATCTGT 2312

QY 319 ----- 319
Db 2313 AGAGTCGTTGGCCCCAGTTTGCAGAGAAGAAAGCGGAGCTTATTCAAAGTCTAGAGGAG 2372
QY 319 ----- 319
Db 2373 TGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGTTCAGCGCGAGTGTGCCCTCTGTCT 2432
QY 319 ----- 319
Db 2433 CCCCCAACGACTTTCACAAATAATCTCACAGCGCCTTCCAGCTCAGGCGTCTCTAGAAGGG 2492
QY 319 ----- 319
Db 2493 TCTTGAAGCCTATGGCAGCTGTCTTGTGTTCCTCTCACCCGCTCTCCCTCACAGCTG 2552
QY 319 ----- 319
Db 2553 AGACTCCAGGAAACCTTCAGACTACCTTCTCTGCTTTCAGCAAGGGCGTGTGCCACA 2612
QY 319 ----- 319
Db 2613 TTCTCTGAGGTCAGTGAAGAACCTAGACTCCCAFTGCTAGAGGTAGAAAGGGAAGGG 2672
QY 319 ----- 319
Db 2673 TGCTGGGAGCAGGCGTGTGTCCACAGCAGGTCTCTGTGAGCAGGTACCTGTGGTTCCGCC 2732
QY 319 ----- 319
Db 2733 TTCTCATCTCCCTGAGACTGTCTCCAGCCCTTCCCTCCAGGCTCTGTCTGTGGCCCCCTC 2792
QY 320 -----GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerIle 336
Db 2793 TCCCTCTGAGCGTTCGATGGGCGCTGTGGCTGTTCCTGTGAGTGGCCATCTCCCT 2852
QY 336 uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrsr 356
Db 2853 GGTCTTCTCTCTGTGTATGAGCCGCTGTGTGAGGATTCGCACTCCAGCAGCTATTT 2912
QY 356 uAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl 376
Db 2913 GGCCAGTGTGGCAGCTTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2972
QY 376 aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 396
Db 2973 CGTGTGTGACGCTTCAGCGCCCTCAGCGGTTTACCTTCTCAGCCCTGCAGATCTGCC 3032
QY 396 oTyrsrThrLeuAlaSerLeuTyrsrHisArgGluLysGlnValPheLeuProLysTyrsrArgG 416
Db 3033 CTACACACTGGCTCCCTCTACCCACCGGAGAGCAGGTGTTCCTGCCCAATACCGAGG 3092
QY 416 yAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLy 436
Db 3093 GGACACTGGAGTGTAGCAGTGAGCAGCAGCTGTATGACAGCTTCTCTGCCAGGCCCTAA 3152
QY 436 sProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProPr 456
Db 3153 GCCTGTGAGCTCTCCCTTCCCTAATGGACACGTGGGTGTGTGGAGGAGTGGCCTGCCACC 3212
QY 456 oProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyG 476
Db 3213 TCCACCCCGCTGTGGGGGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3272
QY 476 uProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAs 496
Db 3273 GCCCAGCCAGGCGAGGTGTTCGGGCGCGGCGCATCTGTGTGTGTGTGTGTGTGTGTGTGT 3332
QY 496 pSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLe 516
Db 3333 TAGTGCCCTTCTGT 3392

Qy	516	uSerGlnSerValThrAlaTyrWetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyr	536
Db	3393	CAGCCAGTCGTGCATGCCTATATGGTGTCGCCGACGCCCTGGTCTGGTCGCATTTA	3452
Qy	536	rPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla	553
Db	3453	CTTTGGTACACAGGTAGTATTTGACAAGAGCGACCTGGCCAAATACTCAGCG	3504

RESULT 19

US-09-895-793-702

: Sequence 702, Application US/09895793

: Publication No. US20020192763A1

: GENERAL INFORMATION:

: APPLICANT: Xu, Jiangchun

: APPLICANT: Dillon, Davin C.

: APPLICANT: Mitcham, Jennifer L.

: APPLICANT: Harlocker, Susan L.

: APPLICANT: Jiang, Yuqiu

: APPLICANT: Kalos, Michael D.

: APPLICANT: Retter, Marc W.

: APPLICANT: Stolk, John A.

: APPLICANT: Day, Craig H.

: APPLICANT: Vedvick, Thomas S.

: APPLICANT: Carter, Barrick

: APPLICANT: Li, Samuel X.

: APPLICANT: Wang, Aijun

: APPLICANT: Skeiky, Yasir A.W.

: APPLICANT: Hepler, William T.

: APPLICANT: Henderson, Robert A.

: APPLICANT: Hural, John

: APPLICANT: McNeill, Patricia D.

: APPLICANT: Houghton, Raymond L.

: APPLICANT: Vinals de Bassols, Carlota

: APPLICANT: Foy, Teresa

: APPLICANT: Fanger, Gary R.

	;	TITLE OF INVENTION:	COMPOSITIONS AND METHODS FOR THE THERAPY AND
	;	TITLE OF INVENTION:	DIAGNOSIS OF PROSTATE CANCER

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; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 702

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: LENGTH: 48

LENGTH: 40
TYPE: DNA

TYPE: DNA
ORGANISM: Homo sapiens

ORGANISM: HOMIO
115-09-895-793-702

701-661-60-50

24-00000-119

Alignment Scores:

pred. No.:	5,33e-229	Length:	4894
Score:	2538.50	Matches:	551
Percent Similarity:	51.11%	Conservative:	0
Best Local Similarity:	51.11%	Mismatches:	2
Query Match:	88.73%	Indels:	526
DB:	9	Gaps:	2

US-09-593-793A-113 (1-553) x US-09-895-793-702 (1-4894)

Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
 |||
 Db 274 ATGCTCCAGAGGCTGTGGTTCAGCCCTGTCTCGGACCGGAAAGCCAGCTTTTGTG 333

DD Z74 A TGGTCCAGAGGCTGTGGGTGAGCCGCCCTGCTGCTGCGGCACCGGAAAGCCAGCTCTTGTGCTG 333

27 Val den I am f am f b b o c l u f a u c l u v a l c u e f a u a l a l c l u f a m f a u a l b o c l o

QY 21 VALASHLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40

334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285

334 GTCACCTGCTAACCTTTGGCCTGGAGGTGTTTGGCCGAGGCATCACCTATGTGCCG 393

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[illegible]

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Qy 57

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Qy	57	-----	57
Db	693	AAATGCTCACCTTTGGCTAGCCCCCTTTAATAATTATAGGATTATCTCATTTAATGC	752
Qy	57	-----	57
Db	753	TTACAACCACTTTGAGGTGATCCATTTTACAGAGAAGAACAGAGGCTTTTAAGAGG	812
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Db	993	CCCAGGAAGAGGGGCCCTGTGAGGANTGCAGGCTCTGGAGTCACACTGCTGTGTGAAC	1052
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Db	1113	ATGCTCAGTTTGTCCATCTGAANAATGGGGGCATCTGTAATGCCCTGCTGTATGAGAGTA	1172
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Qy	57	-----	57
Db	1233	TTCTCAGGAGCTTGGTTCCCTTCCCTTGGCCCTTTACTTGTCCCCAGCCATTGACTCAT	1292
Qy	58	-----	71
Db	1293	ACTACTTCCCTTCTCCAGGCATTTGTCAGTCTGGGCTGGTCTGTGTCCTCCCTCTTA	1352
Qy	72	GlySerAlaSerAspHisTrpArgGlyArGtyrGlyArGArgProPheIleTrpAla	91
Db	1353	GGCTCAGCCAGTGACCACTGGGTGAGCCTATGGCCGCCGCCGCCCTTTCATCTGGGCA	1412
Qy	92	LeuSerLeuClylleLeuLeuSerLeuPheLeuLleProArgAlaGlyYTrpLeuAlaGly	111
Db	1413	CTGTCTTGGGCATCTGTGTGAGCCTTCTTCATCCCAAGGCGCGCTGGCTAGCAGGG	1472
Qy	112	LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuLleLeuGlyValGlyLeu	131
Db	1473	CTGCTGTGCCCGATCCAGGCCCTTGGAGCTGGCAGCTGCTCATCTGGGGCTGGGGCTG	1532
Qy	132	LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe	151
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QY 152 ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
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 QY 192 LeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
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 Db 2013 TACACGGATTTCTGGGGAGGGGTGTACCAAGGCGTGTGCCAGAGCTGAGCGGGCAC 2072
 QY 312 GluAlaArgArgHisTyrAspGlu----- 319
 Db 2073 GAGGCCGGAGACACTATGATGAAGGTAAAGCCTTGGGACGCCAGCAGAGGCTGGTGGG 2132
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 Db 2193 CCCGACTTCTCTCAGGAAAGTGGGATGGACCCCATCTGCATACAGGCTTCTCATGG 2252
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 Db 2793 TCCCTCTCAGGCGTTCCGATGGGAGCCTGGGGCTGTTCCTGCAGTGGCCATCTCCCT 2852
 QY 336 uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe 356
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 QY 476 uProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAs 496
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 QY 536 rPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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 RESULT 20
 US-09-895-814-702
 ; Sequence 702, Application US/09895814
 ; Publication No. US20020193296A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
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 ; APPLICANT: Jiang, Yuqiu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 702
LENGTH: 4894
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-814-702

Alignment Scores:
Pred. No.: 5,33e-229 Length: 4894
Score: 2538.50 Matches: 551
Percent Similarity: 51.11% Conservative: 0
Best Local Similarity: 51.11% Mismatches: 2
Query Match: 88.73% Indels: 526
DB: 9 Gaps: 2

US-09-593-793A-113 (1-553) x US-09-895-814-702 (1-4894)

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QY 41 ProLeuLeuGluValGlyValGluGlyLysPheMetThrMetValLeu----- 57
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Db 394 CCTCTGCTGGAAGTGGGGTAGAGGAGAAGTTTCATGACCATTGCTGCT-GGGTGAGTC 452
QY 57 ----- 57
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QY 57 ----- 57
Db 573 GGAGGTGACCTGGGCTGAGGGGGCACACCAAGAGAAGAGAGAAATACCAAGACATA 632
QY 57 ----- 57
Db 633 CCCAGTCACCTCTGGATCCCTGGTCTGCACAGAGCCCTGGCTCATAGGACACCTGGAG 692
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QY 112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu 131
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RESULT 21
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; Sequence 702, Application US/09759143
; Patent No. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 702
; LENGTH: 4894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-702

Alignment Scores:
Pred. No.: 5.33e-229 Length: 4894
Score: 2538.50 Matches: 551
Percent Similarity: 51.11% Conservative: 0
Best Local Similarity: 51.11% Mismatches: 2
Query Match: 88.73% Indels: 526
Db: 10 Gaps: 2
US-09-593-793A-113 (1-553) x US-09-759-143-702 (1-4894)


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; Sequence 702, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 702
; LENGTH: 4894
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-780-669-702

Alignment Scores:
Pred. No.: 5,33e-229 Length: 4894
Score: 2538.50 Matches: 551
Percent Similarity: 51.11% Conservative: 0
Best Local Similarity: 51.11% Mismatches: 2
Query Match: 88.73% Indels: 526
DB: 10 Gaps: 2

US-09-593-793A-113 (1-553) x US-09-780-669-702 (1-4894)

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QY 312 GluAlaArgArgHisTyrAspGlu 319
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US-10-012-896-705

; Sequence 705, Application US/10012896

; Publication No. US20020183251A1

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Db	1604	CTGGGCACCCAGGAGGAGTGCCCTCTTTTGGCCCTGCTCACCCCTCATCTTCTCCTCACCTTGGGTA	1663
Qy	212	AlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGly	231
Db	1664	GCAGCCACACTGTGTGTGGCTGAGGAGGCAGCGCTGGCCCCCAGCAGCCAGCAAGAGG	1723
Qy	232	LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg	251
Db	1724	CTGTGCGCCCTCTCTGTGTGCGCCCACTGCTGTCCATGCGCGGCGCGTTCGGCTTCCTCGG	1783
Qy	252	AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu	271
Db	1784	AACCTGGCGCCCTGCTTCCCCGGCTGCACCAAGCTGTGTGCGCATGCCCGCACCGCTG	1843
Qy	272	ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe	291
Db	1844	CGCGCGCTCTTCGTGGCTGAGCTGTGCACGTGATGGCACTCATGACCTTCACCGCTGTT	1903
Qy	292	TyrThrAspPheValGlyGluGlyLeuTyrGlnGlyAlaProArgAlaGluProGlyThr	311
Db	1904	TACACGATTTCTGTGGCGAGGGGCTGTACCAGGGCGTGCACAGAGCTGAGCGCGGCACC	1963
Qy	312	GluAlaArgArgHisTyrAspGlu	319
Db	1964	GAGGCGCGAGACACTATGATGAAGTAAGCGCTTGGCAGCCAGCAGAGGCTGTGTGGG	2023
Qy	319	-----	319
Db	2024	AGCGCGCCACCAGAGACACTCGGGGCTGTCTGTGGCTGGTGCCTTCCATCCTGGC	2083
Qy	319	-----	319
Db	2084	CCCGACTTCTCTGCAGAAAGTGGGATGGACCCCATCTGCATACACGGCTTCTCATGG	2143
Qy	319	-----	319
Db	2144	GTGTGGAAACATCTCTCTGTCGGGTTTCAGGAAGGCTCTGGCTGCTTAGGAGTCTGATC	2203
Qy	319	-----	319
Db	2204	AGAGTCGTTGCCCCAGTTTGACAGAAGAAAGCGCGAGCTTATTCAAAGTCTAGAGGGAG	2263
Qy	319	-----	319
Db	2264	TGGAGGAGTTAAGGCTGGATTTTCAGATCTGCCTGTCTCCAGCGCAGTGTGCCCTCTGCT	2323
Qy	319	-----	319
Db	2324	CCCCAACGACTTTCACAAATAATCTACACAGCGCCTTCCAGCTCAGGCGTCTAGAGCG	2383
Qy	319	-----	319
Db	2384	TCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCTCTCACCCCGCTGTCTCTACAGCTG	2443
Qy	319	-----	319
Db	2444	AGACTCCAGGAACCTTCAGACTACCTTCTCTGCCTTTCAGCAAGGGCGGTGCCACACA	2503
Qy	319	-----	319
Db	2504	TTCTCTGAGGGTCAGTGGGAAGAACCTAGACTCCCATTTGCTAGAGGTAGAAGGGGAAGG	2563
Qy	319	-----	319
Db	2564	TGCTGGGAGCAGGCTGTGTCCACAGCAGGTCTCTGTGAGCAGGTACCTGTGTGTCGCC	2623
Qy	319	-----	319
Db	2624	TTCTCATCTCCCTGAGACTGCTCCGACCTTCCCTCCCGAGCTCTGTCTGATGGCCCTC	2683
Qy	320	-----GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe	336
Db	2684	TCCTCTGCAGCGCTTCGATGGCAGCTGTGGGCTGTCTCTGAGTGCAGTGCAGCTATCCCT	2743

QY	336	uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe	356
Db	2744	GGTCTTCTCTGTGTCATGACCGGGTGGTGCAGCGATTTCGCACATCGAGCAGTCTATT	2803
QY	356	uAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl	376
Db	2804	GGCCAGTGTGCACGCTTTCCTGTGGCTGCCGTGCACATGCCCTGCCACAGTGTGGC	2863
QY	376	aValIThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr	396
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QY	396	oFyrThrLeuAlaSerLeuTyrHisArgGluIysGlnVal	409
Db	2924	CTACACATGGCCCTCCCTCTACCAACGGGAGAGCAGGT- ACTCATTTGCCAGTGGGTGG	2982
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Db	2983	AGTCAGGTGGAGGGGTGTCTGGGTTTTCGGAGGCCAACTAGCTCAGAACCTGGTAT	3042
QY	409	-----	409
Db	3043	CTGGCAACCACTTTTGAGAAATGCTTCTTTGAATCAGAGAAGACTTATCCTAGCCCCA	3102
QY	409	-----	409
Db	3103	GGCCAGCAGGCTTGGGCTGCAGAACAGTGTATATTAGATTCTTGGGAATGACTTCTGTGGG	3162
QY	409	-----	409
Db	3163	TCAGACTGTGTAGCACTTCAATGGATGATTGCAGGAATGCAAAATACGATAGTGGGAA	3222
QY	409	-----	409
Db	3223	TCCGAAGGGTCAGGCCAGCAGGAGCCCTAGGCTTCTAGGCTGGTTGTCTATGGAGAGG	3282
QY	409	-----	409
Db	3283	CAGGGCGCTGAATCAGATGACCCCTTGGGCAATTCAGCCTCAGCAGCGGAGTGGGAATG	3342
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Db	3343	GTCCAGCCTTAGCAACACCTTTCTTCAGGGAGCAGCAACCTGACTTAGCCTGTATCCTAC	3402
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Db	3403	TCTGGTCTCTGAGATGGGCGAGCTCTTCTTCCCTACCCCTTTCTTCTGGCTATTTTTCT	3462
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Db	3523	TCCCTTCCCTTCCCTCTGGGCAGATATCTGAGCTTGACACCTGACCCACTCACTTGGG	3582
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QY	409	-----	409
Db	3643	GGGCCCTTTCCTTGGGAAGCCACCTAACCCAGATAGTGTGTATCTTGTCCCTTCCA	3702
QY	409	-----	409
Db	3703	CTGACCTCACTGAGCTACAAACCTGGTGCTGGACTCTGGAGGGCATGAAGTTGG	3762
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Db	3763	GGTGTCCCAAGGAGGAGGATGCAAGACTGCTCTCATAGAGCTCTCAGACTGTAGGGA	3822

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Db 3883 GGCTGGTTAACTAGTAGGTAGCTGCAGGGGTAGAGATATGGAGGGGAGGGGCTAAAGGT 3942
QY 409 ----- 409
Db 3943 TTTGGTTGGGGAGCCTGGTCCCTGAGACCCCTGTTAGCCCCACTGATAACCTTCTTCAGC 4002
QY 409 ----- 409
Db 4003 CTTCACTCTTCTGCTTGCTGGCTGGGGCAGGGGCTGGCATCAGCGGCCAGGSCCTGA 4062
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QY 409 ----- 409
Db 4123 ATGTCTGCTCGGACCACTCCAGACTCCAACCTCAGCGGACATTCCTGGGGTGGCAGGC 4182
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Db 4183 AGGGAGGAGAAGTCTCTGGGAGGCCCTTTCCTTAACAGCAGCTGATGGCAGACTTGGCACTG 4242
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Db 4483 CAGCAGGAGGAAGTGAGAACCTTCAACATTAGCACAGCTGGGGCTGGGGGAGGTGGGA 4542
QY 409 ----- 409
Db 4543 AGAGGACATTCCCTCCTGCTTGGGTCTACTGGATTCTCCCTGCCCAAGGCTGGGACA 4602
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Db 4603 AGGAGCTCATGGCAGGCAGCTACCTAGTGGCATCTGGGACCCCGAGAGGAGAGCT 4662
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Db 4663 TCTCTGCACCGGCAATGAGGATTTCCAGATGTCGGAGTGGAGGCGCAGGAGGAAG 4722
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Db 4783 TGTTCTGFCATCTTACCACCGCTCTCAFTCCCTGTGTCTTTTCTTACCTTGGAG 4842
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Db 4843 CTCGTCTCTCTGATCTGTGATATTGAGTTTGTCTGCTTCTTACCTGTTCTTAAGAGGCT 4902
QY 409 ----- 409

Db 4903 AGAGGAGACCTAGACTTCTGGGTTTCACATTTGTCCCCCCTACCCGTTACCTTCTCC 4962
QY 409 ----- 409
Db 4963 CACTCTCAGGAAGGTCTCTGGTTAGACTTGGACCAAGTAGGGTCTCCATCTTCTCTCCT 5022
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Db 5023 GCTCCTGATTCTCATGAAGTCCCATTTGCCCTGGGATGGAGGAGGCTGTGTTCTCACA 5082
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Db 5143 GCCTTAGGTGTCTCTGCCAAATACCGAGGGGACACTGGAGGTCTAGCAGTGGAGCAG 5202
QY 426 rLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisVa 446

Db 5203 CCTGATGACCACTTCTGCGCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT 5262
QY 446 lGlyAlaGlySerGlyLeuLeuProProProAlaLeuLeuCysGlyAlaSerAlaCy 466

Db 5263 GGTGCTGGAGGCACTGGCCTGCTCCACCTCCACCGCTCTGCGGGGCTCTGCGCTG 5322
QY 466 sAspValSerValArgValValValGlyGluProThrGluAlaArgValValProGlyAr 486

Db 5323 TGATGCTCTCCGTAGCTGTGGTGGGTGAGCCACCGAGGCCAGGGTGGTTCGGGGCCG 5382
QY 486 gGlyLeuCysLeuAspLeuAlaLeuLeuAspSerAlaPheLeuLeuSerGlnValAlaPr 506

Db 5383 GGGCATCTGCTGGACCTCGCCATCTCGGATAGTGCCTTCTGTGCTCCAGGTGGCCCC 5442
QY 506 oSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSe 526

Db 5443 ATCCCTGTTATGGCTCCATTTGCCAGCTCAGCAGCTGTCACTGCCTATATGTTGTC 5502
QY 526 rAlaAlaGlyLeuGlyLeuValAlaAlaIleTyrPheAlaThrGlnValValPheAspLysSe 546

Db 5503 TGCGCAGGCTGGGTCTGGTCCGCAATTTACTTTGTACACAGGTAGTATTGTACAAGAG 5562
QY 546 rAspLeuAlaLysTyrSerAla 553

Db 5563 CGACTTGGCCAAATACTCAGCG 5584
RESULT 25
US-09-895-793-705
: Sequence 705, Application US/09895793
: Publication No. US20020192763A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yuqiu
: APPLICANT: Kalos, Michael D.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William T.
: APPLICANT: Henderson, Robert A.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Vinals de Bassols, Carlota
: APPLICANT: Foy, Teresa

Db 1964 GAGGCCGAGACACTATGATGAAGGTAAAGCCCTTGGCAGCCAGCAGAGGCTGTGTGGG 2023
Qy 319 ----- 319
Db 2024 AGCCGCCACCAGACACACTCGGGGCTGTGTCTGGCTGGTGCCTCTCCATCCTGGC 2083
Qy 319 ----- 319
Db 2084 CCCGACTTCTGTCTGACGAAAGTGGGATGGACCCCATCTGCATACACGGCTTCTCATGG 2143
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Db 2744 GGTCTTCTCTGTCTATGACCGCGCTGGTGACGATTCGGCACTCGACGACTCATATT 2803
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Db 2804 GGCCAGTGTGGCAGCTTTCCTCTGTGGCTGCGCGTGCCACATGCCTGCCACAGCTGTGGC 2863
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Db 2864 CGTGGTGACAGCTTTCAGCCGCCCTTCACCGGGTTTCACCTTCTCAGCCCTGCAGATCCTGCC 2923
Qy 396 oTyrThrLeuAlaSerLeuTyrHisArgGluLysGluVal----- 409
Db 2924 CTACACACTGGCCCTTCCCTCTACACCCGGAGACAGGT-ACTCATTTGGCCAGTGGGTGG 2982
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Db 2983 AGTCAGGTTGGAGGGTGTCTGGGTTTTTGGGAGGCCAACTAGCTCAGAACTGGTAT 3042
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Db 4543 AGAGGACATTCCTCCTGCTTGGGGTCTACTGGATTCTCCCTGCCCAAGGCTGGGACA 4602
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Db 4603 AGGAGCTCATGCGAGGCGAGCTACCTAGTGGCATCTGGACCCCGAGAGAGCT 4662
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Db 4663 TCTCTCACCGGCAATGAGGATTTCCAGATGTCGGAGTGGAGGCGAGCAGAGGAAG 4722
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Db 4903 AGAGGAGACCTAGACTTCTGGGTTTACATTTGTCCCGCCCTACCCGTTACCCCTTCTCC 4962
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Db 4963 CACTCTGAGGAGGCTCTGTTAGACTTGGACCAAGTAGGGTCTCCATCTCTCTCTCT 5022
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Db 5023 GCTCTGATTCTCATGAAGTCCCATTTGCCCTGGGATGGAGCAAGGGTCTGTCTCACA 5082
QY 409 ----- 409
Db 5083 GCTGGGGTGTGCCAGTCTGTGGGTACACACCTGTCTCTTCCCTTTTCTTCCACCCCTCT 5142
QY 410 ----- PheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAspSe 426
Db 5143 GCCTTAGGTGTCTCTGCCCAATACCGAGGGGACACTGGAGGTGTAGCAGTGGAGACAG 5202
QY 426 rLeuMetThrSerPheLeuProGlyProLysProGlyAlaPheProAsnGlyHisVa 446
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QY 446 lGlyAlaGlySerGlyLeuLeuProProAlaLeuCysGlyAlaSerAlaCys 466

Db 5263 GGTGTCTGGAGCAGTGGCTCTCTCCACCTCCACCGGCTCTCGGGGCTCTGCTGCTG 5322
QY 466 sAspValSerValArgValValValGlyGluProThrGluAlaArgValValProGlyAr 486
Db 5323 TCATGTCTCCGTACGTGTGGTGGTGAGCCGCCAGGAGCCAGGGTGTTCGGGGCCG 5382
QY 486 gGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaPr 506
Db 5383 GGGCATCTCCCTGGACCTCGCCATCTGTGATAGTCTCTCTCTGCTCCAGGTGGCC 5442
QY 506 oSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSe 526
Db 5443 ATCCCTGTTTATGGGTCATTTGTCAGCTCAGCCAGCTGTGCTACTGCTATATGTTGC 5502
QY 526 rAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSe 546
Db 5503 TCCCGCAGGCCCTGGGTCTGGTCCCATTTTGTCTACACAGGTAGTATTTGACACAGAG 5562
QY 546 rAspLeuAlaLysTyrSerAla 553
Db 5563 CGACTTGGCCAAATACTCAGCG 5584
RESULT 26
US-09-895-814-705
; Sequence 705, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
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; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-705
Alignment Scores:
Pred. No.: 1.16e-191 Length: 6976
Score: 2144.00 Matches: 551
Percent Similarity: 30.48% Conservative: 0
Best Local Similarity: 30.48% Mismatches: 2
Query Match: 74.94% Indels: 1257
DB: 9 Gaps: 3
US-09-593-793a-113 (1-553) x US-09-895-814-705 (1-6976)

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QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 225 GTCAACCTGCTAACCTTTGGCTGGAGGTGTGTTGGCCGCGAGGCATCACCTATGTGCGG 284
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeu----- 57
Db 285 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGGTGCT-GGGTGAGTTC 343
QY 57 ----- 57
Db 344 ACTACATCCTCTCTTCCTTCTCCAGATACATGCCACCTGGCATGTGGACAGGAGTA 403
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QY 57 ----- 57
Db 704 TTAGGTAGTCTTTAGCCAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 763
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Db 824 GATAAATCTACAAGGCCACAGAAGGCAAGTAGTAACCATTTGTGTGACAACCCCTCACC 883
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Db 884 CCCAGGAAGAGGGCCCTGTGAGGATTGCAGGCTCTGGAGTCACACTGCTTGTGTAAC 943
QY 57 ----- 57
Db 944 GTCGCTCTTACCCCTCCCTAGTCTGCGCCTTTGAATAGATATCATCTTMTAGTTGCTCC 1003
QY 57 ----- 57
Db 1004 ATGCCTCAGTTTGTCCATCTGAAATGGGGGCATCTGTAATGCCCTGTATTATGAGGAGTA 1063
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Db 1064 AATTACAGCATCCCTGTGAAGAGGTAGCACAGTGTGCGAGTACGGAATGTTATTTCCATCC 1123
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Db 1124 TTCTCAGGAGCTTGGTTCCCTTCCCTTGGCCCTTTACTTGTCCAGCCATTGACTCAT 1183
QY 58 -----GlyIleGlyProValLeuGlyLeuValCysValProLeuLeu 71
Db 1184 ACTACTTCCCTTCTTGCAGGCATTTGTCAGTGTGCGCTGGGCTGTGTCGCCGCTCTTA 1243
QY 72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgProPheIleTrpAla 91

Db 1244 GGCTCAGCAGTGCACACTGGCTGGACGCTATGGCGCGCGGCTTCATCTGGGCA 1303
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Db 1304 CTGTCTCTGGGATCCTGCTGAGCCCTCTTTCATCCCAAGGGCCGGCTGGGTAGCAGGG 1363
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RESULT 27

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US-09-759-143-705
; Sequence 705, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-705

Alignment Scores:
Pred. No.: 1.16e-191 Length: 6976
Score: 2144.00 Matches: 551
Percent Similarity: 30.48% Conservative: 0
Best Local Similarity: 30.48% Mismatches: 2
Query Match: 74.94% Indels: 1257
DB: 10 Gaps: 3

US-09-593-793A-113 (1-553) x US-09-759-143-705 (1-6976)

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Db 5263 GGTGCTGGAGGAGTGGCTGTCTCCACCTCCACCCGCGCTCTGGGGGCGCTCTGCCCTG 5322
QY 466 saspValSerValArgValValValGlyGluProThrGluAlaArgValValProGlyAr 486
Db 5323 TGATGTCCTCGTACGTGTGGTGGGTGAGCCACCGAGCCAGGGTGGTTCGGGGCCG 5382
QY 486 gGlylleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaLpr 506
Db 5383 GGCATCTGCTGGACCTGCCCATCTCGGATAGTCTCTCTCTCTCTCTCTCTCTCTCTCT 5442
QY 506 oSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSe 526
Db 5443 ATCCCTGTTTATGGGTCCATTGTCAGCTCAGCCAGTCTGTCACTGCCTATATGTTGTC 5502
QY 526 rAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSe 546
Db 5503 TGCCGAGGCGCTGGGTCTGGTCCCATTTACTTTGTACACAGGTAGTATTTGACAAGAG 5562
QY 546 rAspLeuAlaLysTyrSerAla 553
Db 5563 CGACTTGGCCAAATACTACGCG 5584

RESULT 28

US-09-780-669-705
; Sequence 705, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09

; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 13.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-705
Alignment Scores:
Pred. No.: 1,16e-191 Length: 6976
Score: 2144.00 Matches: 551
Percent Similarity: 30.48% Conservatives: 0
Best Local Similarity: 30.48% Mismatches: 2
Query Match: 74.94% Indels: 1257
DB: 10 Gaps: 3
US-09-593-793A-113 (1-553) x US-09-780-669-705 (1-6976)
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QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIlePheTrpValPro 40
Db 225 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTGGCCGACGAGCATCACTATGTGCC 284
QY 41 ProLeuLeuLeuGluValGlyValGlyValGluGluLysPheMetThrMetValLeu 57
Db 285 CCTCTGCTGCTGGAAGTGGGGTAGAGGAGAGTTCATGACCATGTGTCT-GGGTGAGTC 343
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Db 524 CCCAGTACCTCTCGATCCCTGGTCTCTGACAGAGCTGGCTCATAGGAGACATGGAG 583
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Db 704 TTAGGTAAGTCTTAGCCAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 763
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Db 1304 CTGTCTTGGGCATCTGTGTGACCTCTTCTCATCCCAAGGCGCGCTGGCTAGCAGG 1363
QY 112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu 131
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Db 1544 GGCTGCTGGGTACTCTCTGCTGCCATTGACTGGACACCACTGCCCTGCCCTTAC 1603
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QY 212 AlaAlaThrLeuLeuValAlaGluAlaAlaLeuGlyProThrGlnProAlaGlyLeu 231
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QY 252 AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271
Db 1784 AACCTGGGGCCCTGTCTCCCGGCTGCACCACTGTGTGCGCATGCCCGCACCCCTG 1843
QY 272 ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291
Db 1844 CCCCCGCTCTTCTGGCTGAGCTGTGACCTGGATGGACTCATGACCTTCAGCTGTGTT 1903
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QY 312 GluAlaArgArgHisTyrAspGlu----- 319
Db 1964 GAGGCCCGGAGACACTATGATGAAGTAAGGCTTGGCAGCCAGCAGAGGCTGGTGTGG 2023
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Db	3343	GTCCAGCCTTAGCAACACCTTTCTTCAGGGAGCAGCAACTGACTAGCCTGTATCCTAC	3402
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Db	3403	TCTGGTCTCTGAGATGGGCGAGCTCCTTCCTACCCCTTCTTCTGGCTTATTTTCT	3462
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Db	3643	GGCCCCCTTCTTGGGAAGCCACCTAACCCAGGTAGTGTGGTCACTCCTTGTCCTCCCA	3702
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Db	3943	TTTGGTTGGGGAGCCTGGTCCCTGAGACCCCTGTAGCCCACTGATAACCTTCTTCAGC	4002
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Db	4003	CTTCACTCTTCTGCTTGCTGGCTGGGGCAGGGGCTGGCATCAGCGCCAGGCTGA	4062
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Db	4123	ATCTCTGCTCGGACCCTCCAGACTCCAACTCAGCGGACATTCCTGGGGTGGCAGGC	4182
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Db	4183	AGGAGGAGAAGTCTCTGGGAGGCCCTTCTTAACAGCAGCTGATGCGACTTGGCACTG	4242
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Db	4303	CTGGTGTCAAGTTTGTAGCTCTGCCATGGCTCCACCTCGCAATGCAGCCAACTCAACTC	4362
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Db	4423	GCCATCAAGGCGAGGGTTGGGGGATGGTGTGCAGCAGTCACTCTGTATCTAAGTCAGA	4482
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Db	4483	CAGCAGGAAGGAAGTCAGAAAGCCCTTCAACATTAGCACAGCTGGGGCTGGGGAGGTGGGA	4542
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Db	4783	TGTTCTGTGCATCTCTTACCACCGTCTTCATTTCCCCCTGTGTCTTTTCCTTACCTTGGAG	4842
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Db	4843	CTCTGTCTCTGTGATCTGTGATATTGAGTTTGTCTGCCTCTTACCTGTTCTAAGAGGCT	4902
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Db	4903	AGAGGAGACCTAGACTTCTGGGTTTCAATTTGTCGCCGCTTACCCGCTTACCTTCTCC	4962
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Db	4963	CACCTCTGAGGAAGGTCTCTGTTAGACTTGGACCAAGTAGGCTCTCCATCTTCTCTCCT	5022
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Db	5023	GCTCTGATTCTCATGAAGTCCCATTTGCCCTGGGATGGAGCAAGGCTGTGTTCTCACA	5082
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Qy	426	rLeuMetThrSerPheLeuProLysProGlyAlaProPheProAsnGlyHisVa	446
Db	5203	CCTGATGACCAGCTTCTGCCAGGCCCTAAGCTGGAGCTCCCTTCCCTAATGGACACGT	5262
Qy	446	lGlyAlaGlySerGlyLeuLeuProProAlaLeuCysGlyAlaSerAlaCy	466
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Qy	466	saspValSerValArgValValValGlyGluProThrGluAlaArgValValProGlyAr	486
Db	5323	TGATGTCTCCGTACGTGTGTGGTGAGCCACCGAGGCCAGGGTGTGTTCCGGGCCG	5382

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Qy 486 gglyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaPr 506
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Db 5383 GGGCATCTGCTGGACCTCGCATCTCGATAGTGCCCTTCTGCTGCCAGTGCCCC 5442
Qy 506 oSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSe 526
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Db 5443 ATCCCTGTTTATGGGCTCCATTGTGCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGT 5502
Qy 526 rAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSe 546
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Db 5503 TCCCGCAGCCCTGGGTCTGGTGGCCATTACTTTGCTACACAGGTAGTATTGACAAGAG 5562
Qy 546 rAspLeuAlaLysTyrSerAla 553
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Db 5563 CGACTTGGCCAAATACTCAGCG 5584

RESULT 29
US-09-822-827-705
; Sequence 705, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 705
; LENGTH: 6976
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-705

Alignment Scores:
Pred. No.: 1,16e-191 Length: 6976
Score: 2144.00 Matches: 551
Percent Similarity: 30.48% Conservative: 0
Best Local Similarity: 30.48% Mismatches: 2
Query Match: 74.94% Indels: 1257
DB: 10 Gaps: 3

US-09-593-793A-113 (1-553) x US-09-822-827-705 (1-6976)
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Qy 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeu----- 57
Db 285 CCTGTGCTGCTGGAAGTGGGGTAGAGGAGAAGTTCATGACCATTGGTCT-GGGTGAGTC 343
Qy 57 ----- 57
Db 344 ACTACATCCTCTCTCTTCTTCTTCCAGATACATGCCACCTGGCATGTGGGACAGGACTA 403
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Db 824 GATAAATTTACAAAAGCCACAGAAGCAAGTAGTAACCATTTGTGTGACACCCCTCACC 883
Qy 57 ----- 57
Db 884 CCCAGAAAGAGGGGCCCTGTGAGGATTGCAGGCTCTGGAGTCACACTGCTTGTGTGAAC 943
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Db 944 GCTGCCTCTTACCCTCCCTAGGTCTGCGCCTTTGAATAAGTATCATCTTMTAGTTGCTCC 1003
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Db 1064 AATTACAGCATCCCTGTGAAGACGTAGCACAGTGCAGTAAGGAATGTTATTTCCATCC 1123
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Db 1124 TTCACGAGGCTTGGTTCCCTTCCCTTCCCTTGTCCCTTTACTTGTCCAGCCATTGACTCAT 1183
Qy 58 -----GlyIleGlyProValLeuGlyLeuValCysValProLeuLeu 71
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Db 1244 GGCTCAGCCAGTGCACACTGGCGTGGAGCTATGGCCCGCCGCCCTTTCATCTGGGCA 1303
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Db 1304 CTGCTCTTGGGCATCTGCTGAGCCCTCTTCTCATCCCAAGGCGCGCTGGCTAGCAGGG 1363
Qy 112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu 131
Db 1364 CTGCTGTGCCCGGATCCCGAGCCCTTGGAGCTGGCACTGCTCATCTGGCGGTGGGGCTG 1423
Qy 132 LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151
Db 1424 CTGGACTTCTGTGGCAGGTGTGCTTCACTCCACTGGAGGCGCTGCTCTCTGACCTCTC 1483
Qy 152 ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
Db 1484 CGGGACCCGGACCACTGTCGCCAGGCCCTACTCTGTATGCCCTTCATGATAGTCTTGGG 1543
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Db 1544 GGCTGCTGGGCTACTCTGCTGCCATTGACTGGGACACAGTGCCCTGGCCCCCTAC 1603
Qy 192 LeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
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QY 212 AlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGly 231
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QY 292 TyrThrAspPheValGlyGluGlyLeuTyrGlnGlnValProArgAlaGluProGlyThr 311
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Db 2864 CGTGGTGCAGCTTCAGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCC 2923
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Db 3823 AGACCTGCCCCCTGCGTCTCGTAGCACATTGAGGAGAGGAGTAGGTAAGTTCTCGTAGCTGAGA 3882
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Db 3883 GGCTGGTTAACTGAGTAGGTAGCTGACAGGGGTGAGAGGTATGAGGGGAGGGGCTAAGGT 3942
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Db 3943 TTTGGTTGGGGAGCCTGGTCCCTGAGACCCTGTGTAGCCCACTGATAAACCTTCTTCAGC 4002
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Db 4003 CTTCACTCTTCTGCTGCTGGGTGGGGCAGGGGCTGGCATCAGCGGCCAGGCGCTGA 4062
Qy 409 ----- 409
Db 4063 GTATGTGCTGCTGCCAGGGAACGTTCTGGGGCTAGCCATCTTCTCCAGATGGAGGAGC 4122
Qy 409 ----- 409
Db 4123 ATGTCTGTCTCGGACCACCTCCAGACTCCAACTCAGCGGACATTCTCTGGGGTGGCAGGC 4182
Qy 409 ----- 409
Db 4183 AGGAGGAGAAAGTCTGGGAGGCCCTTCTTAACAGCAGCTGTATGGCAGACTTGGCACTG 4242
Qy 409 ----- 409
Db 4243 CACGCTGTCTGCCCTGTTCTTGGCCACTGTTGACGTGCTGATGGTGGCCGTGGGCTTCC 4302
Qy 409 ----- 409
Db 4303 CTGCTGTCAAGTTTGAGCTCTGCATGCTCCACCTCGCAATGCAAGCAACTCAACTC 4362
Qy 409 ----- 409
Db 4363 TTCTGGCATGGGGAATGTTGGATAAGACCTGGCCCTGTGCTTAAATAGGAGGCTCTGG 4422
Qy 409 ----- 409
Db 4423 GCCATCAAGGCAGGGGTTGGGGGATGGTGGTGACAGTCACTCTGATCTAAGTCAGA 4482
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Db 4483 CAGCAGGAAGAGTAGAGAGCCCTTCAACATTAGCACAGCTGGGGCTGGGGAGGTGGGA 4542
Qy 409 ----- 409
Db 4543 AGAGGACATTCCCTCTGCTTGGGGTCTACTGGATTCTCCTGCCCCAAGGCTGGGGACA 4602
Qy 409 ----- 409
Db 4603 AGGAGCTCATGGCAGGCAGCTACCTATGTGGCATCTGGACCCCAAGAGGCAGAGCT 4662
Qy 409 ----- 409
Db 4663 TCTCTGCCCGGCAATGAGGATTTCCAGATGTCGGAGTGGAGGCGCAGGAGGAAG 4722
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Db 4723 GTTAGGAGGCTCGTGGGTTTGGGCCATCAGGGGCCCTGCTTGGCTTTTGTCTCCTC 4782
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Db 4783 TGTCTCTGCATCTCTTACCACCGCTCTTCATTCCTCCCTGTGCTTTTCTTACCTTGGAG 4842
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Db 4843 CTCGTCTCTCTCATCTGTATATTGAGTTGTGCTCTTACCTGTTCTTAAGAGGCT 4902
Qy 409 ----- 409
Db 4903 AGAGGAGACCTAGACTTCTGGGTTACATTTGTCCCGCCCTACCCGTTTACCCTTCTCC 4962

Qy 409 ----- 409
Db 4963 CACTCTGAGGAAGGGTCTCGTTAGACTTGGACCAAGTAGGGTCTCCATCTTCTCTCCT 5022
Qy 409 ----- 409
Db 5023 GCTCCTGATTCTCATGAAGTCCCATTTGCCCTGGGATGGAGCAAGGGTCTGTTCTCACA 5082
Qy 409 ----- 409
Db 5083 GCTGGGTGGTGCCAGTGTGGGTACACACTGTCTCTTCCCCCTTTTCTTACCCCTCT 5142
Qy 410 -----PheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAspSe 426
Db 5143 GCCTTAGGTGTCTCTGCCCAATAACCGAGGGACACTGGAGGTCTAGCAGTAGGACAG 5202
Qy 426 rLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHIsVa 446
Db 5203 CCTGATGACCAGCTTCTCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTTAATGGACAGT 5262
Qy 446 lGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCy 466
Db 5263 GGGTGTCTGGAGGAGTGGCTTCCACCTCCACCGCTCTCGGGGCGCTCTGGCTG 5322
Qy 466 sAspValSerValArgValValValGlyGluProThrGluAlaArgValValProGlyAr 486
Db 5323 TGATGTCTCGTAGCTGTGGTGGGTGAGCCACCGAGGCCAGGGTGTCTCCGGGCGG 5382
Qy 486 gGlyLeuCysLeuAspLeuAlaLeuLeuAspSerAlaPheLeuLeuSerGlnValAlaPr 506
Db 5383 GGGCATCTGCTGGACCTCGCCATCTCTGGATAGTGCCTTCTGTGTCTCCAGGTGGCCCC 5442
Qy 506 oSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSe 526
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Qy 526 rAlaAlaGlyLeuGlyLeuValAlaLalleTyrPheAlaThrGlnValValPheAspLysSe 546
Db 5503 TGCCGCGAGGCTGGGTCTGTGCGCCATTACTTTGCTACAGAGTAGTATTGACAAGAG 5562
Qy 546 rAspLeuAlaLysTyrSerAla 553
Db 5563 CGACTTGGCCAAATACTCAGCG 5584
RESULT 30
US-10-012-896-703
; Sequence 703, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro

APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 703
LENGTH: 2904
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-703

Alignment Scores:

Pred. No.: 3,6e-171 Length: 2904
Score: 1920.50 Matches: 390
Percent Similarity: 77.23% Conservative: 0
Best Local Similarity: 77.23% Mismatches: 1
Query Match: 67.13% Indels: 115
DB: 9 Gaps: 1

US-09-593-793A-113 (1-553) x US-10-012-896-703 (1-2904)

QY 163 ValTyrAlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAsp 182
DB 1 GTCTATGCTTCATGATCAGTCTTGGGGGCTGCTGGGCTACCTCCTGCCTGCCATTGAC 60
QY 183 TrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeu 202
DB 61 TGGGACACGAGTGGCTGGCCCTTACCTGGGACCCAGGAGGAGTGGCTCTTTGGCCCTG 120
QY 203 LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGluAla 222
DB 121 CTCACCTCATCTTCTTACCTGCTGAGCAGCCACACTGCTGGTGGCTGAGGAGGACGG 180
QY 223 LeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCys 242
DB 181 CTGGGCCCCACCCAGGACGACAGAGGGCTGTGGGCCCTCTTGTGCCCCACTGCTGT 240
QY 243 ProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGln 262
DB 241 CCATGCCGGGGCCGCTTGGCTTTCGGGAACCTTGGGCGCCCTCTTCCCGGGCTGCACGAG 300
QY 263 LeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrp 282
DB 301 CTGTGCTGCCGATGCCCGCACCTGCGCGGCTCTTCTGCTGGCTGAGCTGTGACGCTGG 360
QY 283 MetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGln 302
DB 361 ATGGCACTCATCAGCTTACCGCTGTTTACACGGATTTCTGTTGGGAGGGGCTGTACCAG 420
QY 303 GlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal --- 321
DB 421 GCGCTGCCAGAGCTGAGCGGGGACCGAGGCGCCGAGGACACTATGATGAAGGAAG -GCC 479
QY 321 ----- 321
DB 480 TCTGGCTGCTTAGGAGTCTGATCAGAGTCTGTGGCCCGGTTTGACAGAAGAGGCGG 539
QY 321 ----- 321
DB 540 AGCTTATTCAAAGTCTAGAGGAGTGGAGGAGTTAAGGCTGGATTTTCAGATCTGCTGGT 599
QY 321 ----- 321
DB 600 TCCAGCCGAGTGTGCCCTCTGCTCCCGCAAGACTTTTCCAAATAATCTCACCAGCGCT 659
QY 321 ----- 321
DB 660 TCCAGCTCAGGGCTCTAGAACGCTGTTGAAGCCTATGGCCAGCTGCTTTGTGTTCCT 719
QY 321 ----- 321

DB 720 CTCACCCGCTGTCTCTCAGCTGAGACTCCAGGAAACCTTTCAGACTACCTTCTCTCTGC 779
QY 322 ----- ArgMetGlySerLeuGlyLeu 328
DB 780 CTTTACGAAGGGGCGTGGCCACATTTCTTGAGGGCGTTTCGGATGGGACGCTGGGGCTG 839
QY 329 PheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArg 348
DB 840 TTCCTGCACTGGCCATCTCCCTGCTCTCTCTGGTCATGACCGGCTGTGTCAGCGA 899
QY 349 PheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAla 368
DB 900 TTCGCACTCGAGCAGTCTATTTCGCGAGTGTGGAGCTTTCCCTGTGGCTGCGGTGCC 959
QY 369 ThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuThrGlyPheThr 388
DB 960 ACATGCTCTGCCACAGTGTGGCCGTGGTGGACAGCTTACGCGCCCTCACCGGGTTACCC 1019
QY 389 PheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluGlyGln 408
DB 1020 TTCCTCAGCCCTGCAGATCTGCCCTACACACTGGCTCCTCTACACCGGGAAGACG 1079
QY 409 ValPheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMet 428
DB 1080 GTGTTCTCTGCCAAATACCGAGGGGACACTGGAGGTGTAGCAGTAGGACAGCCTGATG 1139
QY 429 ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAla 448
DB 1140 ACCAGCTTCTTCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTTAATGGACACGCTGGTGT 1199
QY 449 GlyGlySerGlyLeuLeuProProProAlaLeuLeuCysGlyAlaSerAlaCysAspVal 468
DB 1200 GGAGCAGTGGCTGCTCCACCTCCACCGGCTCTGGGGGCTCTGCGGTGTGATGTC 1259
QY 469 SerValArgValValValGlyGluProThrGluAlaArgValValProGlyArgGlyIle 488
DB 1260 TCCGTACGTGTGGTGGGTGAGCCACCGAGGCGAGGGTGTTCGGGCGGGGCGATC 1319
QY 489 CysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeu 508
DB 1320 TCCCTGGACCTCGCCATCTGGATAGTGCCTTCTCTGCTGCTCCAGTGGCCCCATCCCTG 1379
QY 509 PheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAla 528
DB 1380 TTTATGGGCTCCATGTCCAGCTCAGCAGCTGTCTGCTATATGCTGTGTCGCCGA 1439
QY 529 GlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeu 548
DB 1440 GGCCTGGGTCTGGTGGCATTTTACTTTGCTACACAGTAGTATTTTGACAAGAGCGACTTG 1499
QY 549 AlaLysTyrSerAla 553
DB 1500 CCAAAATACCTCAGCG 1514
RESULT 31
US-09-895-793-703
; Sequence 703, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun

```
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-703

Alignment Scores:
Pred. No.: 3.6e-171 Length: 2904
Score: 1920.50 Matches: 390
Percent Similarity: 77.23% Conservative: 0
Best Local Similarity: 77.23% Mismatches: 1
Query Match: 67.13% Indels: 115
DB: 9 Gaps: 1

US-09-593-793A-113 (1-553) x US-09-895-793-703 (1-2904)

Qy 163 ValTyrAlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAsp 182
Db 1 GTCTATGGCTTCATCATCAGCTTGGGGCTGCCCTGGGGTACCTCTGCTGCCATTGAC 60

Qy 183 TrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPheGlyLeu 202
Db 61 TGGGACACAGTGGCCCTGGCCCTACCTGGGSCACCCAGGAGAGTGGCTCTTTGGCCTG 120

Qy 203 LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluAlaAla 222
Db 121 CTCACCCCTCATCTTCCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGCAGG 180

Qy 223 LeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCys 242
Db 181 CTGGCCCCCAGCCAGCAGAGGGCTGTGGCCCCCTCTTGTGGCCCCACTGCTGT 240

Qy 243 ProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGln 262
Db 241 CCATGCGGGCCCGCTTGCTTTCCGGAACCTGGGCGCCCTCTTCCCGGGCTGCACCCAG 300

Qy 263 LeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrp 282
Db 301 CTGTGCTGCGGATGCCCGCCACCTTGGCGCGGCTCTTGGTGGCTGAGCTGTGACAGTGG 360

Qy 283 MetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGln 302
Db 361 ATGGGCACATACCTTCACGCTGTTTACACGGATTTCGTGGGGAGGGGCTGTACCCAG 420

Qy 303 GlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal --- 321
Db 421 GCGGTGCCAGAGCTGAGCCGGGACCCAGGCGCCGAGACACTATGATGAAGGAAG-GCC 479

Qy 321 ----- 321
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Qy 321 ----- 321
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Qy 321 ----- 321
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Qy 322 ----- ArgMetGlySerLeuGlyLeu 328
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Qy 329 PheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArg 348
Db 840 TTTCTGTCAGTGGCCATCTCCCTGGTCTTCTCTGCTGATGACCGGCTGGTGAGCGGA 899
Qy 349 PheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAla 368
Db 900 TTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGTGCC 959
Qy 369 ThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThr 388
Db 960 ACATGCTCTGCCACAGTGTGGCGGTGACAGCTTCAGCGCCCTCACCGGGTTCCACC 1019
Qy 389 PheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGln 408
Db 1020 TTTCTCAGCCCTGCAGATCTGCCCTACACACTGGCCCTCTTACCACCGGAGAGACAG 1079
Qy 409 ValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMet 428
Db 1080 GHGTTCTGCCCAATACCCAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATG 1139
Qy 429 ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAla 448
Db 1140 ACCAGCTTCTGCCAGCGCCTAAGCGTGGAGCTCCCTTCCCTAATGGACACGTTGGTGCT 1199
Qy 449 GlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspVal 468
Db 1200 GGAGCAGTGGCTGCTCCACCTCCACCGCGCTCTGCGGGGCTCTGCCCTGTGATGT 1259
Qy 469 SerValArgValValValGlyGluProThrGluAlaArgValValProGlyArgGlyIle 488
Db 1260 TCCGTACGTGCTGGTGGTGAGCCACCCAGGAGCCAGGTTGGTCCGGGGCGGGCATC 1319
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Db 1320 TGCCCTGGACCTCGCCATCTGGATAGTGGCTTCTCTGCTGCCAGGTGGCCCATCCCTG 1379
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Db 1380 TTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGCACCTATATGTTGTGTGCCGGA 1439
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Db 1440 GGCCTGGGTCTGCTGCCCATTTTACTTTGCTACAGGTAGTATTTGCACAGAGGACGACTG 1499
Qy 549 AlaLysTyrSerAla 553
Db 1500 GCCAAATACCTCAGCG 1514

RESULT 32
US-09-895-814-703
; Sequence 703, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
```


APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 703
LENGTH: 2904
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-814-703

Alignment Scores:
Pred. No.: 3,6e-171 Length: 2904
Score: 1920.50 Matches: 390
Percent Similarity: 77.23% Conservative: 0
Best Local Similarity: 77.23% Mismatches: 1
Query Match: 67.13% Indels: 115
DB: 9 Gaps: 1

US-09-593-793A-113 (1-553) x US-09-895-814-703 (1-2904)

QY 163 ValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAsp 182
DB 1 GTCATGGCTTCATGATCAGTCTGTGGGGCTGCCTGGGCTACCTCTGCCTGCCATTGAC 60
QY 183 TrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeu 202
DB 61 TGGGACACCAGTGCCCTGGCCCCCTACCTGGGACCCAGGAGAGTGCCTCTTGGCCCTG 120
QY 203 LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluAlaAla 222
DB 121 CTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGACGG 180
QY 223 LeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCys 242
DB 181 CTGGGGCCCCCAGGACGACGAGAAGGGCTGTGGCCCCCTCTTGTGCCCCCACTGCTGT 240
QY 243 ProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGln 262
DB 241 CCATGCGGGCCCGCTTGGCTTTCGGAACCTGGGCGCCCTGCTTCCCGGGCTGCACACG 300
QY 263 LeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrp 282
DB 301 CTGTGTGCGCATGCCCGCACCTCTGCGCGGCTCTTGGTGGCTGAGCTGTGCACTGG 360
QY 283 MetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValClyGluLeuTyrGln 302
DB 361 ATGGCACTCATGACCTTCACGCTGTTTTACAGGATTTCTGGGGGAGGGGCTGTACCAG 420
QY 303 GlyValProArgAlaGluProGlyThrGluAlaArgHisTyrAspGluGlyVal --- 321
DB 421 GGGGTGCCAGAGCTGAGCGGGGACCGAGGCCGAGACACTATGATGAAGGAG-GCC 479
QY 321 ----- 321

DB 480 TCTGGGTGCTCTTAGAGAGTCTGATCAGAGTGTGTGCCCCAGTTTGTACAGAAGAAAGCGG 539
QY 321 ----- 321
DB 540 AGCTTATTCAAAGTCTAGAGGGAGTGGAGAGTTAAGGCTGGATTTCAGATCTGCCTGGT 599
QY 321 ----- 321
DB 600 TCCAGCGCAGTGTGCCCTCTGTCTCCCCCAACGACTTTCCAAATAATCTCACCAGGCGCT 659
QY 321 ----- 321
DB 660 TCCAGTCAAGCGCTCTAGAACGCTTTGAAGCCTATGGCCAGCTGTCTTTGTGTCCCT 719
QY 321 ----- 321
DB 720 CTCACCCGCTGTCTTCACAGCTGAGACTCCCGAGGAACCTTCAGACTACCTTCCTCTGC 779
QY 322 ----- ArgMetGlySerLeuGlyLeu 328
DB 780 CTTTCAGCAAGGGCGGTTGCCACATTTCTGTAGGGCGGTTTCGGATGGCAGCCTGGGGCTG 839
QY 329 PheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArg 348
DB 840 TTCTCTGAGTGGCGCATCTCCCTGTCTCTCTGTCTGTGTCATGACCGGCTGTGTCAGCGA 899
QY 349 PheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAla 368
DB 900 TTCGGCACTCGAGCAGCTATTTTGGCCAGTGTGGCAGCTTTTCCCTGTGGCTGGCGGTGCC 959
QY 369 ThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThr 388
DB 960 ACATGCTGTCCACAGTGTGGCGGTGGTGACAGCTTCAGCGCCCTCACCAGGTTTCAAC 1019
QY 389 PheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGln 408
DB 1020 TTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCCTCCTTACCACCGGGAGAGCAG 1079
QY 409 ValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMet 428
DB 1080 GTGTCTCTCCCAATACAGAGGGGACACTGGAGGTGTAGCAGTAGGACACCTGTATG 1139
QY 429 ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAla 448
DB 1140 ACCAGCTTCTGCCAGGCCCTTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTCT 1199
QY 449 GlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspVal 468
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QY 469 SerValArgValValValGlyGluProThrGluAlaArgValValProGlyArgGlyIle 488
DB 1260 TCCGTACGTGTGGTGGGTGAGCCCCAGGCGCAGGGTGGTTCCGGGCGGGGCATC 1319
QY 489 CysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeu 508
DB 1320 TGCTGGACCTGGCATCTGGATAGTGTCTTCTGTCTCCAGGTGGCCCATCCCTG 1379
QY 509 PheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAla 528
DB 1380 TTTATGGGTCCATTGTCCAGCTCAGCCAGTCTGTCTCCTGTATATGTTGTGTGCGCA 1439
QY 529 GlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeu 548
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QY 549 AlaLysTyrSerAla 553
DB 1500 GCCAAATACACGC 1514
RESULT 33
US-09-759-143-703

; Sequence 703, Application US/09759143
; Patent No. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaqun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Panger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-703

Alignment Scores:
Pred. No.: 3,6e-171 Length: 2904
Score: 1920.50 Matches: 390
Percent Similarity: 77.23% Conservative: 0
Best Local Similarity: 77.23% Mismatches: 1
Query Match: 67.13% Indels: 115
DB: 10 Gaps: 1
US-09-593-793a-113 (1-553) x US-09-759-143-703 (1-2904)

QY 163 ValThrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAsp 182
|||||
Db 1 GTCTATGCCTTCATGATCAGTCTTTGGGGCTGCTGGGTACCTCTCGCTGCCATTGAC 60
QY 183 TrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeu 202
|||||
Db 61 TGGGACACCAGTGCCCTGGGCCCTACCTGGGCACCCAGGAGGTGCTTTGGCCTG 120
QY 203 LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuValAlaGluAlaAla 222
|||||
Db 121 CTCACCTCATCTCTCTACCTCGGTAGGACCCACACTGCTGGTGGCTGAGGAGGACGG 180
QY 223 LeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCys 242
|||||
Db 181 CTGGGCCCCACCGACGACGAGAGGCTGTCGGCCCCCTCTCTGTCGCCCATGCTGT 240
QY 243 ProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGln 262
|||||
Db 241 CCATGCGGGCGGCTTGGCTTTCCGGAACTGGGGCGCTGCTTCCCGGCTGCACACG 300
QY 263 LeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrp 282
|||||
Db 301 CTGTGCTGGCGATGCCCGCACCCCTGGCGCGGCTCTTGTGGCTGAGCTGTCAGCTGG 360
QY 283 MetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGln 302
|||||
Db 361 ATGGCACTCATGACCTTCAGCTGTGTTTACACGGATTTCGTGGCGAGGGGCTGTACCAG 420
QY 303 GlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal --- 321
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Db 421 GCGTGCCCCAGAGCTGAGCGGCGACCGGAGCCCGGAGACATATGATGAAGGAG-GCC 479
QY 321 ----- 321
Db 480 TCTGGCTGCTCTAGGAGTCTGATCAGAGTCTGTTGCCCCAGTTTGACAGAAGAAAGCGG 539
QY 321 ----- 321
Db 540 AGCTTATCAAGTCTAGAGGGAGTGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGT 599
QY 321 ----- 321
Db 600 TCCAGCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCAAAATAATCTCACAGCGCCT 659
QY 321 ----- 321
Db 660 TCCAGCTCAGCGCTCTAGAGCGCTTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCT 719
QY 321 ----- 321
Db 720 CTCACCGCGCTGCTCACAGTGTGAGACTCCCGAGAAACCTTCAGACTACCTTCTCTGTC 779
QY 322 -----ArgMetGlySerLeuGlyLeu 328
Db 780 CTTCAAGAGGGCGTTGCCACATTTCTGAGGGCTTCGGATGGCGACGCTGGGGCTG 839
QY 329 PheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArg 348
|||||
Db 840 TTCCTGCACTGGCCCATCTCCCTGGTCTCTCTGCTGATGGACCGGCTGGTGACAGCA 899
QY 349 PheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAla 368
|||||
Db 900 TTCGGCACTCGAGCAGTCTATTTTGGCCAGTGTGGCAGCTTTCCTCTGCTGGCTGCGGTGCC 959
QY 369 ThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThr 398
|||||
Db 960 ACATGCTCTCCACAGTGTGGCGGTGACAGCTTCAGCCGCCCTCACCGGGTTTCAAC 1019
QY 389 PheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGln 408
|||||
Db 1020 TTCTCAGCCTCGAGATCTTGCCTTACACTGGCCTTCCCTTACCACCGGAGAGACAG 1079
QY 409 ValPheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAspSerLeuMet 428
|||||
Db 1080 GTGTTCTGCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACACGCTGATG 1139
QY 429 ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAla 448
|||||
Db 1140 ACCAGCTTCTCTGCGAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTTGGTGT 1199
QY 449 GlyGlySerGlyLeuLeuProProAlaLeuCysGlyAlaSerAlaCysAspVal 468
|||||
Db 1200 GGAGGAGTGGCTGCTCCACCTCCACCGCGCTCTCGGGGCCCTCTGCGTGTGATGTC 1259
QY 469 SerValArgValValGlyGluProThrGluAlaArgValValProGlyArgGlyIle 488
|||||
Db 1260 TCCGTACGTGTGTGGTGGGTGAGCCACCGAGGCCAGGTGTTCCGGCGCGGCGATC 1319
QY 489 CysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeu 508
|||||
Db 1320 TGCCTGAGCTCGCCATCTGGATAGTCTTCCCTGTCCAGGTGGCCCATCCCTG 1379
QY 509 PheMetClySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAla 528
|||||
Db 1380 TTTATGGGCTCCATTTCTCCAGCTCAGCCAGTGTGTCACCTATATGTTGTTGCTGCCGCA 1439
QY 529 GlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeu 548
|||||
Db 1440 GGCTGGTCTGGTCCCATTTACTTTGCTACACAGGTAGTATTTTGCACAGGCGACTTG 1499
QY 549 AlaLysTyrSerAla 553
|||||
Db 1500 GCCAAATACTCAGCG 1514

RESULT 34

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US-09-780-669-703
; Sequence 703, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-703

Alignment Scores:
Pred. No.: 3,6e-171
Score: 1920.50
Percent Similarity: 77.23%
Best Local Similarity: 77.23%
Query Match: 67.13%
DB: 10

US-09-593-793A-113 (1-553) x US-09-780-669-703 (1-2904)
Length: 2904
Matches: 390
Conservative: 0
Mismatches: 1
Indels: 115
Gaps: 1

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Qy	283	MetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluLeuTyrGln	303
Db	361	ATGCACATCATGACCTTCAACGCTGTTTTACACAGGATTTCTGGGGAGGGGTGTACACG	420
Qy	303	GlyValProArgAlaGluProGlyThrGluAlaAtrArgHisTyrAspGluGlyVal---	321
Db	421	GGCTGCCACAGCTGAGCGCGACCGAGGCGCGGAGACACTATGATGAAGAAG-GCC	479
Qy	321	-----	321
Db	480	TCTGGCTGCTCAGGAGCTCTGATCATCAGATCGTGTGCCCAAGTTTGACAGAAAGAGCGG	539
Qy	321	-----	321
Db	540	AGCTTATTCAAAGTCTAGAGGAGTGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGT	599
Qy	321	-----	321
Db	600	TCCAGCGCAGTGTGGCTCTGCTTCCCAAGCAGCTTTCCTCAAAATAATCTCACACAGCGCT	659
Qy	321	-----	321
Db	660	TCCAGCTCAGCGCTCTAGAAAGCGTCTTGAAAGCCTATGCGCAGCTGTCTTTGTGTTCCT	719
Qy	321	-----	321
Db	720	CTCACCCGCTGTCTCACAGCTGAGACTCCACAGAAACCTTCAGACTACCTTCTCTCTGC	779
Qy	322	-----	322
Db	780	CTTCAGCAAGGGCGTTGGCCACATTTCTCTGAGGGCTTCGGATGGCAGCGCTGGGGCTG	839
Qy	329	PheLeuGlnCysAlaIleSerLeuValPheSerLeuValIleAspArgLeuValGlnArg	348
Db	840	TTCTCGCAGTGGCCATCTCCCTGGTCTCTCTGTGTCTATGACCGGCTGTGTGACGGA	899
Qy	349	PheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAla	368
Db	900	TTCGGCACCTCGACGAGTCTATTGGCCAGTGTGGCAGCTTTCCTGTGGCTGCCGGTGCC	959
Qy	369	ThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThr	388
Db	960	ACATGCTGTCCCACAGTGTGGCGTGTGCACAGCTTCACGCGCGCTCACCGGGTTCACC	1019
Qy	389	PheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGln	408
Db	1020	TTCTACGCGCTGCAGATCTCGCCCTACACACTGGCTCTCCCTCTACACCGGGAGAAGCAG	1079
Qy	409	ValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMet	428
Db	1080	GTGTTCTGCCCCAAATACCCAGGGGACACTGGAGGTGCTAGCAGTCAGGACAGCCTGATG	1139
Qy	429	ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAla	448
Db	1140	ACCAGCTTCTGCGAGCGCTTAAGCCTGGAGTCTCCCTTCCCTTAATGGACACGTGGGTGCT	1199
Qy	449	GlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspVal	468
Db	1200	GGAGGAGTGGCTGCTCCACCTCCACCGCGCTCTGGGGGCTCTGCTGTGATGTCT	1259
Qy	469	SerValArgValValGlyGluProThrGluAlaArgValValProGlyArgGlyIle	488
Db	1260	TCCGTACGTGTGTGGTGGTGAGCCACCGAGGCCAGGGTGTCCGGCGCGGGGCATC	1319
Qy	489	CysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeu	508
Db	1320	TGCCTGGACCTCGCCATCTCTGGATAGTGCTTCTCTGCTTCCAGGTGGCCCATCTCCCTG	1379
Qy	509	PheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAla	528
Db	1380	TTTATGGGCTCAATGTGCCAGCTACGCCAGTCTGTCTACCTGTCTATATGGTGTCTGCCCA	1439
Qy	529	GlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeu	548

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|||||
Db 1440 GGCCTGGCTGCTGGCGCCATTACTTTGCTACAGGAGTAGTATTGACAAGAGGCACCTTG 1499
Qy 549 AlalystyrSerAla 553
Db 1500 GCCAAATACTCAGCG 1514

RESULT 35
US-09-822-827-703
; Sequence 703, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 703
; LENGTH: 2904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-703

Alignment Scores:
Pred. No.: 3.6e-171 Length: 2904
Score: 1920.50 Matches: 2904
Percent Similarity: 77.23% Conservative: 0
Best Local Similarity: 77.23% Mismatches: 1
Query Match: 67.13% Indels: 115
DB: 10 Gaps: 1

US-09-593-793A-113 (1-553) x US-09-822-827-703 (1-2904)
Qy 163 ValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAsp 182
Db 1 GTCTATGCTTCATGATCAGTCTTTGGGGCTGCCTGGGCTACCTCCTGCCTGCCATTGAC 60
Qy 183 TrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPheGlyLeu 202
Db 61 TGGGACACCAAGTGGCCCTGGCCCTACCTGGGACCCAGGAGGAGTGCTCTTTGGGCGTG 120
Qy 203 LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluAlaAla 222
Db 121 CTCACCTCATCTTCCTCACCTGCTAGCAGCCACACACTGCTGGTGGCTGAGGAGCAGC 180
Qy 223 LeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCys 242
Db 181 CTGGGCCCCACCGAGCCAGCAGAAGGCTGTCGGCCCCCTCCTTGTGCGCCCCACTGCTGT 240
Qy 243 ProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGln 262
Db 241 CCATGCGCGGCGCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCCTCCCGCGCTGCACCG 300
Qy 263 LeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrp 282
Db 301 CTGFGCTGCCGATGCCCGCCGACCTCGCGCGCTCTTCGGTGGCTGAGCTGTGACGCTGG 360
Qy 283 MetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGln 302
Db 361 ATGGCACTCATGACCTTCACGCTGTTTACAGGATTTCTGGGGGAGGGGCTGTACCAG 420
Qy 303 GlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal--- 321
Db 421 GGCCTGCCAGAGCTGAGCGCGGCGCAGCGGCGGAGACACTATGATGAAGGAAG-GCC 479
Qy 321 ----- 321
Db 480 TCTGGCTGCTTAGAGTCTGATCAGAGTCGTTGCCCGCAGTTTGACAGAAGAAAGCGG 539
Qy 321 ----- 321
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Db 540 AGCTTATTCAAAGTCTAGAGGAGTGGAGAGTTAAGGCTGGATTTTCAGATCTGCCTGGT 599
Qy 321 ----- 321
Db 600 TCCAGCCCGCAGTGTGCCCTCTGCTCCCCCAACGAGCTTTCCAAATAATCTCACCAGCGCT 659
Qy 321 ----- 321
Db 660 TCCAGCTCAGGCGTCTTAGAAGCGTCTTTGAAGCCTATGSCCAGCTGTCTTTGTGTCCCT 719
Qy 321 ----- 321
Db 720 CTCACCCCGCTGTCTCTACAGCTCAGACTCCAGGAAACCTTCAGACTACCTTCTCTGCG 779
Qy 322 ----- ArgMetGlySerLeuGlyLeu 328
Db 780 CTTCAGCAAGGGCGTGTGCCCATCTCTCTGAGGCGCTTCGATGGGCGAGCGCTGGGGCTG 839
Qy 329 PheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArg 348
Db 840 TTCCTGCAGTGGCCATCTCCTCGTCTCTCTGTGTCATGAGCCGCTGGTGACGCA 899
Qy 349 PheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAla 368
Db 900 TTCGGCACTCGAGCAGTCTATTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGCTGCC 959
Qy 369 ThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThr 388
Db 960 ACATGCTGTCTCCACAGTGTGGCGTGTGACAGCTTCAGCGCCCTCACCAGGTTACCC 1019
Qy 389 PheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGln 408
Db 1020 TTCACGCGCTGCAGATCTGCCCTACACTGGGCTCCTCTACCCACGGGAGAGCAG 1079
Qy 409 ValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerSerGluAspSerLeuMet 428
Db 1080 GTGTTCTCTGCCAAATACCGAGGGGACACTGGAGTGTAGCAGTGGAGCAGCGCTGATG 1139
Qy 429 ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAla 448
Db 1140 ACCAGCTTCTCGCCAGGCGCTTAAGCTGGAGCTCCCTTCCCTTAATGGACAGCTGGGTGCT 1199
Qy 449 GlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspVal 468
Db 1200 GGAGCAGTGGCGCTGCTCCACCTCCACCGCGCTCTCGGGGCGCTCTGCCTGTGATGTC 1259
Qy 469 SerValArgValValValGlyGluProThrGluAlaArgValValProGlyArgGlyIle 488
Db 1260 TCCGTTACGTGTGGTGGTGGTGAGCCACCGAGCGGCGGTGGTTCGCGGGCGGGGCATC 1319
Qy 489 CysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeu 508
Db 1320 TGCCTGGACCTCGGCATCTCTGGATAGTCCCTTCCTGCTGCCAGGTGGCCCGCCATCCCTG 1379
Qy 509 PheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAla 528
Db 1380 TTTATGGGCTCCATGTGCCAGCTCAGCCAGTCTGTCACTGCTATATGCTGTGCCGA 1439
Qy 529 GlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeu 548
Db 1440 GGCCTGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTGACAAGAGCGACTTG 1499
Qy 549 AlalystyrSerAla 553
Db 1500 GCCAAATACTCAGCG 1514
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RESULT 36
US-10-012-896-851
; Sequence 851, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 851
LENGTH: 1203
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-851

Alignment Scores:
Pred. No.: 4,58e-123 Length: 1203
Score: 1403.50 Matches: 267
Percent Similarity: 97.45% Conservative: 0
Best Local Similarity: 97.45% Mismatches: 2
Query Match: 49.06% Indels: 5
DB: 9 Gaps: 1

US-09-593-793A-113 (1-553) x US-10-012-896-851 (1-1203)

QY 30 ValCysLeuAlaAlaGly-----IleThrTyrValProProLeuLeuLeu 44
Db 379 GTGACATTGGCCGAGGAGCCCGCCGGAATTATCATCCTATGTGCCGCTCTGCTGCTG 438

QY 45 GluValGlyValGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGly 64
Db 439 GAAGTGGGGTAGAGAGAGATTCATGACCATGGTCTGGGCATTGGTCCAGTGGCTGGGC 498

QY 65 LeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGlyArg 84
Db 499 CTGGTCTGTGTCGCCGCTCCTAGGCTCAGCAGTGACCATGGCTGGCGATGCGCCG 558

QY 85 ArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIlePro 104
Db 559 CGCCGGCCCTTCATCTGGGCATGCTCTGGGCATCCTCTGAGCCCTCTTCTCATCCCA 618

QY 105 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeu 124
Db 619 AGGGCCGGCTGGCTAGCAGGGCTGCTGTGCCGGATCCAGGCCCTGGAGCTGGCAGCTG 678

QY 125 LeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGlu 144
Db 679 CTCATCTGGCGTGGCGCTGGGACTTCTGTGGCCAGGTGTCTCACTCCACTGGAG 738

QY 145 AlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyr 164
Db 739 GGCCTGCTCTGACCTTCTCCGGGACCGGACCACTGTGCGCAGGCGCTTACTCTGTCTAT 798

QY 165 AlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAsp 184
Db 799 GCCTTATGATCAGTCTTTGGGGCTGCTTGGGCTACTCTGCTGCATGACTGGGAC 858

QY 185 ThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeuLeuThr 204
Db 859 ACCAGTGGCTGGCCCTTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACC 918

QY 205 LeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluAlaLeuGly 224
Db 919 CTCATCTTCTCCTACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGAGGCTGGC 978

QY 225 ProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCys 244
Db 979 CCCACCGAGCCAGCAAGGGCTGTGCGCCCTCTCTTGTGCGCCCACTGCTGTCCATGC 1038

QY 245 ArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCys 264
Db 1039 CGGGCCCGCTTGGCTTTCGGAACTTGGCGGCTGCTTCCCGCGCTGCACAGCTGTGC 1098

QY 265 CysArgMetProArgThrLeuArgLeuPheValAlaGluLeuCysSerTrpMetAla 284
Db 1099 TGGCGCATGCCCGCACCTGCGCGGCTTCTGCTGGCTGAGCTGTGACAGTGGATGGCA 1158

QY 285 LeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlu 298
Db 1159 CTCATGACCTTACGCTGTTTTTACACGGATTCGTGGCGGAG 1200

RESULT 37
US-09-895-793-851
Sequence 851, Application US/09895793
Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 851
LENGTH: 1203
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-793-851

Alignment Scores:
Pred. No.: 4,58e-123 Length: 1203
Score: 1403.50 Matches: 267
Percent Similarity: 97.45% Conservative: 0

; APPLICANT: Kalos, Michael D.

D9		/55	GCCCTTCATGATCAGTCTTTGGGGGGGTACCTCCCTGCCTTGCCCATTCAGTGGGAC	853	
D9					
Qv	185	ThrSerAlaLeuAlaprotvtrLengVtHrGngInsgnucystleuphegVleuLeuthr	2047		

D9		/55	GCCCTTCATGATCAGTCTTTGGGGGGGTACCTCCCTGCCTTGCCCATTCAGTGGGAC	853	
D9					
Qv	185	ThrSerAlaLeuAlaprotvtrLengVtHrGnGnGnCysLeupheGVLentLeutHr	2047		

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Db 859 ACCAGTGGCCCTGGCCCTACCTGGGACACCCAGGAGGTGCTCTTTGGCCCTGCTCACC 918
QY 205 LeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGluAlaLeuGly 224
Db 919 CTCATCTTCTACCTGGGTAGCAGCACACTGCTGGTGGTGAGGAGCGCTGGGC 978
QY 225 ProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCys 244
Db 979 CCCACCAGGACGACGAGGCGTGTGGCCCTCTCTGTGGCCCTGCTGTCTCCATGC 1038
QY 245 ArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCys 264
Db 1039 CGGGCCCGCTGGCTTTCCGGAACCTTGGGCGCCCTGCTTCCCGGCTGCACCACTGTGC 1098
QY 265 CysArgMetProArgThrLeuArgAlaGluPheValAlaGluLeuCysSerTrpMetAla 284
Db 1099 TGGCGGATGCGCCGACCTTGGCCGCGCTTCTGCTGGCTGAGCTGTGCAGCTGGATGGCA 1158
QY 285 LeuMetThrPheThrLeuPheThrLeuPheThrAspPheValGlyGlu 298
Db 1159 CTCATGACCTTACGCTGTTTACACGGATTTCGTGGCGGAG 1200

RESULT 39
US-09-759-143-851
; Sequence 851, Application US/09759143
; Patent No. US200202248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-851

Alignment Scores:
Pred. No.: 4,58e-123 Length: 1203
Score: 1403.50 Matches: 267
Percent Similarity: 97.45% Conservative: 0
Best Local Similarity: 97.45% Mismatches: 2
Query Match: 49,06% Indels: 5
DB: 10 Gaps: 1

US-09-593-793A-113 (1-553) x US-09-759-143-851 (1-1203)
QY 30 ValCysLeuAlaAlaGly-----IleThrTyrValProLeuLeuLeu 44
Db 379 GTACATTTGGCCGAGGACCCCGCGGCAATTCATCACTATGTGGCGCTCTGCTGCTG 438
QY 45 GluValGlyValGluGluCysPheMetThrMetValLeuGlyIleGlyProValLeuGly 64
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Db 439 GAAGTGGGGGTAGAGGAGAAAGTTTCATGACCATGGTCTGGGCATTTGGTCCAGTGTGGGC 498
QY 65 LeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGlyArg 84
Db 499 CTGGTCTGTGTCCCGTCTTAGCTAGGCTAGCCAGTACGACCTGGCGTACGCTATGGCCG 558
QY 85 ArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIlePro 104
Db 559 CGCGCGCCCTTCATCTGGGCACTGTCTTGGGCATCTCTGTGAGCCTCTTCTTCATCCCA 618
QY 105 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeu 124
Db 619 AGGGCGCGGTGGCTAGCAGGGGTGCTGTGCCGAGATCCAGGCCCCCTGGAGTGGCACTG 678
QY 125 LeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGlu 144
Db 679 CTCATCTGGGGTGGGGTGTGGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAG 738
QY 145 AlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyr 164
Db 739 GCCCTGCTCTGACCTTCCGGGACCCGGACCACTGTCCGACGGCCTACTCTGTCTAT 798
QY 165 AlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAsp 184
Db 799 GCCTTCATCATGCTTGGGGGTGCTGGGCTACCTCTGCTGCCCATTTGACTGGGAC 858
QY 185 ThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPheGlyLeuLeuThr 204
Db 859 ACCAGTGGCTGGCCCTACCTGGGACCCAGGAGGAGTGCCTCTTTGGCCCTGCTCACC 918
QY 205 LeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGluAlaLeuGly 224
Db 919 CTCATCTTCTCCTCCTGCTAGCAGCACACTGCTGGTGGCTGAGGAGGACGCTGGGC 978
QY 225 ProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCys 244
Db 979 CCCACCGAGCCAGCAGAGGGGTGCTGGCCCTCTCTGCGCCCACTGCTGTCATGC 1038
QY 245 ArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCys 264
Db 1039 CGGGCCCGCTTGGCTTTCGGAACCTGGGCGCCCTGCTTCCCGGCTGCACCACTGTGC 1098
QY 265 CysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAla 284
Db 1099 TGGCGCATGCCCGCACCTGCGCGGCTTCTGCTGGCTGAGCTGTGCAGCTGGATGGCA 1158
QY 285 LeuMetThrPheThrLeuPheThrLeuPheThrAspPheValGlyGlu 298
Db 1159 CTCATGACCTTACGCTGTTTACACGGATTTCGTGGCGGAG 1200

RESULT 40
US-09-780-669-851
; Sequence 851, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
```



```
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780.669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-851

Alignment Scores:
Pred. No.: 4.58e-123 Length: 1203
Score: 1403.50 Matches: 267
Percent Similarity: 97.45% Conservative: 0
Best Local Similarity: 97.45% Mismatches: 2
Query Match: 49.06% Indels: 5
DB: 10 Gaps: 1

US-09-593-793A-113 (1-553) x US-09-780-669-851 (1-1203)
Qy 30 ValCysLeuAlaAlaGly-----lleThrTyrValProProLeuLeuLeu 44
Db 379 GTGACATTGGCGAGGAGCCCGCCGCAATTCATCAGCTATGTGCCCGCTCTGCTG 438
Qy 45 GluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGly 64
Db 439 GAAGTGGGGGTAGAGGAGAGTTCATGACCATGTGCTGGCGATGTCCTGAGTGGCG 498
Qy 65 LeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGlyArg 84
Db 499 CTGGTCTGTGCTCCGCTCTAGGCTCAGCCAGTACCATGGCGTGGAGTGGCGCGC 558
Qy 85 ArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIlePro 104
Db 559 CGCGCGCCCTTCATCTGGGCACTGTCTGGCATCTCTGCTGAGGCTCTTCTCATCCCA 618
Qy 105 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuAlaLeu 124
Db 619 AGGGCGGCTGGCTAGCAGGCTGTCTGGCCGATCCAGGCCCTTGGAGCTGGCACTG 678
Qy 125 LeuIleLeuGlyValGlyLeuAspPheCysGlyGlnValCysLeuPheGlyLeuThr 144
Db 679 CTCATCTCTGGCGTGGGCTGTCTGAGTCTCTGTGGCCAGGTGTCTTGTGGCTGCTC 738
Qy 145 AlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyr 164
Db 739 GCCCTGCTCTGTGACCTCTTCCGGGACCCGAGCCAGTCTGCTGCTATCTGCTAT 798
Qy 165 AlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAsp 184
Db 799 GCCTTCATGATCAGTCTTGGGGGCTGCTGGGCTACCTCCCTGCTGCTGCTGCTGCT 858
Qy 185 ThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPheGlyLeuThr 204
Db 859 ACCAGTGCCTTGGCGCCCTACCTGGGCACTGGGAGGAGGAGTGCCTTTTGGCGCTG 918

US-09-593-793A-113 (1-553) x US-09-822-827-851 (1-1203)
Qy 30 ValCysLeuAlaAlaGly-----lleThrTyrValProProLeuLeuLeu 44
Db 379 GTGACATTGGCGAGGAGCCCGCCGCAATTCATCAGCTATGTGCCCGCTCTGCTG 438
Qy 45 GluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGly 64
Db 439 GAAGTGGGGGTAGAGGAGAGTTCATGACCATGTGCTGGCGATGTCCTGAGTGGCG 498
Qy 65 LeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGlyArg 84
Db 499 CTGGTCTGTGCTCCGCTCTAGGCTCAGCCAGTACCATGGCGTGGAGTGGCGCGC 558
Qy 85 ArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIlePro 104
Db 559 CGCGCGCCCTTCATCTGGGCACTGTCTGGCATCTCTGCTGAGGCTCTTCTCATCCCA 618
Qy 105 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuAlaLeu 124
Db 619 AGGGCGGCTGGCTAGCAGGCTGTCTGGCCGATCCAGGCCCTTGGAGCTGGCACTG 678
Qy 125 LeuIleLeuGlyValGlyLeuAspPheCysGlyGlnValCysLeuPheGlyLeuThr 144
Db 679 CTCATCTCTGGCGTGGGCTGTCTGAGTCTCTGTGGCCAGGTGTCTTGTGGCTGCTC 738
Qy 145 AlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyr 164
Db 739 GCCCTGCTCTGTGACCTCTTCCGGGACCCGAGCCAGTCTGCTGCTATCTGCTAT 798
Qy 165 AlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAsp 184
Db 799 GCCTTCATGATCAGTCTTGGGGGCTGCTGGGCTACCTCCCTGCTGCTGCTGCTGCT 858
Qy 185 ThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPheGlyLeuThr 204
Db 859 ACCAGTGCCTTGGCGCCCTACCTGGGCACTGGGAGGAGGAGTGCCTTTTGGCGCTG 918

US-09-822-827-851
; Sequence 851, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822.827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-851

Alignment Scores:
Pred. No.: 4.58e-123 Length: 1203
Score: 1403.50 Matches: 267
Percent Similarity: 97.45% Conservative: 0
Best Local Similarity: 97.45% Mismatches: 2
Query Match: 49.06% Indels: 5
DB: 10 Gaps: 1

US-09-593-793A-113 (1-553) x US-09-822-827-851 (1-1203)
Qy 30 ValCysLeuAlaAlaGly-----lleThrTyrValProProLeuLeuLeu 44
Db 379 GTGACATTGGCGAGGAGCCCGCCGCAATTCATCAGCTATGTGCCCGCTCTGCTG 438
Qy 45 GluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGly 64
Db 439 GAAGTGGGGGTAGAGGAGAGTTCATGACCATGTGCTGGCGATGTCCTGAGTGGCG 498
Qy 65 LeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGlyArg 84
Db 499 CTGGTCTGTGCTCCGCTCTAGGCTCAGCCAGTACCATGGCGTGGAGTGGCGCGC 558
Qy 85 ArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIlePro 104
Db 559 CGCGCGCCCTTCATCTGGGCACTGTCTGGCATCTCTGCTGAGGCTCTTCTCATCCCA 618
Qy 105 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuAlaLeu 124
Db 619 AGGGCGGCTGGCTAGCAGGCTGTCTGGCCGATCCAGGCCCTTGGAGCTGGCACTG 678
Qy 125 LeuIleLeuGlyValGlyLeuAspPheCysGlyGlnValCysLeuPheGlyLeuThr 144
Db 679 CTCATCTCTGGCGTGGGCTGTCTGAGTCTCTGTGGCCAGGTGTCTTGTGGCTGCTC 738
Qy 145 AlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyr 164
Db 739 GCCCTGCTCTGTGACCTCTTCCGGGACCCGAGCCAGTCTGCTGCTATCTGCTAT 798
Qy 165 AlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAsp 184
Db 799 GCCTTCATGATCAGTCTTGGGGGCTGCTGGGCTACCTCCCTGCTGCTGCTGCTGCT 858
Qy 185 ThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlyCysLeuPheGlyLeuThr 204
Db 859 ACCAGTGCCTTGGCGCCCTACCTGGGCACTGGGAGGAGGAGTGCCTTTTGGCGCTG 918
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RESULT 44
US-10-012-896-10
; Sequence 10, Application US/10012896
; Publication No. US2002018325A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.

```

QY 494 IleLeuAspSerAlaPheLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
Db 423 ATCTGGATAGTC - TTCCTGGCTCCANGTGGCCCCATCCCTGTTATGGGCTCCATT 481
QY 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuVal 533
Db 482 GTCCAGCTACAGCAGTCTGTCACTGGCTATATGCTGTGCCCCAGCCCTGGGTCCTGGTC 541
QY 534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 542 CC-ATTACTTCTGTACACAGGTTANTATTGACAAAGCAGGANTTGGCCAAATACTCAGCG 600

RESULT 45

US-09-895-793-10
; Sequence 10, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(789)
; OTHER INFORMATION: n = A,T,C or G
US-09-895-793-10

Alignment Scores:

Pred. No.:	9,79e-78	Length:	789
Score:	919.00	Matches:	192
Percent Similarity:	96.50%	Conservative:	1
Best Local Similarity:	96.00%	Mismatches:	7
Query Match:	32.12%	Indels:	2
DB:	9	Gaps:	0

US-09-593-793A-113 (1-553) x US-09-895-793-10 (1-789)

QY 354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
Db 3 GTCTATNTGCCAGTGTGGCAGCTTTCCTGCTGGCTGCCGCTGCCACATGCTGCCAC 62
QY 374 SerValAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
Db 63 AGTGTGGCGGTGTGTGACAGCTTACAGCCGCTCAGCGGGTTACCTTCTCAGCCCTGCAG 122

QY 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413
Db 123 ATCTGCTCCCTACACACTGGCTCCCTCTACCACCGGAGACAGGTGTTCCTGCCCAAA 182
QY 414 TyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
Db 183 TACCGAGGGAGACTGGAGGTGCTAGCAGTAGGACAGCCTGATGACCACTTCCTGCCA 242
QY 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeu 453
Db 243 GGCCTTAAGCCTGGAGCTCCCTTCCCTAATGGACAGCTGGGTGCTGGAGGAGTGGCCTG 302
QY 454 LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473
Db 303 CTCCTCCACTCCACCCGCGCTCTGCGGGGCTCTGCTGTGTGATGCTCTCCCTAGCTGTGGTG 362
QY 474 ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 493
Db 363 GTGGGTGAGCCACCACCGANGCAGGGTGTTCGGGGCGGGGCATCTGCCCTGGACCTCGCC 422
QY 494 IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513
Db 423 ATCTGGATAGTGC - TTCCTGCTGTCCCGCCCATCCCTGTTATGGGCTCCATT 481
QY 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuVal 533
Db 482 GTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGAGGCTGGGTCTGGTC 541
QY 534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 542 CC-ATTACTTGTGTACACAGGTTANTATTGACAAAGCAGGANTTGGCCAAATACTCAGCG 600

Search completed: February 19, 2003, 05:16:48

Job time : 402 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 19, 2003, 03:45:09 ; Search time 1694 Seconds
(without alignments)
5286.956 Million cell updates/sec

Title: US-09-593-793A-113
Perfect score: 2861
Sequence: 1 MVQRLWVSRLRHRKAQLL.....AIYFATQVVFKDSLAKYSA 553

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Command line parameters:
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-O=/cgn2.1/USPNO_spool/SUFFIX-rst -MINMATCH=0.1 -DOOPEXT=0
-DB=EST -QFMT=fastcap -SUFFIX=human40.cdi -LIST=100
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=45 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09593793 -CGEN_1.1_959 @runat_13022003 161308 21565 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THRAPDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
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2: em_esthum:*
3: em_estin:*
4: em_estmu:*
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6: em_estpl:*
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8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
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19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
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23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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5	1033	36.1	786	12	BG174399 602334219
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7	904	31.6	592	10	AW412402 uo78h02.y
8	897.5	31.4	929	12	BF785813 602112437
9	886	31.0	934	14	BQ934815 AGENCOURT
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11	858	30.0	969	12	BG173136 602335411
12	829	29.0	482	9	AF109299 AF109299
13	826.5	28.9	700	12	BF581244 602100464
14	817	28.6	872	12	BG864609 602798469
15	796	27.8	894	12	BG469520 603532833
16	781	27.3	901	13	BI650119 603296208
17	780	27.3	850	12	BF972601 602243025
18	742	25.9	700	10	BB610495 BB610495
19	698	24.4	509	10	BB701488 BB701488
20	682	23.8	1060	14	BM914562 AGENCOURT
21	660	23.1	759	12	BF789072 602104930
22	659	23.0	578	17	AZ418156 IM0194E12
23	620	21.7	800	12	BG469487 602532993
24	616	21.5	844	12	BG246497 602360526
25	607	21.2	692	10	BG627667 BB627667
26	601	21.0	630	13	BI145201 602909395
27	578	20.1	520	12	BG364300 GAB86B09.
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34	487.5	17.0	1037	12	BE914848 601667874
35	485	17.0	564	13	BG964810 602829364
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37	455	15.9	317	10	BB707065 BB707065
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42	399.5	13.6	1020	17	CNS050VL Tetraodon
43	385	13.5	906	12	BF680993 602156279
44	384	13.4	228	9	AA112574 zm28c12.s
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56	304.5	10.6	925	14	BQ679269 AGENCOURT
57	303	10.6	997	13	BM471166 AGENCOURT
58	299.5	10.5	970	14	BQ883505 AGENCOURT
59	298	10.4	919	14	BQ894058 AGENCOURT
60	297	10.4	959	14	BQ682666 AGENCOURT
61	295.5	10.3	661	14	BQ442313 UT-M-EXO-
62	290.5	10.2	894	14	BQ676555 AGENCOURT
63	290	10.1	572	13	BI345407 374221 MA
64	290	10.1	924	14	BQ677908 AGENCOURT


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Db 720 GGATGCCCGGAACCTCCGCGGCTTCGTGGCTGAGCTGTCAGCTGGCATGGCAACT 779
Qy 285 uMetThrPheThrLeuPheTyr---ThrAspPheValGlyGluGlyLeuTyrGlnGlyVa 304
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 780 CATGACCTTCAGCCTGTTTACCCGCGCATCTCGCTGGCGGACGGGCTGTCCCCACGGCGT 839
Qy 304 lProArgAlaGluProGlyThr-GluAlaArgArgHisTyrAspGluGlyValArgMetG 324
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 840 TGCACAGAGCTAGCGCGGACCGGAGCCGAGAACCTATGCTGAACGCGTCCGCGATGG 899
Qy 324 lySer 325
Db 900 CCGCC 904

RESULT 2
BI107873
LOCUS 602901816F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5031771 5',
DEFINITION mRNA sequence.
ACCESSION BI107873
VERSION BI107873.1 GI:14558766
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 858)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11088 row: o column: 04
High quality sequence stop: 810.
FEATURES
source
location/Qualifiers
1..858
/organism="Mus musculus"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5031771"
/clone_lib="NCI_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
/note="organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
```

133 a 265 c 245 g 215 t

BASE COUNT

ALIGNMENT SCORES

Pred. No.: 1.28e-104 Length: 858

Score: 1196.50 Matches: 236

Percent Similarity: 89.4% Conservative: 11

Best Local Similarity: 85.5% Mismatches: 25

Query Match: 41.8% Indels: 4

DB: 13 Gaps: 1

US-09-593-793a-113 (1-553) x BI107873 (1-858)

Qy 122 LeuAlaLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThr 141

Db 13 GTTGGCCCTGCTGATCTGGGAGTGGGCTGTGGACTTTTGTGGCAGGTGTGCTTTACT 72

Qy 142 ProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyr 161

Db 73 CCATTGGAGGCGCTTACTCTCCGACCTCTCCGGGACCCAGACCACTGCCCAAGCCTTC 132

Qy 162 SerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIle 181

Db 133 TCTGTCTAGCCCTTCATGATCAGCCTTGGGGCTGCGCTACCTCTTACCTGCAAT 192

Qy 182 AspTyrAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGly 201

Db 193 GACTGGACACACAGCGTTCTGGCCCCCTACTGGGTACTCAGGAAGAATGCCCTCTTTGGC 252

Qy 202 LeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGluAla 221

Db 253 CTCCTCACCTCATTTTCTCATCTGCATGGCAGCCACTCTCTTTCTGACGGAGGAGGCA 312

Qy 222 AlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCys 241

Db 313 GTACTGGGCCACACCGAGCCGCGAGAGGGTTGTGGTCTCTGCCGTGTCGCGCCGATGC 372

Qy 242 CysProCysArgAlaLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHis 261

Db 373 TGCCCCATGCCACGTTGGCTTTCCGGAATCTGGGTACCTGTTTCCCCGGCTGCAG 432

Qy 262 GlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSer 281

Db 433 CAGCTGTGTCGCGCATGCTCGCACCTTACGCCGACTCTTTGTGGCTGAGCTGTGCAGC 492

Qy 282 TrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyr 301

Db 493 TGGATGGCACTTATGACTTTTACACCTGTTCTACACGACTTCTCGTGGAGAGGGCTGTAC 552

Qy 302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal 321

Db 553 CAGGGTGTACCCAGAGCCGAGCCAGCCAGCCGAGCCGAGCCGAGCATTATGTAAGCATT 612

Qy 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341

Db 613 CGAATGGGAGCCTGGGGCTCTTCTGTCAGTGTGCCATCTCCCTGGTCTCTCCCTGGTC 672

Qy 342 -MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAl 361

Db 673 ATTGGACAGGCTGGTACAGAAGTTCGGCACACGGTCAGTCTATCTGCCCATGTGTGATGAC 732

Qy 361 aPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal-ValThr-Ala 380

Db 733 CTTTCTCTGTGGTGGCG---CTGCACCTGCTGTCCACAGCGTGGTGAAGTGACAAGCC 789

Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIle 394

Db 790 TCAATGGGCTCACCGGGTTTCACTTTCTCGGCTTGAAGATC 831

RESULT 3

LOCUS BG242597

DEFINITION BG242597.1 GI:12752412

ACCESSION BG242597

VERSION BG242597.1

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1116)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10319 row: c column: 03
High quality sequence stop: 666.
Location/Qualifiers
1. .1116
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="IMAGE:4482362"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site.1: Sali;
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 209 a 349 c 314 g 244 t
ORIGIN

Alignment Scores:
Pred. No.: 3.9e-94 Length: 1116
Score: 1089.50 Matches: 232
Percent Similarity: 81.13% Conservative: 13
Best Local Similarity: 76.82% Mismatches: 42
Query Match: 38.08% Indels: 18
DB: 12 Gaps: 2

US-09-593-793A-113 (1-553) x BG242597 (1-1116)
QY 248 LeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMet 267
Db 11 CTGCTTTCGGGAATCGGGTACCTCTTTCCCGCGCTGCAGCAGCTGTGCTGCCGATG 70
QY 268 ProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTirpMetAlaLeuMetThr 287
Db 71 CCTCGCACCTACGCCGACTTTTGTGGCTGAGCTGTGCAGCTGGATGGACATTATGACT 130
QY 288 PheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAla 307
Db 131 TTCACACTGTCTACACGGACTTCGTGGGAGAGGGGCTGTACCAGGCTGTACCAGAGCC 190
QY 308 GluProGlyThrGluAlaArgArgHisTyrAspGluGlyValArgMetGlySerLeuGly 327
Db 191 GAGCCAGGCCAGGCCGCGGAGACACTATGATGAAGGCATTGAAATGGGCACCTGGGG 250
QY 328 LeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGln 347
Db 251 CTCTTCTGCAGTGTGCCATCTCCCTGGCTCTTCCCTGGTCTATGACAGCGCTGGTACAG 310
QY 348 ArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGly 367
Db 311 AACTTGGCCACACGGTCAGTCTATCTGCCAGGTGTATGATGACCTTTCTCTGGCTGCCGCT 370
QY 368 AlaThrCysLeuSerHisSerValAlaValValThAlaSerAlaAlaLeuThrGlyPhe 387
Db 371 GCCACCTGCTGTCACACAGCGTGGTGTAGTAGACAGCCTCAGCTGCCCTCACCGGGTTC 430
QY 388 ThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLys 407
Db 431 ACCTTCTGGCCCTTGAGATCTCGCTTACCGCTCGCTTCCCTCTACCACTGAGAGAG 490
QY 408 GlnValPheLeuProLysTyrArgGlyAspThrGlyAlaSerSerGluAspSerLeu 427
Db 491 CAGGTGTCTCTGCCAAATACCCAGGGAGCGCTGGAGGTAGCAGCGGTGAGGACGCCAG 550
QY 428 MetThrSerPheLeuProGlyProLysPheProGlyAlaProPheProAsnGlyHisValGly 447
Db 551 ACAACCAAGCTTCTTGGCAGGCCCTTAAGCCAGGAGCTCTCTTCCCAATGGACACGTGGG 610

QY 448 AlaGlyCysSerGlyLeuLeuProProProAlaLeuLeuCysGlyAlaSerAlaCysAsp 467
Db 611 TCTGGCAACACGCGATCCTGGC-CCTCCACT-GCACTCTGTGGGCTCTTGTGCGAT 668
QY 468 ValSerValArgVal-ValValGlyGluProThrGluAlaArgValValProGlyArgG1 487
Db 669 GTTTCATCGATCGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 728
QY 487 YileCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaPro-- 506
Db 729 CATTTGCTGGC-CTGGCCATTTCTGGCGGTGCTTCTGTCTGTCCAGGTGGTGGCGCTG 787
QY 507 -----SerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAl 522
Db 788 TCCTGGCCCATGCACGCTGACACTC-----TGCACCTGG 820
QY 522 atyMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValVa 542
Db 821 CCATATGGGATCAGTGCAGGCATGGCTTGTGCGCGATACTTTTGACACACCGGACTGG 880
QY 542 LPhe 543
Db 881 GTTC 884
RESULT 4
LOCUS BE867241 718 bp mRNA linear EST 20-OCT-2000
DEFINITION 601442309F1 NTH_MGC_65 Homo sapiens cDNA clone IMAGE:3846411 5',
mRNA sequence.
ACCESSION BE867241
VERSION BE867241.1 GI:10316017
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 718)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9559 row: a column: 04
High quality sequence stop: 693.
Location/Qualifiers
1. .718
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:3846411"
/clone_lib="NIH_MGC_65"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: Sali; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
BASE COUNT 112 a 227 c 210 g 168 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 1.4e-89 Length: 718
Score: 1039.00 Matches: 212
Percent Similarity: 98.15% Conservative: 0
Best Local Similarity: 98.15% Mismatches: 2
Query Match: 36.32% Indels: 2

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DB: 12 Gaps: 0
US-09-593-793A-113 (1-553) x BE867241 (1-718)

QY 340 LeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerVal 359
Db 2 C7GGGTCATGGACGGGTGGTGCAGCGATTCCGACACTCGACAGTCTATTGTGGCCAGTGTG 61
QY 360 AlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThr 379
Db 62 GCAGCTTCCCTGGTGGTCCGGTCCACATGCCGTCTCCACAGTGTGCCGTGGTGA 121
QY 380 AlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnInLeuLeuProTyrThrLeu 399
Db 122 GCTTCAGCGCGCTCACCGGGTTCACCTTCTCAGCCCTCAGATCCTGCCCTACACACTG 181
QY 400 AlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGly 419
Db 182 GCCTCCCTTACCCAGCGGAGAGAGGTGTTCTTCCCAATAACCGAGGGACACTGGA 241
QY 420 GlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAla 439
Db 242 GTGTGTAGCAGTGCAGACAGCTGTATGACCACTTCTCCAGGCGCTTAAGCTGGAGCT 301
QY 440 ProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAla 459
Db 302 CCCTTCCCTTAATGGACACGCTGGTGTGGAGGACGTGGCTGCCACCTCCACCCGGG 361
QY 460 LeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGlu 479
Db 362 C7CTCGGGGGCTCGCCCTGTATCTCCGTACGTGTGGTGGTGGTGGAGCCACCCAG 421
QY 480 AlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPhe 499
Db 422 GCCAGGGTGTCCGGCGGGGGCATCTGCTGGACCTCCCATCCCATCTGGATAGTGCCTTC 481
QY 500 LeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSer 519
Db 482 CTGCTGTCCAGTGGCCCATCCCTGTTATGGCTCCATTGTCCAGCTCAGCCAGTCT 541
QY 520 -ValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIle-TyrPheAlaT 539
Db 542 TGTCACTNGCTATATGGTGTCTTGGCCAGGCGCTGGTGTGGTGGCATTTTACTTTGCTA 601
QY 539 hrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
Db 602 CACAGGTAGTATTACACAGACGAGCTTGGCCAAATACTACGCG 645

RESULT 5
BG174399
LOCUS
DEFINITION 602334219F1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:4457452 5',
mRNA sequence.
ACCESSION BG174399
VERSION BG174399.1 GI:12681102
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 786)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabps-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Plate: LLAM10254 row: e column: 05
High quality sequence stop: 666.
Location/Qualifiers
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4457452"
/clone_lib="NCI_CGAP_Maml"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/Note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 121 a 246 c 234 g 185 t
ORIGIN

Alignment Scores:
Pred. No.: 6,1e-89 Length: 786
Score: 1033.00 Matches: 209
Percent Similarity: 83.14% Conservative: 8
Best Local Similarity: 80.08% Mismatches: 35
Query Match: 36.11% Indels: 9
DB: 12 Gaps: 5

US-09-593-793A-113 (1-553) x BG174399 (1-786)
QY 104 ProArgAlaGlyTyrPheLeuAlaGlyLeuLeuCysProAspPheProLeuGluLeuAla 123
Db 1 CCGAGGGCTGGCTGGCTGGCAGACTGCTGTACCCAGACAGCCGCCCTGGAGTAGGCC 60
QY 124 LeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeu 143
Db 61 CTGCTGATCTTGGGAGTGGGCTGCTGGACTTTTGTGGCCAGGTGTCTTACTCCATTG 120
QY 144 GluAlaLeuLeuSerAspLeuPheArgAspProAspPheIleCysArgGlnAlaTyrSer-Va 163
Db 121 GAGGCTTACTCTCCGACCTCTCCGGGACCAGACCACTGCCGCCAACCCCTCTCTGGG 180
QY 163 lTyrAlaPheMetIleSerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspTr 183
Db 181 GTACGCTTCATGATCAGCTTGGGGCTGCTGGGCTACCTTACCTGCCATTGACTG 240
QY 183 pAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeuLe 203
Db 241 GGACACCCAGCGTCTGGCCCTTACTGCGTACTCAGGAAGAAATGCTCTTTGGCCTCCT 300
QY 203 uThrLeuIlePheLeuThrCysValAlaAlaAlaThrLeuLeuValAlaGluGluAlaLe 223
Db 301 CACCCTCATTTTCTTCATCTGTCATGGCACCCTCTGTTGTGACGGAGAGGAGTACT 360
QY 223 uGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysPr 243
Db 361 GGGCCACCCGAGCGCGCAGAAAGGTTGTGCTCTCTGCGGTGTCGCGCGGCTGTGCGCC 420
QY 243 cCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnle 263
Db 421 ATGCCACGTTGGCTGGCTTCCGAAATCTGGGTACCCCTGTTTCCCGGCTCGACGAGCT 480
QY 263 uCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuLeuCysSerTrpMe 283
Db 481 GTGCTGCCGATGCTCCGACCTACGCCGACTCTTGTGGCTGAGCTGTGAGCTGGAT 540
QY 283 tAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGlnGl 303
Db 541 GGCACCTTATGACTTTCACACTGTTTACACGAGCTTCTGTTGGGAGAGGGGCTGTAACCCAG 600
QY 303 yValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyValArgMe 323
Db 601 TGTACCCAGAGCCGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 660
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QY 323 tGlySerLeu---GlyLeuPheLeuGln---CysAlaIleSerLeuValPhe----- 338
Db 661 TGGGGCAGCCCTCTTCCTGGAGGTGTCACATTCCTCCCTGCTTCCTCCCTGG 720
QY 339 -SerLeuValMetAspArgLeuValGlnArgPhe---GlyThrArgAlaValTyrLeuAl 357
Db 721 CTATTG-----GACAGGCTGGCTCCCGAAATTTGCGGCCCGCCAGGCAATTAATCTTCG 774
QY 357 a 357
Db 775 G 775

RESULT 6
BO948390
LOCUS
DEFINITION
BO948390 885 bp mRNA linear EST 21-AUG-2002
IMAGC:6198823 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 885)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapps-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13611 row: b column: 08
High quality sequence stop: 615.
Location/Qualifiers
1..885
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6198823"
/clone_lib="Lupski_sciatic_nerve"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
Note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TGACCCAGCGTCCG-3' and
5'-GACTAGTTCTAGTCCGAGCGCCGCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."
BASE COUNT 129 a 286 c 294 g 176 t
ORIGIN

Alignment Scores:
Pred. No.: 1-24e-76 Length: 885
Score: 906.00 Matches: 180
Percent Similarity: 92.86% Conservative: 2
Best Local Similarity: 91.84% Mismatches: 11
Query Match: 31.67% Indels: 3
DB: 14 Gaps: 0

US-09-593-793A-113 (1-553) x BO948390 (1-885)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20

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Db 259 ATGCTCAGAGGCTGTGGGTGAGCCGCTCTCGCGCACCGAAAGCCAGCTCTTCTG 318
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 319 GTCAACCTGCTAACCTTTGGCCCTGGAGGTGTGTTTGGCCGACGATCACCATTGTCGG 378
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 379 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGTGTGCTGGCATTTGG 438
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
Db 439 CCAGTGTGGGCTGTGCTGTGCTCCGCTCTAGGCTCAGCCAGTGACCATCGCGTGA 498
QY 81 ArgTyrClyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 499 CGCTATGGCCGCCGCCGCTTTCATCTGGGCACTGTCTTGGGCACTCTGCTGAGGCTC 558
QY 101 PheLeuIleProArgAlaGlyTyrLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 559 TTTCTCATCCCAAGGCCGCTGCTAGCAGGCTGCTGTGCCGGATCCAGGCCCTG 618
QY 121 GluLeuAlaLeuLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 619 GAGCTGGCACTGCTCATCTCTGGCGTGGGCTGCTGGACTTCTGTGGCCCGGTGTGCTTC 678
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAsp-ProAspHisCysArgGlnAl 160
Db 679 ACTCCACTGGAGGCCCTGCTCTGAACCTCTCCGGGACCCCGACCATGTGCCAGGC 738
QY 160 atySerValTyrAlaPheMetIle--SerLeuGlyGlyCysLeuGlyTyrLeuLeuPro 179
Db 739 CTACTCTGTCTATGCTCTCATGATCCGCTCTTGGGGGCTGGCCGGGCTACCTCTGCCC 798
QY 180 AlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGly 193
Db 799 TGCCTTGGTGGGGAACACGAGGCGCTGGGCCCTAACTGGGC 840

RESULT 7
AW412402
LOCUS
DEFINITION
AW412402 592 bp mRNA linear EST 08-FEB-2000
uo78h02.y1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:2648691 5'
similar to TR:Q39231 Q39231 SUCROSE-PROTON SYMPORTER. [1] ;, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AW412402
AW412402.1 GI:6938274
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 592)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Other ESTs: uo78h02.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapps-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
MGI:1029143
Seq primer: -40Rp from Gibco
High quality sequence stop: 421.
Location/Qualifiers
1..592
FEATURES
source

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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:2648691"
/clone_lib="NCI_CGAP_Maml"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site.1: SalI;
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 91 a 193 c 168 g 140 t
ORIGIN

Alignment Scores:
Pred. No.: 1,01e-76 Length: 592
Score: 904.00 Matches: 172
Percent Similarity: 89.85% Conservatives: 5
Best Local Similarity: 87.31% Mismatches: 20
Query Match: 31.60% Indels: 1
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x AW412402 (1-592)
QY 149 AspleuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIle 168
Db 2 GACCTCTCCGGGACCCAGACCACCTGCCGCCAAGCCTTCTGTCTACGCTTCATGATC 61
QY 169 SerLeuGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeu 188
Db 62 AGCCTTGGGGGCTGCCCTGGGCTACCTCTTACCTGCCATTGACTGGGACACCGCTGCTG 121
QY 189 AlaProTyrLeuGlyThrGlnGluGluCysLeuPheGlyLeuThrLeuIlePheLeu 208
Db 122 GCCCCCTACTGGGTACTCAGGAAGAATGCCTCTTTGGGCTCCTCACCCCTCATTTTCCTC 181
QY 209 ThrCysValAlaAlaThrLeuLeuValAlaGluAlaLeuGlyProThrGluPro 228
Db 182 ATCTGCATGGCAGCCACTCTGTTGTGACGAGGAGGAGTACTGCGCCACCCAGACCG 241
QY 229 AlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeu 248
Db 242 GCAGAAAGGTTGTGTGCTCTGCGGTGCGCGCGATGCTGCCATGCCACGTTGGCGTG 301
QY 249 AlaPheArgAsnLeuGlyAlaLeuProArgLeuHisGlnLeuCysCysArgMetPro 268
Db 302 GCTTCCGGAACTGGGTACCTGTTTCCCGGCTGCAGCAGCTGTGCGCGCATGSCCT 361
QY 269 ArgThrLeuArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPhe 288
Db 362 CGCACCTACGCGGACTCTTGTGGCTGAGCTGCGAGCTGGATGGCACTTATGACTTTC 421
QY 289 ThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGlu 308
Db 422 ACACCTGTTCTACACGACTTCGTGGGAGAGGGGCTGTACAGGGTGTACCCAGACCGAG 481
QY 309 ProGlyThrCluAlaArgHisTyrAspGluGlyValArgMetGlySerLeuGlyLeu 328
Db 482 CCAGGCACCGGCGCGGAGACACTATGATGAAGGCAATTCGAATGGGCGAGCCTGGGCTC 541
QY 329 PheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeu 345
Db 542 TTCCTGCATGTGCCATCTCCCTGGTCTCTCCCT-GTCATGGACAGGCTG 591

RESULT 8
BF785813 929 bp mRNA linear EST 12-JAN-2001
LOCUS 602112437F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4240617
DEFINITION 5', mRNA sequence.
ACCESSION BF785813
VERSION BF785813.1 GI:12090849
KEYWORDS EST.
```

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 929)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM9855 row: j column: 10
High quality sequence stop: 610.
Location/Qualifiers
1..929
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4240617"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: kidney; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT 190 a 275 c 262 g 202 t
ORIGIN

Alignment Scores:
Pred. No.: 8.85e-76 Length: 929
Score: 897.50 Matches: 195
Percent Similarity: 83.54% Conservatives: 8
Best Local Similarity: 80.25% Mismatches: 40
Query Match: 31.37% Indels: 5
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BF785813 (1-929)

QY 177 LeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGlu 196
Db 13 CTCCTTACCTGCCAT-GACTGGGACACCGAGTCTCGGCCCTTACCTGGTACTCAGGAA 71
QY 197 GluCysLeuPheGlyLeuLeuIlePheLeuThrCysValAlaAlaThrLeuLeu 216
Db 72 GAATGCTCTTAGGCCCTCTCACCCCTCATTTTCTCATCTGCGAGCCGACTCTGTTT 131
QY 217 ValAlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSer 236
Db 132 GTACGAGGAGGAGGAGTACTGGGCCCCACCGAGCCGAGAGGGTGTGTTGTTCTGCG 191
QY 237 LeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeu 256
Db 192 GTGTCCGCCGATGCTGCCCATGCCACGTTGGCTTCCGGAATCTGGGTACCCCTG 251
QY 257 LeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheVal 276
Db 252 TTTCCCGGCTGCAGCAGCTGTGCTGCCGATGCTCGACCTAGCCGACTCTTTGTTG 311
QY 277 AlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheVal 296
Db 312 GCTGAGCTGTGAGCTGGATGGCACTTATGACTTTTACACTGTTTACACGAGCTTCGTG 371
QY 297 GlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrCluAlaArgHis 316
Db 372 GGAGAGGGGCTGTACAGGGTGTACCCAGAGCCAGGACCCAGGACCCGAGACAC 431
QY 317 TyrAspGluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeu 336

```
|||||
Db 432 TATGATGAAGGCATTCGAATGGGCAGCTGGGCTCTCTCCAGTGTGCATCTCCCTG 491
QY 337 ValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeu 356
Db 492 GTCTTCCTCCCTGGTCATGGACAGCTGGTACAGAAGTTCGGCACACGGTCAGTCTATCTG 551
QY 357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaValThrCysLeuSerHisSerValAla 376
Db 552 GCCAGTGTGATGACCTTTTCCTGTGGCTGCC--TGTCACTGTCTGTCCCACACGGTGGT 609
QY 377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396
Db 610 GTAGTGACAGCCC--AGTGGCCCTCACGGGTGCACCTTCTCGGG-CTGAGAGATACCGGCT 666
QY 397 TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly 416
Db 667 TACAGCAGCAGCTTC-CTCTACCAACCGTGGCAAGCAGTGTCTGCCCAATACCGAGGGGC 725
QY 417 AspThrGly 419
Db 726 ACCTGAGGT 734

RESULT 9
BQ934815
LOCUS BQ934815
DEFINITION AGENCOURT_B881033 NCI_CGAP_Co24 Mus musculus cDNA clone
IMAGE:6396364 5', mRNA sequence.
ACCESSION BQ934815
VERSION BQ934815.1 GI:22350198
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL 1 (bases 1 to 934)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13892 row: 1 column: 05
High quality sequence stop: 634.
Location/Qualifiers
1..934
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6396364"
/clone_lib="NCI_CGAP_Co24"
/lab_host="PH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 Kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 164 a 278 c 273 g 219 t
ORIGIN
```

Alignment Scores:
Pred. No.: 1.14e-74
Score: 886.00
Length: 934
Matches: 189
Percent Similarity: 81.17%
Conservative: 5
Best Local Similarity: 79.08%
Mismatch: 23
Query Match: 30.97%
Indels: 22
Gaps: 4
DB:

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US-09-593-793A-113 (1-553) x BQ934815 (1-934)
QY 1 MetValGlnArgLeuTrpValSerArgLeuArgHisArgLysAlaGlnLeuLeuLeu 20
Db 246 ATGATCAGAGGCTGTGGCCAGCCGCTCTACGGACCCGGAAGCTCAGCTCCTGCTG 305
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
Db 306 GTCAACCTGCTACCTTTTGGCCCTGGAGGTGCTGCTGGCTGCCGCATTAACCTATG 365
QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
Db 366 CCCCTTCTGCTGGAAGTCGGGGTGGAGGAAATTCATGACCATGGT----- 413
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTTrpArgGly 80
Db 414 -----TTGGGCTCAGCCAGTGCACCTGAGTGGG 443
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Db 444 CGCTATGGCCGCGGAGACCTTTATCTGGGCTTTGTCCCTGGGTGCTCTGCTAAGCCTC 503
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Db 504 TTTTCTCATCCGAGGCTGGCTGGCTGGCAGGACTGCTGTACCCAGACACAGGCCCCCTG 563
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Db 564 GAGTTGGCCCTGCTGATCTTGGGAGTGGGCTGCTGCACCTTTTGGGCCAGGTGCTCTT 623
QY 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Db 624 ACTCCATTGGAGGCTTACTCTCCGACCTTCTCCGGGACCCAGACCTGCCGCCAAGCC 683
QY 161 TyrSerValTyrAlaPheMetIleSerLeu-GlyGlyCysLeuGlyTyrLeuLeuProAl 180
Db 684 TTTCTCTGTCTACGCTTTCATGATCAGCCTTTGGGGCTTGGGGCTGCTGGGTACTGCT 743
QY 180 alleAspTrpAspThrSerAlaLeu-AlaProTyrLeuGlyThrGln-GluGluCysLeu 199
Db 744 CATTGACTGGGACACGAGCTTCTGGGCCCTTACTCTGGGTACTCAGGGAAATGCTT 803
QY 200 -PheGlyLeu---LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu----- 216
Db 804 CTTTGGCCCTCCCTCACCCTCATTTTCTCTCATCTGCAATGGCAACCCACTGCTGTTT 863
QY 216 uValAlaGluGluAlaAlaLeuGlyProThr---GluProAlaGluGly 231
Db 864 GACCGGAAGAAGCAATACTTTGGGCCCCCACCACCCCAACCCGCCCAAGGG 912

RESULT 10
BQ081576
LOCUS BQ081576
DEFINITION H3066G04-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3066G04 5', mRNA sequence.
ACCESSION BQ081576
VERSION BQ081576.1 GI:12564144
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 549)
JOURNAL Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka
COMMENT Verification and initial annotation of NIA mouse 15K cDNA clone set
Unpublished (2001)
Other ESTs: H3066G04-3
Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
```

This clone set has been freely distributed to the community. Please visit <http://lgsun-grc.nia.nih.gov/cDNA/15k.html> for details.

Plate: H3066 row: G column: 04

Seq primer: -21M13 Reverse

High quality sequence stop: 549

POLYA=No.

FEATURES

source

Location/Qualifiers

1..549

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="niaEST:H3066G04-5"

/db_xref="taxon:10090"

/clone="H3066G04"

/clone_lib="NIA Mouse 15K cDNA Clone Set"

/sex="Clones arrayed from a variety of cDNA libraries"

/dev_stage="Clones arrayed from a variety of cDNA libraries"

/lab_host="DH10B"

/note="vector: pSPORT1; Site_1: SalI; Site_2: NotI; This

clone is among a rearranged set of 15,247 clones from 11

embryo cDNA libraries (including preimplantation stage

embryos from unfertilized egg to blastocyst, embryonic

part of E7.5 embryos, extraembryonic part of E7.5 embryos

and E12.5 female mesonephros/gonad) and one newborn

ovary cDNA library. Average insert size 1.5 kb. All

source libraries are cloned unidirectionally with Oligo(dT

)-Not primers. References include: (1) Genome-wide

expression profiling of mid-gestation placenta and embryo

using a 15,000 mouse developmental cDNA microarray, 2000,

Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2)

Large-scale cDNA analysis reveals phased gene expression

patterns during preimplantation mouse development, 2000,

Development, 127: 1737-1749; (3) Genome-wide mapping of

unselected transcripts from extraembryonic tissue of

7.5-day mouse embryos reveals enrichment in the t-complex

and under-representation on the X chromosome, 1998, Hum

Mol Genet 7: 1967-1978."

Mol Genet 7: 1967-1978."

BASE COUNT 98 a 176 c 160 g 115 t

ORIGIN

Alignment Scores:

Pred. No.: 2,63e-73 Length: 549

Score: 868.00 Matches: 165

Percent Similarity: 93.96% Conservative: 6

Best Local Similarity: 90.66% Mismatches: 11

Query Match: 30.34% Indels: 0

DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BG081576 (1-549)

Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300

Db 3 ACCTGGATGGCACTTATGACTTTCACCTGTTCTACCGACTTCGTGGAGGGGCTG 62

Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320

Db 63 TACCAGGCTGTACCCAGAGCCGAGCACCAGCCGAGCCGAGACATGATGAGGC 122

Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340

Db 123 ATTCGAATGGGCGAGCTGGGGCTCTTCCTGCAGTGTGCATCTCCGCTCTTCCTG 182

Qy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360

Db 193 GTCATGGACAGCTGGTACAGAAAGTTCGCACACCGTCTATCTGGCCAGTGTGAG 242

Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380

Db 243 ACCTTTCTGTGGCTGCCGCTGCCACCTGCCCTGCCAGCGGTGTAGTGACAGCC 302

Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400

Db 303 TCAGTGGCCCTACCGGGTTCACCTTCTCGGCTTGCAGATCCTCCCTTACACGCTGCC 362

Qy 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
 Db 363 TCCCTCTACCCACCGTGAGAGCAGGTGTCTTCCCTGCCAATACCGAGGCGCTGGAGT 422
 Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
 Db 423 AGCAGCGGTGAGGACAGCCAGACACACAGCTTCTTCCAGAGCCCTAAGCCAGGCTCTC 482
 Qy 441 PheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProProAlaLeu 460
 Db 483 TTCCCAATGGACACGTGGGCTCTGGCAGCAGCGGATCTTGGCCCTCCACCTGCACTC 542
 Qy 461 CysGly 462
 Db 543 TCTGGG 548

RESULT 11

BG173136

LOCUS

DEFINITION 602335411F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4458602 5',

ACCESSION BG173136

VERSION BG173136.1 GI:12679748

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10257 row: e column: 03

High quality sequence stop: 608.

Location/Qualifiers

1..969

/organism="Mus musculus"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:4458602"

/clone_lib="NCI_CGAP_Mam1"

/tissue_type="tumor, biopsy, sample"

/dev_stage="10 months, virgin"

/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigator

providing samples: Gilbert Smith, NIH"

BASE COUNT 199 a 289 c 287 g 194 t

ORIGIN

Alignment Scores:

Pred. No.: 6.01e-72 Length: 969

Score: 858.00 Matches: 195

Percent Similarity: 79.46% Conservative: 10

Best Local Similarity: 75.58% Mismatches: 50

Query Match: 29.99% Indels: 8

DB: 12 Gaps: 2

US-09-593-793A-113 (1-553) x BG173136 (1-969)

Qy 186 SerAlaLeuAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeuThrLeu 205

Db 111

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Db 1 AGCGTTCTGCGCCCTACCTGGGTACTCAGGAAGAATGCGCTCTTTGGCCTCTCACCCCTC 60
QY 206 ILePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGluAlaLeuGlyPro 225
Db 61 ATTTTCTCATCTGCATGGCAGCCTCTGTTGTACGAGGAGGAGCAGTACTGGGCCCA 120
QY 226 ThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCysArg 245
Db 121 CCCGAGCGGACAGAGGTTGTTGGTCTCTGCGCGTGTGCGCGCGATGCTGCCCATGCCAC 180
QY 246 AlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCys 265
Db 181 GTTGGCCTGGCTTTCCGGAATCTGGGTACCTCTGTTCCCGGCTGCAGCAGCTGTCTGC 240
QY 266 ArgMetProArgThrLeuArgAsnLeuPheValAlaGluLeuCysSerTrpMetAlaLeu 285
Db 241 CGATGCTCGCACCTACGCCCACTCTTGTGGCTGAGCTGTGCAGCTGGATGGCACTT 300
QY 286 MetThrPheThrLeuPheThrAspPheValGlyGluGlyLeuThrGlnGlyValPro 305
Db 301 ATGACTTTTACACTGTTTACACGGACTTCTGCGGAGAGGGGCTGTACCA-GGTGTACCC 359
QY 306 ArgAlaGluProGlyThrGluAlaAlaArgHisTyrAspGluGlyValArgMetGlySer 325
Db 360 AGAGCCGAGCCAGGCAACCGAGGC-CGGAGACACTATGATGAAGGCATTCGAATGGGCAGC 418
QY 326 LeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeu 345
Db 419 CTGGGCTCTTCTGAGTGTGCATCTCCCTGGTCTTCTCCCTGGTATGGACAGGCTG 478
QY 346 ValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAla 365
Db 479 GTACAGAAGTTGGCACACCGCTCAGTCTATCTGGCCAGTGTGTATGACCTTTCTCTGGCT 538
QY 366 AlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuThr 385
Db 539 GCGCTGCCACCTGCTG-TCCCCACAGCTGGTGTGTAGTACAGC-TCAGGTGCCCTCACC 596
QY 386 GlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArg 405
Db 597 GGGTTACCTTCTCCGGCTGACAGTCTTGAC-TTAAAGATCGCCTCTCTACACCGTG 655
QY 406 -GluGlyGlnValPheLeuProGlyTyrArgGlyAspThrGlyGlyAlaSerSerGluAs 425
Db 656 AGAAGACCACTTCTCCGGCAAAAT---AAGGAGGAGGACCTGAAGCATGCCGTGAAGA 712
QY 425 pSerLeuMetThrSerPheLeuProGlyProGlyProGlyAlaProPhePro 442
Db 713 ACGGCAAAACCGGTTTT---GGCGGGCTTAAAGCAGGAGCATCTCTCCCA 761

RESULT 12
AF109299 482 bp mRNA linear EST 28-JAN-2000
LOCUS AF109299 Homo sapiens prostate adult Homo sapiens cdna ipca-2
DEFINITION , mRNA sequence.
ACCESSION AF109299
VERSION AF109299.1 GI:6782692
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 482)
JOURNAL Walker M.G., Volkmutz W., Sprinzak E., Hodgson D. and Klingler T.
MEDLINE Prediction of gene function by genome-scale expression analysis:
COMMENT prostate cancer-associated genes
20082966 Genome Res. 9 (12), 1198-1203 (1999)
Contact: Walker MG
Incyte Pharmaceuticals
3174 Porter Drive, Palo Alto, CA 94304, USA
co-expressed with known prostate-cancer genes.
Location/Qualifiers

FEATURES
source 1..482
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IPCA-2"
/clone_lib="Homo sapiens prostate adult"
/tissue_type="prostate"
/dev_stage="adult"
/note="multiple clone assembly from multiple libraries and donors"
BASE COUNT 57 a 179 c 141 g 105 t
ORIGIN
Alignment Scores:
Pred. No.: 1,21e-69 Length: 482
Score: 829.00 Matches: 157
Percent Similarity: 98.12% Conservative: 0
Best Local Similarity: 98.12% Mismatches: 2
Query Match: 28.98% Indels: 1
DB: 9 Gaps: 0
US-09-593-793A-113 (1-553) x AF109299 (1-482)
QY 129 ValGlyLeuLeuAspPheCys-GlyGlnValCysPheThrProLeuGluAlaLeuLeuSe 148
Db 4 GTGGGCTCTGGACATCTCTGGGCCAGGTGTCTTCACTCCACTGGAGCCCTGCTCTC 63
QY 148 rAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIl 168
Db 64 TGACCTCTTCCGGGACCCGAGCAGCAGTGTGCCAGGCTACTCTGTCTATGCTTCATGAT 123
QY 168 eSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLe 188
Db 124 TAGTCTTTGGGGCTGCTGGGCTACCTCTGCTGCCATTGACTGGACACCAAGTGCCT 183
QY 188 uAlaProTyrLeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLe 208
Db 184 GGGCCCTTACCTGGGACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCTCATCTTCCT 243
QY 208 uThrCysValAlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluPr 238
Db 244 CACCTCGTAGAGCCACACACTGCTGTGTGGCTGAGGAGGAGGAGGCTGGGCCACAGCC 303
QY 228 oAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLe 248
Db 304 AGCAGAAGGCTGTGCGCCCTCTGCTGCGCCACTGCTGCCATGCGGGCCGCTT 363
QY 248 uAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetPr 268
Db 364 GGGTTTCCGGAACCTGGGCGCCCTGCTTCCCGGCTGCACAGCTGTGCGCGCATGCC 423
QY 268 oArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThr 287
Db 424 CCGCACCTTGGCGGCTCTTCTGTGGCTGAGCTGTGCAGCTGGATGGCACTCATGACC 481

RESULT 13
BF581244 700 bp mRNA linear EST 12-DEC-2000
LOCUS BF581244 Mus musculus cdna clone IMAGE:4220415 5',
DEFINITION mRNA sequence.
ACCESSION BF581244
VERSION BF581244.1 GI:11654956
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 700)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
```

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AW9803 row: p column: 16
High quality sequence start: 2
High quality sequence stop: 680.
Location/Qualifiers

FEATURES

source
1..700
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4220415"
/clone.lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 110 a 227 c 197 g 166 t
ORIGIN

Alignment Scores:
Pred. No.: 3.84e-69 Length: 700
Score: 826.50 Matches: 194
Percent Similarity: 85.90% Conservative: 7
Best Local Similarity: 82.91% Mismatches: 31
Query Match: 82.89% Indels: 9
DB: 12 Gaps: 1

US-09-593-793A-113 (1-553) x BF581244 (1-700)

Qy 177 LeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGlu 196
|||||
Db 3 CTCCTACCTGCCAT-GACTGGACACCAAGCGTCTGGCCCTACTGGGTACTCAGGAA 61
Qy 197 GluCysLeuPheGlyLeuLeuThrLeuPheLeuThrCysValAlaAlaThrLeuLeu 216
|||||
Db 62 GAATGCTCTT-GGCTCTCTACCTCATTTTCTCACTGCTGATGGCAGCCACTCTGTT- 119
Qy 217 ValAlaGluGluAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSer 236
|||||
Db 120 GTGACGGAGGAGGAGTACTGGGCCCCACCGAGCGCGAGAGGTTGTG-GTCTCTGCC 178
Qy 237 LeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeu 256
|||||
Db 179 GTGTCGCCCGCATGTGCCCATGCCACGTTGGCCTGGCTTCCGGAATCTGGGTACCCCTG 238
Qy 257 LeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheVal 276
|||||
Db 239 TTTCCCGCGCTGCACAGCTGTGCTGCCGATGCTCGACCTCGACCGCTACTTTGTG 298
Qy 277 AlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheVal 296
|||||
Db 299 GCTGAGCTGTGCAGCTGGATGACATTATGACTTTCACACTGTTCTACAGGACTCTGTG 358
Qy 297 GlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHis 316
|||||
Db 359 GGAGAGGGGCTGTACACCGTGTATCCAGCCGAGCCAGGACCGAGCGCCGGAGACAC 418
Qy 317 TyrAspGluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeu 336
|||||
Db 419 TATGATGAGGCAATTCGAATGGGACAGCTGGGGCTCTTCTTCAGTGTGCCATCTCCCTG 478
Qy 337 ValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeu 356
|||||
Db 479 GTCTTCTCCCTGTCATGGACAGGCTGTACAGAAGTTCGGCACACAGGTCAGTCTATCTG 538
Qy 357 AlaSer-ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl 376
|||||
Db 539 GCCACGTGTGATGACCTTTCTGTGGCTTTCCTGCTTTCCTCCACCTGCTG-TCCACAGCGTGT 597

Qy 376 aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 396
|||||
Db 598 GGTAGTGACAGCCTCAGCTGC-CTCACGGGTTACCTTCTCGGC-TTGACATCTCG-- 653
Qy 396 oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnVal 409
|||||
Db 654 -CTTACAGCTCGTCCCTCTACACCGTGAAGCGGTG 692

RESULT 14

BG864609

LOCUS 602798469F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4919513 5',
DEFINITION mRNA sequence.

ACCESSION BG864609

VERSION BG864609.1 GI:14215147

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 872)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1AM10834 row: i column: 18

High quality sequence stop: 738.

FEATURES

source

1..872
/organism="Mus musculus"
/strain="NMRI"
/db_xref="taxon:10090"
/clone="IMAGE:4919513"
/clone.lib="NCI_CGAP_Mam4"
/tissue_type="tumor, gross
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."

BASE COUNT 157 a 242 c 276 g 197 t

ORIGIN

Alignment Scores:
Pred. No.: 4.49e-68 Length: 872
Score: 817.00 Matches: 173
Percent Similarity: 90.91% Conservative: 7
Best Local Similarity: 87.37% Mismatches: 15
Query Match: 28.56% Indels: 5
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BG864609 (1-872)

Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
|||||

Db 280 ATGATCCAGAGGCTGTGGCCAGCGCTGTCTACGGCACCAGGAAAGCTCAGCTCTGCTG 339

Qy 21 ValAsnLeuLeuThrPheClyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||||

Db 340 GTCAACCTGCTCACCTTTTGGCTGGAGGTGTGCTGGCTGGCGCATTTACCTATGTGCCA 399

QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
|||||
Db 400 GCCCTTCTGCTGCAAGTCGGGGTGGAGGAAATTCATGACCATTGTTGGCCATTGGC 459
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
|||||
Db 460 CCAGTGTAGCCCTGGTGTCTGCTCCACTCTAGGCTCAGCCAGTACCAGTGGCGTGGG 519
QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
|||||
Db 520 CGTATGGCCCGCGGAGACCCTTATCTGGCTTTGTCCCTGGGTGTCTGCTTAAGCCCTC 579
QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
|||||
Db 580 TTTCTCATCCGAGGCTGGCTGGCTGGCAGGACTGCTGTA-CCAGACACCAGGCCCTG 638
QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCys-GlyGln-ValCysP 140
|||||
Db 639 GAGTTGGCCCTGTGTATCTTGGAGTGGGCTGTCTGGACTTTTGGTGGCCAAAGGTGTGCT 698
QY 140 heThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnA 160
|||||
Db 699 TTACTCATTTGGAGGCTTACTCTCCGAGCTCTTCGGGACGCGAGAACATGGCGCAAG 758
QY 160 laTyrSer-ValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuPro 179
|||||
Db 759 CCTTCTCTGTCTACGCTTTCATGATCAGCCTTGGGGCTGCCTGGGTACTTTTACCT 818
QY 180 AlaIleAspTrpAspThrSerAlaLeuAlaProTyrIleuGlyThrGln 195
|||||
Db 819 GGCATTGACTGGAACACAAG-GTGCTGGGCGCCCTACTCTGGGTAATCAG 865
RESULT 15
BG469520 894 bp mRNA linear EST 21-MAR-2001
LOCUS 602532833F1 NTH_MGC_15 Homo sapiens cDNA clone IMAGE:4660496 5',
DEFINITION mRNA sequence.
ACCESSION BG469520
VERSION BG469520.1 GI:13401795
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 894)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>,
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1458 row: a column: 09
High quality sequence stop: 671.
Location/Qualifiers
1. .894
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4660496"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Orgn: colon; Vector: pOTB7; Site:1; Xhol; Site_2:
EcoRI; Orgn made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)*

BASE COUNT 173 a 272 c 264 g 185 t
ORIGIN

Alignment Scores:
Pred. No.: 4.92e-66 Length: 894
Score: 796.00 Matches: 163
Percent Similarity: 98.19% Conservative: 0
Best Local Similarity: 98.19% Mismatches: 1
Query Match: 27.82% Indels: 2
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BG469520 (1-894)

QY 390 SerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnVal 409
|||||
Db 3 TCAGCCCTCAGATCTGCCCTACACACTGGGCTCCCTTACCACCGGAGAGAGAGGTG 62
QY 410 PheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThr 429
|||||
Db 63 TTCCTGCCCAATATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGCAGCCTGATGACC 122
QY 430 SerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGly 449
|||||
Db 123 AGCTTCTCCAGGCCCTAAGCCTGGAGCTCCCTTAAATGGACACGCTGGGTGCTGGA 182
QY 450 GlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSer 469
|||||
Db 183 GGCAGTGGGCTGCTCCCACTCCACCGGCGCTCTGCGGGGCGCTCTGCCCTGTGATGCTCC 242
QY 470 ValArgValValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCys 489
|||||
Db 243 GTACGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 302
QY 490 -LeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPh 509
|||||
Db 303 CTGGACCTCGCCATCTCTGGATAGTCCCTTCTGCTGTCCAGGTGGCCCATCCCTGTT 362
QY 509 eMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAla-G 529
|||||
Db 363 TATGGCTCCATGTGTCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGACGG 422
QY 529 lYleuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuA 549
|||||
Db 423 GCCTGGTCTGGTGGCCATTACTTTGCTACACAGGTAGTATTGTACAGAGCGACTTGG 482
QY 549 laLysTyrSerAla 553
|||||
Db 483 CCAATACTCAGCG 496

RESULT 16
BI650119 901 bp mRNA linear EST 12-SEP-2001
LOCUS 603296208F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5337073 5',
DEFINITION mRNA sequence.
ACCESSION BI650119
VERSION BI650119.1 GI:15564355
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 901)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>,
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1855 row: p column: 02
High quality sequence stop: 778.
Location/Qualifiers

FEATURES

1..901
/organism="Mus musculus"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
/clone_lib="IMAGE:5337073"
/clone_lib="NCI CGAP Mam3"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."

BASE COUNT 151 a 260 c 288 g 202 t

ORIGIN

Alignment Scores:
Pred. No.: 1,38e-64 Length: 901
Score: 781.00 Matches: 174
Percent Similarity: 90.45% Conservativeness: 6
Best Local Similarity: 87.44% Mismatches: 11
Query Match: 27.30% Indels: 9
DB: 13 Gaps: 0

US-09-593-793a-113 (1-553) x BI650119 (1-901)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20

Db 318 ATGATCCAGAGCTGTGGCCAGCGCTGTCTACGGCACCGAAGCTCAGCTCCTGCTG 377

QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTrpValPro 40

Db 378 GTCAACCTGCTCACCTTTGGCCGTGGAGGTGTGCTGTGGTGGCGCATTTATGTGCA 437

QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60

Db 438 CCCCTTCTGCTGGAAGTGGGGTGGAGGAGAAATTCATGACCATGCTGTGGCATTTGC 497

QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80

Db 498 CCAGTGTCTAGGCTGCTTCTGCTCCACTCTAGGCTCAGCCAGTGACCGTGGG 557

QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100

Db 558 CGCTATGGCCGGCGGAGACCTTTATCTGGGCTTTGTCCCTGGGTGTCTGCTAAGCCCTC 617

QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120

Db 618 TTTTCATCCCGAGGGCTGGCTGGCTGGAGGACTGCTGTACCCAGACATCAGGCCCTG 677

QY 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140

Db 678 GAGTTGGCCCTGCTGATCTTGGAGTGGGGCTGTGGACGT-TGTGGCCAGGTGTGCTTG 736

QY 141 -ThrPro-LeuGluAlaLeuLeuSerAsp-LeuPheArg-AspProAspHis-CysArgG 159

Db 737 TACTCCATTTGGAGGCTTTACTCTCCGAACCTCTTCCGGGGAGCCAGACCACTTGC 796

QY 159 InAlaTyrSerVal-TyrAlaPheMetIleSerLeuGlyCysLeu-GlyTyrLeuLe 178

Db 797 AGGCTTCTCTGCTTACGCCCTTCTGTATCAGCCCTGGGGGCTGCTGGGGTTACCTTCT 856

QY 178 uProAlaIleAspTrpAspThr-SerAlaLeuAlaProTyr 191

Db 178 uProAlaIleAspTrpAspThr-SerAlaLeuAlaProTyr 191

Db 857 TACTGGCGTGCTTGGGACACCCAGCGTCTTGGCCCTTAC 897

RESULT 17

BF972601

LOCUS

DEFINITION

BF972601

BF972601

BF972601

BF972601

BF972601

BF972601

BF972601

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BF972601

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2002 row: m column: 14
High quality sequence stop: 485.
Location/Qualifiers
1. .1060
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5480245"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 282 a 294 c 314 g 169 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 6.1e-55 Length: 1060
Score: 682.00 Matches: 135
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 23.84% Indels: 0
DB: 14 Gaps: 0

US-09-593-793A-113 (1-553) x BM914562 (1-1060)

QY 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
|||||
DB 3 GGAGGTGCTAGCAGTGAGACAGCCTGATGACAGCTTCTGCCAGGCCCTAAGCCTGGA 62
|||||

QY 439 AlaProPheProAsnGlyHisValGlyAlaGlySerGlyLeuLeuProProPro 458
|||||
DB 63 GCTCCCTTCCCTATGAGACACGTGGGTGCTGGAGGAGTGGCTGCTCCACCTCCACCC 122
|||||

QY 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr 478
|||||
DB 123 GCGCTCTCGGGGCCCTCTGCTGTATGTCTCCGTACGTGTGGTGGGTGAGCCACC 182
|||||

QY 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498
|||||
DB 183 GAGGCCAGGTGGTTCGGGGCGGGGCATCTGCTGACCTCGCCATCTCGATAGTGC 242
|||||

QY 499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
|||||
DB 243 TTCCCTGCTGCCAGGTGGCCCATCCCTGTTATGGGGTCCATGTCTCCAGCTCAGCCAG 302
|||||

QY 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
|||||
DB 303 TCTGTCACTGCCTATATGTGTCTGCCGAGGCCTGGTCTGGTCCGCAATTTACTTTTGTCT 362
|||||

QY 539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
|||||
DB 363 ACACAGGTAGTATTTGACAAGAGCGACTTTGGCCAAATACTCAGCG 407
|||||

RESULT 21
BF789072 759 bp mRNA linear EST 12-JAN-2001
LOCUS BF789072
DEFINITION 602104930F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4222998

5', mRNA sequence.
BF789072
VERSION BF789072.1 GI:12094108
EST
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE 1 (bases 1 to 759)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9810 row: 1 column: 07
High quality sequence start: 3
High quality sequence stop: 756.
Location/Qualifiers
1. .759
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4222998"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. I"

BASE COUNT 131 a 218 c 243 g 167 t
ORIGIN

Alignment Scores:
Pred. No.: 4.68e-53 Length: 759
Score: 660.00 Matches: 143
Percent Similarity: 90.24% Conservative: 5
Best Local Similarity: 87.20% Mismatches: 12
Query Match: 23.07% Indels: 6
DB: 12 Gaps: 1

US-09-593-793A-113 (1-553) x BF789072 (1-759)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
|||||

DB 282 ATGATCCAGAGGCTGTGGGCCAGCGCTGTCTAGGSCACCGGAAAGCTCAGCTCCTGCTG 341
|||||

QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||||

DB 342 GTCAACCTCTCACCTTTTGGCCTGGAGGTGTGCTGGCTGCCGGCATTAACCTATGTGGCA 401
|||||

QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
|||||

DB 402 CCCCTTCTCTGGAAGTCGGGGTGGAGGAGAAATTCATGACCATGCTGTGGGCATTGGC 461
|||||

QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
|||||

DB 462 CCAGTGTCTAGGCTGTCTTCTGTCTCCACTCTTAGGCTCAGCCAGTGACCCAGTGGCGTGG 521
|||||

QY 81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
|||||

DB 522 CGCTATGGCCG-CGGAGACCTTTTATCTGGGGCTTTTGTCCCTGGGTGCTCTGCTAAGCCCTC 580
|||||

QY 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
|||||

DB 581 TTTTTCATCCCCGAGGCTGGCTGGCTGGCAGGACTGCTGTACCCAGACACACGAGGCCCTCTG 640
|||||

Qy	121	GlutLeuAlaLeuLeuLeuValGlyLeuLeuAspPheCysGlyGlnValCysPhe	140
Db	641	GAGTGTGGCCCTGCATCTTGGGAGTGGGGCTGCTGGACTTTGTGG--CAGGTGTGCTTT	698
Qy	141	ThrProLeuGluAlaLeuLeuSerAsp-LeuPheArgAspProAspHisCysArgGlnAl	160
Db	698	ACTCATTTGGAGGCGTCTACTCTCCGACTCTT-----CCGACCAGACATGGCGCAG	749
Qy	160	aTyrSerVal 163	
Db	750	CTTCTCTGTT 759	
RESULT 22			
AZ418156/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
SOURCE			

```
source
1..800
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:4660703"
/clone_lib="NIH_MGC_15"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pOMB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT 135 a 245 c 239 g 181 t
ORIGIN

Alignment Scores:
Pred. No.: 3,61e-49 Length: 800
Score: 620.00 Matches: 127
Percent Similarity: 99.22% Conservative: 0
Best Local Similarity: 99.22% Mismatches: 1
Query Match: 21.67% Indels: 1
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BG469487 (1-800)
QY 426 SerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHis 445
|||||
Db 3 AGCCTGATGACCAAGCTTCCTGGCAGGCCCTTAAGCCCTGGAGCTCCCTTCCCTAATGACAC 62
|||||
QY 446 ValGlyAlaGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAla 465
|||||
Db 63 GTGGGTGCTGGAGCACTGGCCCTGCCACCTCCACCGCGCTCTCGCGGCGCTCGCC 122
|||||
QY 466 CysAspValSerValArgValValGlyGluProThrGluAlaArgValValProGly 485
|||||
Db 123 TGTGATGTCCTCGCTAGCTGTGGTGGGTGGAGCCACCGAGGCCAGGTG-GTTCGGGC 181
|||||
QY 486 ArgGlyLeuCysLeuAspLeuAlaLeuLeuAspSerAlaPheLeuLeuSerGlnValAla 505
|||||
Db 182 CGGGGATCTGCTGGACCTCGCATCCCTGGATAGTGCCTTCTGCTGCCAGGTGGCC 241
|||||
QY 506 ProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVal 525
|||||
Db 242 CCATCCCTGTTATGGCTCCATGTCACAGTCAGCCAGCTGTCACCTGCTATATGGTG 301
|||||
QY 526 SerAlaAlaGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLys 545
|||||
Db 302 TCTGCCGACGGCTGGGTGTGGCCATTACTTTTGTACACAGGTAGTATTGACAAG 361
|||||
QY 546 SerAspLeuAlaLysTyrSerAla 553
|||||
Db 362 AGCGACTTGGCCAAATACTCAGCG 385

RESULT 24
BG246497
LOCUS BG246497 844 bp mRNA linear EST 13-FEB-2001
DEFINITION 602360526F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:448895 5',
mRNA sequence.
ACCESSION BG246497
VERSION BG246497.1 GI:12756312
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
```

```
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10336 row: c column: 08
High quality sequence stop: 655.

FEATURES
source
1..844
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image="IMAGE:448895"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 152 a 251 c 262 g 179 t
ORIGIN

Alignment Scores:
Pred. No.: 9,55e-49 Length: 844
Score: 616.00 Matches: 135
Percent Similarity: 86.14% Conservative: 8
Best Local Similarity: 81.33% Mismatches: 20
Query Match: 21.53% Indels: 5
DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BG246497 (1-844)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
|||||
Db 315 ATGATCCAGAGGCTGTGGGCCAGCGCTCTGCTACGCCACGGAAAGCTCAGCTCCTGCTG 374
|||||
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||||
Db 375 GTCAACCTCTCACCCTTGGCTGGAGGTGCTGCTGGCTGCCGGCATTTACCTATGTGCCA 434
|||||
QY 41 ProLeuLeuLeuGlu-ValGlyValGluGlyLysPheMetThrMetValLeuGlyIleG 60
|||||
Db 435 CCCCTTCTCTGGACAGCTCGGGGTGGAGGAGAAATTCATGACCATGCTGTGGGCATTGG 494
|||||
QY 60 yProValLeuGlyLeuVal-CysValProLeuLeuGlySerAlaSerAspHisTrpArgG 80
|||||
Db 495 CCCAGTGTAGGCTGGTCTTCTGTTCCTACTCTAGGCTCAGCCAGTGCAGTGGCGTG 554
|||||
QY 80 LysArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerL 100
|||||
Db 555 GCGCGTATGCGCGCGGAGACCTTTATCTGGGCTTCGCTGGGTGCTGCTCTAAGCC 614
|||||
QY 100 euPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProL 120
|||||
Db 615 TCTTTCTCATCCGAGGGCTGCTGCTGGCTGGCAGGACTGCTGTACCCAGACAGCCGCCCT 674
|||||
QY 120 euGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysP 140
|||||
Db 675 G-GAGTGTGGCCCTGGTGATCTTTGGAAGTGGGCTGGTGGACCTTCGTGGCCAGTGGTGT 733
|||||
QY 140 he-ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGln 159
|||||
Db 734 TTAACCTCCATTGGAGGCCCTTAATCTTCAGACCTTTTCGGGAGCCCAACACTGCCG-CAA 792
|||||
QY 160 AlaTyrSerVal 163
|||||
Db 793 GCGTTCAGGTA 804
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLA11137 row: n column: 24
High quality sequence start: 2
High quality sequence stop: 630.

FEATURES

source

```

1. 000
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone IMAGE:5050583"
/clone lib="NCI CCAB L100"

```

/lab_host="DHL0B (T1 phage-resistant)"
 /notes="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.9 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 180 c 137 t 139 g 137 t

RESULT 27
BG364300
LOCUS
DEFINITION
BG364300 520 bp mRNA linear EST 08-MAR-2001
dab6b09.y1 N1CHD XGC Emb2 Xenopus laevis cDNA clone IMAGE:4404424
5' similar to TR:O9VSV1 O9VSV1 CG4484 PROTEIN.: mRNA sequence.

ACCESSION	BG364300	
VERSION	BG364300.1	GI:13253397
KEYWORDS	EST	
SOURCE	African clawed frog.	
ORGANISM	Xenopus laevis	
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus	

REFERENCE
AUTHORS

Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R. |
WASHU Xenopus EST project, 1999
Unpublished (1999)

COMMENT	COUNT
---------	-------

CONTENT

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Library constructed by Life Technologies. DNA Sequencing by:
Washington University Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 435.

TITLE
JOURNAL
COMMENT

WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyT not found
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 348.

FEATURES

source

1. 348
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1629790"
/sex="male"
/tissue_type="schizophrenic brain S-11 frontal lobe"
/dev_stage="34 years old"
/lab_host="SOLR (kanamycin resistant)"
/note="Vector: Bluescript SK-; Site_1: EcoRI; Library
constructed from S-11 frontal lobe, male, 34 years old,
50% caucasian, 50% Aleutian. Schizophrenic suicide.
Random primed into EcoRI site of ZAP II Vector. Mass
excised. Custom library. Avg insert length 1.4kb.
Material obtained by Johnston N., Torrey, E.F., Yolken R.,
and the Stanley Neuropathology Consortium; Analysis of
RNAs from the Brains of Individuals with Psychiatric
Diseases (Unpublished) Stanley Neurovirology Laboratory,
Johns Hopkins School of Medicine, Baltimore MD."

BASE COUNT 78 a 99 c 118 g 53 t

ORIGIN

Alignment Scores:

Pred. No.: 3,81e-42 Length: 348
Score: 541.00 Matches: 113
Percent Similarity: 97.41% Conservative: 0
Best Local Similarity: 97.41% Mismatches: 3
Query Match: 18.91% Indels: 1
DB: 9 Gaps: 0

US-09-593-793A-113 (1-553) x AA984323 (1-348)

QY 326 LeuCluLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeu 345
|||||
Db 348 CTGGGGCTGTTCCTGCAGTCGCCATCTCCCTGGTCTTCTCTGTGTCATGGACCGGCTG 289
QY 346 ValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAla 365
|||||
Db 288 GTCCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGCACGCTTTCCTGTGGCT 229
QY 366 AlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuThr 385
|||||
Db 228 GCCGGTGCCACATGCTGCCACAGTGTGGCGTGGTGACAGCTTCAGCCGACCTCACC 169
QY 386 GlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArg 405
Db 168 GGGTTACCTTCACGCCCTTCAGAGATCCCTGCCCTACACACTGGCCCTCCCTCTACCAACCG 109
QY 406 GLuLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAsp 425
Db 108 GAGACAGAGTGTCTCTGCCCAANTACCGAGGGGACACTGGAGGTGCTGGCAGTGGAGAC 49
QY 426 SerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
Db 48 AGCCTGATGACCAAGCTTCCTGCA-GGCCCTAAGCCTGGAGCTCCCTTC 2

RESULT 30

BQ950805

LOCUS

959 bp

mRNA

linear

EST 21-AUG-2002

DEFINITION

AGENCOURT_8842232 Lupski_sciatic_nerve Homo sapiens cDNA clone

IMAGE:6204253 5', mRNA sequence.

ACCESSION

BQ950805

VERSION

BQ950805.1 GI:22366283

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 959)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

Tissue procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM13625 row: d column: 14

High quality sequence start: 2

High quality sequence stop: 490.

FEATURES

Location/Qualifiers

1. 959

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6204253"

/clone_lib="Lupski_sciatic_nerve"

/sex="male"

/tissue_type="sciatic nerve"

/dev_stage="adult, 70 yr"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:

NotI; Site_2: SalI; cDNA made by oligo-dT priming.

Directionally cloned using the following adaptors:

5'-TCGACCCAGCGTCGCG-3' and

5'-GACTAGTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >

1 kb for average insert length 1.87 kb. This is a primary

library, non-amplified. Library constructed by Life

Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor

College of Medicine) and is available through Life

Technologies."

BASE COUNT 139 a 312 c 308 g 200 t

ORIGIN

Alignment Scores:

Pred. No.: 1.15e-40 Length: 959

Score: 533.00 Matches: 108

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 18.63% Indels: 0

DB: 14 Gaps: 0

US-09-593-793A-113 (1-553) x BQ950805 (1-959)

QY 446 ValGlyAlaGlyCysLeuValValGlyGluProProAlaLeuCysGlyAlaSerAla 465
|||||
Db 8 GTGGGTGCTGGAGGAGTGGCTTGCCTCCACCTCCACCGCGCTCTGCGGGCTCTGCC 67
QY 466 CysAspValSerValArgValValGlyGluProThrGluAlaArgValValProGly 485
|||||
Db 68 TGTGATGTCCTCCGTAGCTGTGGTGGGTGAGCCACCGAGGCGGTGTTCCGGGC 127
QY 486 ArgGlyLeuValValGlyValValGlyValValGlyValValGlyValValGlyValVal 505
Db 128 CGGGGCACTGCTGGACCTCGCATCTGGATAGTCTCTCTGCTGTCCAGGTGGCC 187
QY 506 ProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVal 525
Db 188 CCATCCCTGTTTATGGGCTCCATGTGCCAGCTCAGCCAGTCTGCTACTATATGGTG 247

```

QY 526 SerAlaAlaGlyLeuGlyValAlaLaiIleTyrPheAlaThrGlnValValPheAspLys 545
|||||
Db 248 TCTGCGCAGGCGCTGGTCTGGTCCCATTTACTTTGCTACACAGTAGTATTGCACAG 307

QY 546 SerAspLeuAlaLysTyrSerAla 553
|||||
Db 308 AGCGACTTGGCCAAATACTACGCG 331

RESULT 31
BG828841 602752813F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4905674 5',
LOCUS mRNA sequence. linear EST 22-MAY-2001
DEFINITION BG828841
ACCESSION BG828841
VERSION BG828841.1 GI:14176428
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1035)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1807 row: i column: 03
High quality sequence start: 3
High quality sequence stop: 602.
Location/Qualifiers
1..1035
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4905674"
/clone_lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: muscle; Vector: pOT87; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

BASE COUNT 227 a 273 c 341 g 194 t
ORIGIN

Alignment Scores:
Pred. No.: 1 33e-39 Length: 1035
Score: 522.50 Matches: 127
Percent Similarity: 77.71% Conservative: 9
Best Local Similarity: 72.57% Mismatches: 20
Query Match: 18.26% Indels: 20
DB: 12 Gaps: 7

US-09-593-793A-113 (1-553) x BG828841 (1-1035)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20
|||||
Db 279 ATGGTCCAGAGCGCTGGGTGAGCGCGCTGCTGGCGCACCGAAGCCAGCTCTTGCTG 338

QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
|||||
Db 339 GTCAACCTGCTAACCTTTGGCGCTGGAGGTGTGTTTGGCGCGCAGGCATCACCTATGTGCG 398

QY 41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60
|||||
Db 399 CTTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGGTGGTGGCATGGT 458

QY 61 ProValLeuGlyLeuValCysValPro-LeuLeuGlySer-AlaSerAspHisIleTrpArgG 80
|||||
Db 459 CCAGTCTGGGCGCTGGTCTGTCTGCCGCTATAGGCTCACGCCAGTACCATCTGGCGTG 518

QY 80 LysArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuLeuLeu 98
|||||
Db 519 GACGCTATGGCGCGCGCGCCCTTCATCTGGAGCACTGTCTTGAGGCATCTCGACTT 578

QY 99 --SerLeuPheLeuLeuProArgAla-GlyTrpLeu--AlaGlyLeuLeuCysPro-As 116
|||||
Db 579 GAGCATCTTCTTCATCCCAAGCGCGGCTGGCTAGACAAGGAGTGTCTGTGCCAGGA 638

QY 116 pProArgProLeuGluLeuAlaLeuLeuLeuGlyVal---GlyLeuLeuAspPheCys 135
|||||
Db 639 TACCAGGACCCCTGGAGCTGGA-CTGCTCATCATGGGAGTGGGAGTGTCTGGAACCTCTG 697

QY 135 sGly-----GlnValCysPheThrProLeuGluAlaLeuSerAspLeu----- 150
|||||
Db 698 TGGGGCCAAAGGAGTGTGTCATTCAATCCAAACATGGG-----AGGACCTGGGATCCTC 751

QY 151 -----PheArgAspProAspHis---CysArg 158
|||||
Db 752 TGAACATACACTTCCGGGACCGGACGACACATGTAGG 788

RESULT 32
BF854825/c 322 bp mRNA linear EST 16-JAN-2001
LOCUS RC6-FN0202-271000-011-A03 FN0202 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF854825
ACCESSION BF854825
VERSION BF854825.1 GI:12242569
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 322)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel.: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&t2=RC6-FN0202-
271000-011-A03&t3=2000-10-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 321.
Location/Qualifiers
1..322
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0202"
/dev_stage="Adult"
/notes="Organ: prostate_normal; Vector: puc18; Site_1: SmaI
source
```



```
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue procurement: Gilbert Smith, Ph.D.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM9143 row: c column: 19
          High quality sequence stop: 564.
          Location/Qualifiers
            1..1037
              /organism="Mus musculus"
              /strain="FVB/N"
              /db_xref="taxon:10090"
              /clone="IMAGE:3967818"
              /tissue_type="tumor, biopsy sample"
              /dev_stage="10 months, virgin"
              /lab_host="DH10B"
              /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
              Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
              Library constructed by Life Technologies. Investigator
              providing samples: Gilbert Smith, NIH"
BASE COUNT 202 a 289 c 310 g 234 t 2 others
ORIGIN
Alignment Scores:
Pred. No.: 3,13e-36 Length: 1037
Score: 487.50 Matches: 124
Percent Similarity: 79.65% Conservative: 13
Best Local Similarity: 72.09% Mismatches: 28
Query Match: 17.04% Indels: 10
DB: 12 Gaps: 3

US-09-593-793A-113 (1-553) x BE914848 (1-1037)
QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20
Db ATGATCCAGAGGCTGTGGCCAGCGCTGTGCTACGGCACCGGAAAGCTCAGCTCTGCTG 318
QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTrpValPro 40
Db GTCAACCTGCTCACCTTTGGCTGTGAGGTGTGCTGGTGGCGGATACCTATGTGCCA 378
QY 41 ProLeuLeuGluValGlyValGluGluTysPheMetThrMetValLeuGlyIleGly 60
Db CCCCTTCTGCTGGAAGTCGGGCTGGAGGAGAACTTCATGACCATGGTGTGGCATTTGGC 438
QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis-TrpArgL 80
Db CCAGTGCTAGGCGCTGTTCTCTCCACCTCCCTAGGCTCAGNACAGTGACCATGTGGCGTG 498
QY 80 YArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu-LeuSerL 100
Db GGCCTATGGCTG-CGGAGACCTTT-ATCTGGGCTTTGTCCCTGGGTGTCTCTCTTAAGCC 556
QY 100 euPheLeu---TleProArgAlaGlyTrp-LeuAlaGlyLeuLeuCysProAsp-ProAr 118
Db TCTTTTCTCATTCGCGAAGGGCTGGCTGGCTGGCGGAGCTGGTGTCCAGAAACCAAG 616
QY 118 gProLeuGluLeuAlaLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyGlnVa 138
Db GCCCTGGGAGTGGGCGGCTGGTGGATGGGTCATGGGCTGGCTGGC-TTCTGTGTGCCCGGT 675
QY 138 lCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysAr 158
Db TCTTTTCTCATTCGCGAAGGGCTGGCTGGCTGGCGGAGCTGGTGTCCAGAAACCAAG 616
QY 158 gGlnAlaTyrSerValTrpAlaPheMet 167
Db TCTTTTCTCATTCGCGAAGGGCTGGCTGGCTGGCGGAGCTGGTGTCCAGAAACCAAG 616
```

```
Db 733 CCGC-----TTTCTCTTGTTCGGCCTTATG 757
RESULT 35
LOCUS BG964810
DEFINITION BG964810.1 GI:14352447
ACCESSION BG964810
VERSION BG964810.1
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10589 row: p column: 16
High quality sequence stop: 563.
Location/Qualifiers
  1..564
    /organism="Mus musculus"
    /strain="FVB/N"
    /db_xref="taxon:10090"
    /clone="IMAGE:4984191"
    /clone_lib="NCI_CGAP_Co24"
    /lab_host="DH10B (T1 phage-resistant)"
    /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
    Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
    Average insert size 1.6 kb. Constructed by Life
    Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 95 a 156 c 168 g 143 t 2 others
ORIGIN
Alignment Scores:
Pred. No.: 2,04e-36 Length: 564
Score: 485.00 Matches: 101
Percent Similarity: 94.59% Conservative: 4
Best Local Similarity: 90.99% Mismatches: 6
Query Match: 16.95% Indels: 1
DB: 13 Gaps: 0

US-09-593-793A-113 (1-553) x BG964810 (1-564)
QY 442 ProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCys 461
Db 1 CCCATGGACACGTGGGCTCTGGCAGCAGCGCATCTGGCCCTCCACCTGCACCTCTGT 60
QY 462 GlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAlaArg 481
Db 61 GGGGCTCTGCTGCGCATGCTCTCCATGCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
QY 482 ValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501
Db 121 TT-GTTACGGGACGGGCGCATTTGCCCTGGACCTGGCCATTTCTGGACAGTGCCTTCTGCTG 179
QY 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521
Db 180 TCCAGGTGGCTCCGTCCTCTGTTTCATGGGCTCCATTTGTCAGTGAGCCACTCTGTCACT 239
QY 522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 541
Db 240 GCCTATATGATCAGCTCAGGCTGGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 299
```


10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

FEATURES

source

Location/Qualifiers
1..317
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="7420496101"
/clone_lib="RIKEN full-length enriched, in vitro
fertilized eggs"
/sex="female"
/tissue_type="in vitro fertilized eggs"
/dev_stage="egg"
/lab_host="DH10B"
/note="Site_1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
prepared by using trihalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGATTCGAGTTAAATTAATTAATTCCTCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pluciscript KS(+) after bulk excision from Lambda
FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI"
BASE COUNT 53 a 108 c 91 g 65 t
ORIGIN

Alignment Scores:
Pred. No.: 6.24e-34 Length: 317
Score: 455.00 Matches: 90
Percent Similarity: 90.38% Conservative: 4
Best Local Similarity: 86.54% Mismatches: 9
Query Match: 15.90% Indels: 1
DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x BB707065 (1-317)

QY 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
|||||
Db 3 TCAGCTGCCCTCACCAGGTTACCTCTCGGCTTGCAGATCCTCGCTTACAGCTCGCC 62
QY 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
|||||
Db 63 TCCCTCTACCACCGTGAGAGAGAGGTTTCTTGCCTCCCAATACCGAGGGGACCTGGAGTT 122
QY 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
|||||
Db 123 AGCAGCGGTGAGGAGCAGCAGACACACAGCTTCTTCCAGGCGCCCTAAGCCAGGAGCTCTC 182
QY 441 PheProAsnGlyHisValGlyLysGlySerGlyLeuLeuProProProAlaLeu 460
|||||
Db 183 TTCCCCAATGGACAGTGGGCTCTGGCAGCAGCGCATCTCTGGCCCCCTCCACTGCATC 242
QY 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGlu-Al 480
|||||
Db 243 TGTGGGGCTCTGCTCGCATGCTCTCCATGCGAGTGGTGGTGAACCACTGAGGGC 302
QY 480 aArgValVal 483
|||||
Db 303 CAGGGTTGTT 312

RESULT 38
AW787124

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..537

/organism="Sus scrofa"

/db_xref="taxon:9823"

/clone_lib="MARC lPIG"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: Sall;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."

BASE COUNT 96 a 161 c 186 g 94 t

ORIGIN

Alignment Scores:

Pred. No.: 7.88e-32 Length: 537

Score: 437.00 Matches: 85

Percent Similarity: 98.85% Conservative: 1

Best Local Similarity: 97.70% Mismatches: 1

Query Match: 15.27% Indels: 0

DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x AW787124 (1-537)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20

|||||

Db 276 ATGGTCCAGAGACTTGGATGAGCCCTGCTGCGGCATCGGAAAGCCAGCTCTCTG 335

QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40

|||||

Db 336 GTTACCTGCTGACGTTCCGCTGGAGGTGCTGCTGGCGCAGGATCATCTACGTGCA 395

QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60

|||||

Db 396 CCCCTGCTGTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGGTGTGGCATCGGT 455

QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80

|||||

Db 456 CCAGTGTGGGCTGTCTCCCTCCACTCTCTAGGCTAGGCTAGGCTAGGCTAGGCTAGG 515

QY 81 ArgTyrGlyArgArgPro 87

AW787124 537 bp mRNA linear EST 09-JUL-2000
120845 MARC lPIG Sus scrofa cDNA 5', mRNA sequence.

AW787124

AW787124.1 GI:7843900

EST.

pig.

Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 537)

Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,

Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.

and Keele,J.W.

Design and use of two pooled tissue normalized cDNA libraries for

EST discovery in swine

Unpublished (2000)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18

and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTCACGCG

Plate: 45 row: C column: 12

Seq primer: ATTTAGCTGACACTATAG.

Location/Qualifiers

1..537

/organism="Sus scrofa"

/db_xref="taxon:9823"

/clone_lib="MARC lPIG"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: Sall;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."

BASE COUNT 96 a 161 c 186 g 94 t

ORIGIN

Alignment Scores:

Pred. No.: 7.88e-32 Length: 537

Score: 437.00 Matches: 85

Percent Similarity: 98.85% Conservative: 1

Best Local Similarity: 97.70% Mismatches: 1

Query Match: 15.27% Indels: 0

DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x AW787124 (1-537)

QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20

|||||

Db 276 ATGGTCCAGAGACTTGGATGAGCCCTGCTGCGGCATCGGAAAGCCAGCTCTCTG 335

QY 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40

|||||

Db 336 GTTACCTGCTGACGTTCCGCTGGAGGTGCTGCTGGCGCAGGATCATCTACGTGCA 395

QY 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60

|||||

Db 396 CCCCTGCTGTGGAAGTGGGGGTAGAGGAGAAGTTTCATGACCATGGTGTGGCATCGGT 455

QY 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80

|||||

Db 456 CCAGTGTGGGCTGTCTCCCTCCACTCTCTAGGCTAGGCTAGGCTAGGCTAGGCTAGG 515

QY 81 ArgTyrGlyArgArgPro 87

```

Db 516 CGCTATGGTCCGGAGGCC 536
|||||
RESULT 39
BG745565
LOCUS BG745565 717 bp mRNA linear EST 15-MAY-2001
DEFINITION 602723976F1 NTH_MGC_113 Homo sapiens cDNA clone IMAGE:4850347 5',
mRNA sequence.
ACCESSION BG745565
VERSION BG745565.1 GI:14056218
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 717)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium {LLNL}
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1691 row: 9 column: 20
High quality sequence start: 8
High quality sequence stop: 580.
Location/Qualifiers
FEATURES
source
1..717
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4850347"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; site 1: XhoI; site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 113 a 211 c 209 g 184 t
ORIGIN
|||||
us-09-593-793a-113 (1-553) x BG745565 (1-717)
Pred. No.: 9,46e-30 Length: 717
Score: 417.50 Matches: 122
Percent Similarity: 83.78% Conservatives: 2
Best Local Similarity: 82.43% Mismatches: 9
Query Match: 14.59% Indels: 15
DB: 12 Gaps: 1

Db 418 ThrGlyGlyAlaSerSerGluAspSerLeu-MetThr-SerPheLeuPro-GlyProLys 436
|||||
Db 2 ACTGCAGGTGCTATCAGTGAGGACAGCTGGATGACCAAGCTTCCTGCCATGCCCTAAG 61
|||||
QY 437 ProGlyAlaProPheProAlaGlyHisValGlyAlaGlySerGlyLeuLeuProPro 456
|||||
Db 62 CTTGGAGCTCCCTTCCTTAATGACACGCTGGGTGCTGGAGGAGGCTGCTGCCACCT 121
|||||
QY 457 ProProAlaLeuCysGlyAlaSerAlaCys-AspValSerValArgValValGlyG1 476
|||||
Db 122 CCACCCGCGCTCGCGGGCCCTGCTGCTGTGATGCTCCGTACGTCGTGGTGGTGA 181
|||||
QY 476 uProThrGluAlaArgValValProGlyArgGlyIleCys-LeuAsp-LeuAlaIleLeu 495
|||||

```

```

Db 182 GCCACCGAGGTCCAGGTGCTCCGGCGCGGCATCTGCTCTGGATCTCTGCCATCCTG 241
QY 496 -AspSerAlaPheLeuLeuSer-GlnValAlaPro-SerLeuPheMetGlySerIleVal 514
|||||
Db 242 TGATAGTGCCTTCTGCTGCTCCAGGTGCCCGCATCTGTTTATGGCTCCATGTA 301
|||||
QY 515 -GlnLeuSerGln-SerValThrAlaTyMetValSerAlaAla-GlyLeuGlyLeuVal 533
|||||
Db 302 CCAGCTCAGCCAGTACTGCTCACTGCTATATGCTGCTGCCGCGATCCCTGGCTGCTC 361
|||||
QY 534 Ala---IleTyPheAlaThrGlnValVal-PheAspLys-SerAspLeuAlaLys 550
|||||
Db 362 GGCATATTAACTTGTCTACACAGGTAGTATTTCGACAAATGAGCGACTTGGCCAAA 417
|||||
RESULT 40
BF371417/c
LOCUS BF371417 265 bp mRNA linear EST 24-NOV-2000
DEFINITION RCO-FN0140-040800-023-h03 FN0140 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF371417
VERSION BF371417.1 GI:113333442
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 265)
Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC0&st2=RC0-FN0140-
040800-023-h03&st3=2000-08-04&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 265.
Location/Qualifiers
FEATURES
source
1..265
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0140"
/dev_stage="Adult"
/note="Organ: prostate normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT 68 a 72 c 94 g 31 t
ORIGIN
|||||
Alignment Scores:
Pred. No.: 2,38e-30 Length: 265
Score: 416.50 Matches: 83
Percent Similarity: 96.53% Conservatives: 1
Best Local Similarity: 95.40% Mismatches: 3
Query Match: 14.56% Indels: 2

```

DB: 12 Gaps: 0

US-09-593-793A-113 (1-553) x BF371417 (1-265)

Qy 122 LeuAlaLeuLeuLeuLeuGlyValGlyLeuLeuAspPheCysGlyClnValCysPheThr 141

Db 261 GTGGTGTCTCATCTGGGCGTGGGCGTGTGGAGACTTCTGTGGCAGGTGTGCTACT 202

Qy 142 ProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspPheCysArgGlnAlaTyr 161

Db 201 CCACAGAGCCCTGCTCTGTGACCTCTCCGGGACCGGACCACTGTGCGGACGCTAC 142

Qy 162 SerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIle 181

Db 141 TCTGTCTATGCTTCATGATCAGTCTGGGGGCTGCTGGGTACCTCTGCTGCCATT 82

Qy 182 AspTyrAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnClnCysLeuPheGly 201

Db 81 GACTGGAC-ACCAGTGC-CTGGGCCCTTACCTGGGACCCAGGAGGTGCTCTTTGGC 24

Qy 202 LeuLeuThrLeuIlePheLeu 208

Db 23 CTGCTCACCTCATCTTCCTA 3

RESULT 41

AW822644

LOCUS

DEFINITION

uq13g05.y1 Ren Stubbs mouse thymus Mus musculus cDNA clone

IMAGE:2802392 5', mRNA sequence.

ACCESSION

AW822644

VERSION

AW822644.1 GI:7915661

KEYWORDS

EST.

SOURCE

house musculus.

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 523)

AUTHORS

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

TITLE

The WashU-NCI Mouse EST Project 1999

JOURNAL

Unpublished (1999)

COMMENT

Other_ESTs: uq13g05.x1

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LNL : contact the IMAGE Consortium (info@image.lnl.gov) for further information.

MGI:1041916

Seq primer: Primer name ambiguous

High quality sequence scop: 474.

Location/Qualifiers

1..523

/organism="Mus musculus"

/strain="C3H"

/db_xref="taxon:10090"

/clone_image="IMAGE:2802392"

/clone_lib="Ren Stubbs mouse thymus"

/sex="mixed"

/dev_stage="3 weeks"

/lab_host="DH10B"

/note="Organ: thymus; Vector: pT7T3D-Pac; Site_1: NotI; Site_2: PacI; 1st strand cDNA was primed with an oligo(dT) primer; double-stranded cDNA was ligated using 5' linker gggccgcat and 3' linker aactggaagcttaatt. Library is size-selected >2.5 kb and average insert size is 3.5 kb. Clones were arrayed from primary plating; non-amplified. Library constructed by X. Ren and L. Stubbs (Lawrence

source

Alignment Scores:

Pred. No.: 9.1e-29 Length: 523

Score: 405.00 Matches: 79

Percent Similarity: 96.39% Conservative: 1

Best Local Similarity: 95.18% Mismatches: 3

Query Match: 14.16% Indels: 0

DB: 10 Gaps: 0

US-09-593-793A-113 (1-553) x AW822644 (1-523)

Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20

Db 273 ATGATCAGAGGCTGTGGCCAGCCGCTGTGCTACGCGCAGGAAAGCTGCTGCTG 332

Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaGlyIleThrTyrValPro 40

Db 333 GTCAACCTGCTCACCTTTGGCTTGGAGGTGTGCTGGCTGCCGCAATACCTATGTGCCA 392

Qy 41 ProLeuLeuLeuValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60

Db 393 CCCCTTCTGCTGGAAGCTGGGGTGGAGGAAATTCATGACCATGGTGTGGGCATTGGC 452

Qy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTyrArgGly 80

Db 453 CCAGTGTAGGCTGGTCTTCTGTTCACCTCCTAGGCTCAGCCAGTGACGAGTGGCGTGG 512

Qy 81 ArgTyrGly 83

Db 513 CGCTATGGC 521

RESULT 42

CNS050VL

LOCUS

DEFINITION

Tetraodon nigroviridis genome survey sequence T7 end of clone 006H14 of library C from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION

AL347178

VERSION

AL347178.1 GI:8240948

KEYWORDS

GSS; genome survey sequence.

SOURCE

Tetraodon nigroviridis

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

REFERENCE

1 (bases 1 to 1020)

AUTHORS

Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

TITLE

Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 1020)

AUTHORS

Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

TITLE

Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL

Unpublished

REFERENCE

3 (bases 1 to 1020)

AUTHORS

Genoscope.

TITLE

Direct Submission

JOURNAL

Submitted (12-APR-2000)

COMMENT

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

Location/Qualifiers


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Db 670 TGTGCTGATCCAGGGCCCTGGGAGGTAGACTTGCTCA-----ATCCTGGGTTGGG 723
Qy 130 yLeuLeuaspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLe 150
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 724 GCTGTGCATTCTTGTGGGCCAGGTTTC-GTCCCTTCCCTGGAGGCTGCTCTGGC---CT 779
Qy 150 pPheArgaspPro 154
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AA112574
LOCUS
DEFINITION
  zm28c12.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone
  IMAGE:526966 3', mRNA sequence.
ACCESSION
  AA112574
VERSION
  AA112574.1 GI:1665121
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
REFERENCE
  Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
  Chissoe, S., Dietrich, N., DuBuque, T., Favell, A., Gish, W., Hawkins
  , M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
  , B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
  Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E.,
  Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
  Generation and analysis of 280,000 human expressed sequence tags
  Genome Res. 6 (9), 807-828 (1996)
  97044478
  Contact: Wilson RK
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  WARNING: There is evidence that suggests that the 384-well parent
  plate of this clone contains both human and mouse derived clones.
  Thus, the origin of this clone is uncertain. This caution should be
  kept in mind should you use this clone.
  This clone is available royalty-free through LLNL ; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  Seq primer: -40M13 fwd from Amersham.
  Location/Qualifiers
  FEATURES
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        CTCAGATTTTCTTTTCTTTTCTTTT 3'"
BASE COUNT 40 a 81 c 62 g 45 t
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Alignment Scores:
Pred. No.: 2,51e-27 Length: 228
Score: 384.00 Matches: 76
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.42% Indels: 0
DB: 9 Gaps: 0
US-09-593-793A-113 (1-553) x AA112574 (1-228)

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Qy 361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
Db 1 GCTTTCCCTGTGGTGGCGGTGCCACATGCTGTCCACAGTGTGCCCGTGTGACAGCT 60
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Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 TCAGCGCCCTCACCGGGTTTCACTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 TCCCTCTACCCAGCGAGAGCAGGTGTCTCTGCCCAATACCGAGGGGACACTGGAGT 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
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RESULT 45
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LOCUS
DEFINITION
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ACCESSION
  BF854834
VERSION
  BF854834.1 GI:12242578
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
REFERENCE
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  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 428)
  Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
  Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
  Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
  Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
  , M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
  Simpson, A.J.
  Shotgun sequencing of the human transcriptome with ORF expressed
  sequence tags
  Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  20202663
  Contact: Simpson A.J.G.
  Laboratory of Cancer Genetics
  Ludwig Institute for Cancer Research
  Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
  Brazil
  Tel: +55-11-2704922
  Fax: +55-11-2707001
  Email: asimpson@ludwig.org.br
  This sequence was derived from the FAPESP/LICR Human Cancer Genome
  Project. This entry can be seen in the following URL
  (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC6&t2=RC6-FN0202-
  271000-011-E04&t3=2000-10-27&t4=1)
  Seq primer: puc 18 forward
  High quality sequence start: 20
  High quality sequence stop: 423.
  Location/Qualifiers
  FEATURES
    source
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        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone_lib="FN0202"
        /dev_stage="Adult"
        /note="Organ: prostate_normal; Vector: puc18; Site:1: SmaI
        ; Site:2: SmaI; A mini-library was made by cloning
        products derived from ORESTES PCR (U.S. Letters Patent
        application No. 196,716 - Ludwig Institute for Cancer
        Research) profiles into the puc 18 vector. Reverse
        transcription of tissue mRNA and cDNA amplification were
        performed under low stringency conditions."
BASE COUNT 111 a 111 c 137 g 68 t
ORIGIN
Alignment Scores:
Pred. No.: 1.21e-26 Length: 428
Score: 381.50 Matches: 76
Percent Similarity: 77.57% Conservative: 7

```

Best Local Similarity: 71.03% Mismatches: 11
Query Match: 13.33% Indels: 13
DB: 12 Gaps: 1

US-09-593-793A-113 (1-553) x BF854834 (1-428)

```
QY 22 AsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValProPro 41
   ::::: ||| :::: ||::: :::::
Db 287 AGCTTGGTCCCTTCCCTTGGCCCTTACTTGCCAGCCATTGACTCATACTACTTCC 228
   ::::: ||| :::: ||::: :::::
QY 42 LeuLeuLeuGluValGlyValGluLysPheMetThrMetValLeuGlyIleGlyPro 61
   |||||
Db 227 CTCTTT-----GCAGGCATTGCTCCA 207

QY 62 ValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArg 81
   |||||
Db 206 GTGCTGGGCTGTCTGTCTCCGCTCCAGGCTCAGCCAGTGCACCTGGCGTGGACGC 147
   |||||
QY 82 TyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPhe 101
   |||||
Db 146 TATGGCCGCCGCCCTTCATCTGGGCACCTGCTGGGCATCCTGCTGAGCCTCTTT 87
   |||||
QY 102 LeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuGlu 121
   |||||
Db 86 CTCCTCCCAAGGCCGCGCTGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCCTGGAG 27
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QY 122 LeuAlaLeuLeuIleLeuGly 128
   |||||
Db 26 CTGGCACCTGCTCATCTCTGGGC 6
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